

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 37.6727 Seconds
(without alignments)
71.864 Million cell updates/sec

Title: US-10-691-157-1

Perfect score: 42

Sequence: 1 MQPPPLP 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	7	4 AAB72500	Aab72500 Colostrin
2	42	100.0	7	4 AAB59324	Aab59324 Ewe colos
3	42	100.0	7	4 AAB72246	Aab72246 Colostrin
4	42	100.0	7	4 AAB72532	Aab72532 Colostrin
5	42	100.0	7	5 AAO14577	Aao14577 Neural ce
6	42	100.0	7	5 AAM51036	Aam51036 Colostrin
7	42	100.0	7	5 AAE20228	Aae20228 Colostrin
8	42	100.0	7	8 ADN60295	Adn60295 Constitue
9	42	100.0	7	8 ADS74400	Ads74400 Ovine col
10	42	100.0	8	4 AAB59354	Aab59354 Ewe colos
11	39	92.9	9	8 ADK10336	Adk10336 Human pap
12	39	92.9	10	8 ADK10337	Adk10337 Human pap
13	39	92.9	10	8 ADK10338	Adk10338 Human pap
14	37	88.1	8	8 ADK10335	Adk10335 Human pap
15	36	85.7	12	7 ADC36090	Adc36090 Chemokine
16	36	85.7	12	8 ADR42838	Adr42838 Modulator
17	34	81.0	12	6 AAE32821	Aae32821 Human CEA
18	34	81.0	15	3 AAY8491	Aay8491 Human ced
19	34	81.0	16	3 AAY85494	Aay85494 Human ced
20	33	78.6	7	4 AAM46973	Aam46973 H11 bindi
21	33	78.6	10	2 AAW06853	Aaw06853 Peptide b
22	33	78.6	11	3 AAB21127	Aab21127 Src homol
23	33	78.6	12	2 AAW06845	Aaw06845 Peptide b
24	33	78.6	13	2 AAW38072	Aaw38072 PPPPY mot
25	33	78.6	13	7 ADB49333	Adb49333 Biotinyla

26	32	76.2	6	2 AAR91753	Aar91753 Prolyl en
27	32	76.2	7	2 AAR60997	Aar60997 Fragment
28	32	76.2	7	2 AAR91752	Aar91752 Prolyl en
29	32	76.2	7	4 AAM46827	Aam46827 H11 bindi
30	32	76.2	7	4 AAM46861	Aam46861 H11 bindi
31	32	76.2	7	4 AAM46876	Aam46876 H11 bindi
32	32	76.2	7	4 AAM47027	Aam47027 H11 bindi
33	32	76.2	7	4 AAM46856	Aam46856 H11 bindi
34	32	76.2	7	4 AAM46871	Aam46871 H11 bindi
35	32	76.2	7	4 AAM46851	Aam46851 H11 bindi
36	32	76.2	7	4 AAM46866	Aam46866 H11 bindi
37	32	76.2	8	2 AAR71945	Aar71945 Human 3BP
38	32	76.2	9	7 AAW01573	Aaw01573 Mouse Fnn
39	32	76.2	10	2 AAR77371	Aar77371 SH3 bindi
40	32	76.2	10	2 AAW06861	Aaw06861 Peptide b
41	32	76.2	10	2 AAW38097	Aaw38097 PPPPY mot
42	32	76.2	10	2 AAW38074	Aaw38074 PPPPY mot
43	32	76.2	10	4 AAB86131	Aab86131 Prolin-e-r
44	32	76.2	10	4 AAB86149	Aab86149 Prolin-e-r
45	32	76.2	10	4 AAB70933	Aab70933 Polyoma v
46	32	76.2	10	7 ADB49372	Adb49372 Biotinyla
47	32	76.2	10	7 ADB49335	Adb49335 Biotinyla
48	32	76.2	11	3 AAB21129	Aab21129 Src homol
49	32	76.2	11	3 AAB21132	Aab21132 Src homol
50	32	76.2	11	3 AAB21126	Aab21126 Src homol
51	32	76.2	11	5 ABB99165	Abb99165 Formin-2
52	32	76.2	11	5 ABB99166	Abb99166 Formin-2
53	32	76.2	11	7 AAW01570	Aaw01570 Mouse Fnn
54	32	76.2	11	7 AAW01571	Aaw01571 Mouse Fnn
55	32	76.2	12	2 AAW03154	Aaw03154 Potential
56	32	76.2	12	2 AAW05101	Aaw05101 Prolin-e-r
57	32	76.2	12	2 AAW25457	Aaw25457 SH3 domai
58	32	76.2	12	3 AAB18002	Aab18002 FC-TNF al
59	32	76.2	12	6 ADA50131	Ada50131 Mad2 bind
60	32	76.2	13	2 AAR84641	Aar84641 Grb2-SOS
61	32	76.2	13	4 AAB70928	Aab70928 Polyoma v
62	32	76.2	13	6 ABU10225	Abu10225 Human cyt
63	32	76.2	13	7 AAE39883	Aae39883 Human cyt
64	32	76.2	13	8 ADQ48407	Adq48407 Cytochrom
65	32	76.2	14	2 AAW05490	Aaw05490 SH3-bindi
66	32	76.2	14	2 AAW38067	Aaw38067 PPPPY mot
67	32	76.2	14	7 ADB49257	Adb49257 Biotinyla
68	32	76.2	15	2 AAW39034	Aaw39034 Peptide r
69	32	76.2	15	2 AAW39005	Aaw39005 Peptide r
70	32	76.2	15	2 AAW39050	Aaw39050 Peptide r
71	32	76.2	15	2 AAW38988	Aaw38988 Peptide r
72	32	76.2	15	2 AAW39035	Aaw39035 Peptide r
73	32	76.2	15	2 AAW38959	Aaw38959 Peptide r
74	32	76.2	15	2 AAW39015	Aaw39015 Peptide r
75	32	76.2	15	2 AAW39040	Aaw39040 Peptide r
76	32	76.2	15	2 AAY41635	Aay41635 Mammalian
77	32	76.2	16	2 AAW25411	Aaw25411 Crk N-ter
78	32	76.2	17	2 AAW38977	Aaw38977 Peptide r
79	32	76.2	17	2 AAW38963	Aaw38963 Peptide r
80	32	76.2	18	2 AAR91750	Aar91750 Prolyl en
81	32	76.2	18	2 AAR91746	Aar91746 Prolyl en
82	32	76.2	18	2 AAW38923	Aaw38923 Peptide r
83	32	76.2	18	2 AAW39010	Aaw39010 Peptide r
84	31	73.8	12	3 AAY56628	Aay56628 Virus-lik
85	31	73.8	12	3 AAY56271	Aay56271 Human cat
86	31	73.8	13	2 AAW05447	Aaw05447 SH3-bindi
87	31	73.8	13	2 AAW37655	Aaw37655 PPPPY mot
88	31	73.8	13	7 ADB49202	Adb49202 Biotinyla
89	31	73.8	13	7 ADB49281	Adb49281 Novel WW
90	31	73.8	14	3 ADC16813	Adc16813 Human sin
91	31	73.8	15	2 AAW38905	Aaw38905 Peptide r
92	31	73.8	16	2 AAW38947	Aaw38947 Peptide r
93	31	73.8	17	2 AAW38104	Aaw38104 Peptide r
94	31	73.8	17	7 ADB49204	Adb49204 Biotinyla
95	30	71.4	7	4 AAM47005	Aam47005 H11 bindi
96	30	71.4	7	4 AAM47010	Aam47010 H11 bindi
97	30	71.4	7	8 ADP17735	Adp17735 Prion pro
98	30	71.4	9	2 AAR60998	Aar60998 Sequence

Kam.C.
10/691157
Seq IDs 1-8

99 30 71.4 9 6 ABR28254 Human can
100 30 71.4 9 6 ABR28252 Human can

ALIGNMENTS

RESULT 1

AAB72500
ID AAB72500 standard; peptide; 7 AA.

XX AC AAB72500;
DT 09-MAY-2001 (first entry)
XX Colostrinin peptide #1.
DE Dermatological; oxidative stress regulator; colostrinin.
KW Unidentified.
XX OS
XX WO200112650-A2.
PN 22-FEB-2001.
PD 17-AUG-2000; 2000WO-US022665.
PF 17-AUG-1999; 99US-0149310P.
PR (TEXA) UNIV TEXAS SYSTEM.
XX Stanton GJ, Hughes TK, Boldogh I;
PI WPI; 2001-218342/22.
DR

XX Modulating oxidative stress level in a cell, involves contacting the cell
PT with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations.
XX Claim 6; Page 25; 48pp; English.
XX The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient
XX Sequence 7 AA;
SQ

Query Match 100.0%; Score 42; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
DB 1 MQPPPLP 7

RESULT 2

AAB59324
ID AAB59324 standard; peptide; 7 AA.

XX AC AAB59324;
DT 21-MAR-2001 (first entry)
XX Ewe colostrinin peptide fragment B-9.
DE Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
PI

OS Ovis sp.
XX WO2000075173-A2.
XX 14-DEC-2000.
XX 02-JUN-2000; 2000WO-GB002128.
XX 02-JUN-1999; 99GB-00012852.
PR (REGE-) REGEN THERAPEUTICS PLC.
XX Georgiades JA;
PI WPI; 2001-071058/08.
DR

XX Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.
XX Claim 7; Page 27; 63pp; English.

PS The present invention provides the sequences of a number of peptides
XX found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques
XX Sequence 7 AA;
SQ

Query Match 100.0%; Score 42; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
DB 1 MQPPPLP 7

RESULT 3

AAB72246
ID AAB72246 standard; peptide; 7 AA.

XX AC AAB72246;
DT 14-MAY-2001 (first entry)
XX Colostrinin derived cytokine inducing peptide SEQ ID 1.

DE Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX Synthetic.
XX WO200111937-A2.
XX 22-FEB-2001.
PD 17-AUG-2000; 2000WO-US022818.
PF 17-AUG-1999; 99US-0149311P.
PR (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
PI

DR WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for

PT treating central nervous system diseases and bacterial and viral

PT infections, comprises administering colostrinin as an immunological

PT regulator.

XX

PS Claim 1; Page 34; 50pp; English.

XX

CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,

CC a proline rich polypeptide aggregate contained in colostrum. The peptides

CC have immune response modulatory activity, and are capable of inducing

CC cytokines. Colostrinin and its derived peptides are useful for inducing

CC cytokine production, for modulating an immunological response and for

CC inducing blood cell proliferation. The peptides are useful in the

CC treatment of disorders of the central nervous system, neurological

CC disorders, mental disorders, dementia, neurodegenerative diseases,

CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic

CC disorders of the immune system, bacterial and viral infections and

CC acquired immunological deficiencies

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 42; DB 4; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7

Db 1 MQPPPLP 7

RESULT 4

AAAB72532

ID AAB72532 standard; peptide; 7 AA.

XX

AC AAB72532;

XX

XX 09-MAY-2001 (first entry)

DT

XX

DE Colostrinin peptide #1.

XX

XX Neuroprotective; neural cell differentiation regulator; colostrinin;

KW colostrum.

XX

OS Unidentified.

XX

PN WO200112651-A2.

XX

XX 22-FEB-2001.

PD

XX

XX 17-AUG-2000; 2000WO-US022774.

PF

XX

FR 17-AUG-1999; 99US-0149633P.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

XX Boldogh I;

PI

XX

DR WPI; 2001-226545/23.

XX

XX Use of colostrinin, its constituent peptide or analog as a neural cell

PT regulator, for promoting neural cell differentiation and treating damaged

PT neural cells in a patient.

XX

PS Claim 6; Page 21; 35pp; English.

XX

CC The present invention relates to a method for promoting neural cell

CC differentiation and treating damaged neural cells, using colostrinin and

CC colostrinin constituent peptides (e.g. the present peptide) as a neural

CC cell regulator. Colostrinin is a polypeptide complex found in colostrum

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 42; DB 4; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7

Db 1 MQPPPLP 7

RESULT 5

AAAO14577

ID AAO14577 standard; peptide; 7 AA.

XX

XX AAO14577;

XX

DT 27-MAY-2002 (first entry)

XX

DE Neural cell regulatory colostrinin peptide 1.

XX

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX

OS Unidentified.

XX

XX Key Location/Qualifiers

FH Modified-site 7 /note= "Optional C-terminal amide"

FT

XX

PN WO200213851-A1.

XX

XX 21-FEB-2002.

PD

XX

XX 17-AUG-2000; 2000WO-US022777.

PF

XX

FR 17-AUG-2000; 2000WO-US022777.

XX

XX (TEXA) UNIV TEXAS SYSTEM.

PA

XX

XX Boldogh I, Stanton JG, Hughes TK;

PI

XX

DR WPI; 2002-269152/31.

XX

XX Promoting cell differentiation in a patient involves use of blood cell

PT regulator selected from colostrinin, its constituent peptide and/or

PT analog.

XX

PS Claim 7; Page 21; 37pp; English.

XX

CC The invention comprises a method for promoting cell differentiation (e.g.

CC neural cell differentiation). The method involves contacting cells with a

CC neural cell regulator (i.e. a colostrinin peptide) in order to change the

CC cells in morphology to form neural cells. Colostrinin is a proline-rich

CC polypeptide aggregate that is present in colostrum. The method of the

CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 42; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7

Db 1 MQPPPLP 7

RESULT 6

AAM51036

```

ID  AAMS1036 standard; peptide; 7 AA.
XX
AC  AAMS1036;
XX
DT  30-MAY-2002 (first entry)
XX
DE  Colostrinin constituent peptide.
XX
KW  Colostrinin; colostrum; immunomodulator; cardiovascular;
KW  blood cell regulator; cytokine inducer; beta-casein; human.
XX
OS  Homo sapiens.
XX
FH  Key Location/Qualifiers
FT  Modified-site 7 /note= "optional C-terminal amidation"
FT
XX  WO200213849-A1.
XX
PD  21-FEB-2002.
XX
PF  17-AUG-2000; 2000WO-US022775.
XX
PR  17-AUG-2000; 2000WO-US022775.
XX
PA  (TEXA ) UNIV TEXAS SYSTEM.
PA  (REGE-) REGEN THERAPEUTICS PLC.
XX
PI  Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX  WPI; 2002-269150/31.
XX
PT  Modulation of blood cell proliferation in a patient involves use of blood
PT  cell regulator selected from colostrinin, its constituent peptide and/or
PT  analog.
XX
PS  Claim 1; Page 34; 54pp; English.
XX
CC  The present sequence is that of a colostrinin constituent peptide that is
CC  preferred for use as an immunological regulator and as a blood cell
CC  regulator in claimed methods of the invention. It is classified as having
CC  a beta-casein homologue precursor. Methods are claimed for: inducing a
CC  cytokine in a cell by contact with an immunological regulator, where the
CC  cell is present in a cell culture, a tissue, an organ or an organism, and
CC  the cell is mammalian, including human; modulating an immune response in
CC  a cell by contact with the immunological regulator under conditions
CC  effective to induce a cytokine; modulating an immune response in a
CC  patient by administering an immunological regulator under conditions
CC  administered topically or as part of a dietary supplement, and where the
CC  immune response is specific or non specific, an interferon response or an
CC  antibody response; modulating blood cell proliferation by contacting
CC  blood cells with a blood cell regulator, where the blood cells are
CC  present in a cell culture or an organism, are mammalian or human, and
CC  where the blood cells are increased in number or differentiated; and a
CC  method for modulating blood cell proliferation in a patient. A claimed
CC  cytokine-inducing composition comprises a pharmaceutical carrier and an
CC  active agent such as the present peptide. Cytokines induced by this
CC  peptide in human leucocyte cultures include interferon-gamma, tumour
CC  necrosis factor-alpha, interleukin-4, interleukin-6, interleukin-10 and
CC  interleukin-12. It was one of the best overall inducers in almost all
CC  cytokine and blood cell proliferation experiments conducted
XX
SQ  Sequence 7 AA;

Query Match 100.0%; Score 42; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
Db 1 MQPPPLP 7

RESULT 8
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ADN60295
ID  ADN60295 standard; peptide; 7 AA.
XX
AC  ADN60295;
XX
DT  29-JUL-2004 (first entry)
XX
DE  Constituent peptide of colostrinin SEQ ID NO:1.
XX
KW  modulator; colostrinin; intracellular signaling molecule modulator;
KW  4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;
KW  DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNE inhibitor;
KW  4HNE-protein adduct formation reduction;
KW  4HNE-mediated glutathione depletion inhibition; p53 inhibition;
KW  c-Jun NH2-terminal kinase inhibition.
XX
OS  Synthetic.
XX
PN  WO2004037851-A2.
XX
PD  06-MAY-2004.
XX
PF  22-OCT-2003; 2003WO-US033423.
XX
PR  22-OCT-2002; 2002US-0420369P.
XX
PA  (TEXA ) UNIV TEXAS SYSTEM.
PA  (BOLD/) BOLDGOH I.
PA  (STAN/) STANTON J G.
-PA  (GEOR/) GEORGIADIS J A.
PA  (HUGH/) HUGHES T K.
PA  (KRUZ/) KRUZEL M.
XX
PI  Boldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;
XX
WPI; 2004-365494/34.
XX
DR
XX
PT  Use of colostrinin for e.g. modulating an intracellular signaling
PT  molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a
PT  cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
PT  a cell.
XX
PS  Claim 6; SEQ ID NO 1; 46pp; English.
XX
CC  The present invention describes the use of a modulator selected from
CC  colostrinin, its constituent peptide, its active analogue, and a
CC  combination of these, for modulating an intracellular signaling molecule
CC  in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,
CC  inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
CC  and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
CC  The modulator has cytostatic activity, and can be used as a 4HNE
CC  inhibitor. The modulator is useful in the manufacture of a medicament for
CC  reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated
CC  glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,
CC  and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.
CC  Colostrinin, or its constituent peptide or active analogue is useful for
CC  inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
CC  or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
CC  The present sequence represents a synthetic constituent peptide of
CC  colostrinin, which can be used as a modulator in the present invention.
XX
SQ  Sequence 7 AA;
    Query Match      100.0%; Score 42; DB 8; Length 7;
    Best Local Similarity 100.0%; Pred. No. 1.8e+06;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 MQPPPLP 7
    |||||
DB  1 MQPPPLP 7

RESULT 9
AAB59354
ID  AAB59354 standard; peptide; 8 AA.
XX
AC  AAB59354;
XX
DT  21-MAR-2001 (first entry)
XX
DE  Ewe colostrinin peptide fragment derived sequence #14.

ADN74400
ID  ADS74400 standard; peptide; 7 AA.
XX
AC  ADS74400;
XX
DT  16-DEC-2004 (first entry)
XX
DE  Ovine colostrinin peptide.
XX
KW  Colostrum; colostrinin; sheep; peptide purification.
XX
OS  Ovis aries.
XX
PN  WO2004081038-A1.
XX
PD  23-SEP-2004.
XX
PF  10-MAR-2004; 2004WO-GB001014.
XX
PR  11-MAR-2003; 2003GB-00005552.
PR  08-MAR-2004; 2004GB-00005190.
XX
PA  (REGE-) REGEN THERAPEUTICS PLC.
XX
PI  Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;
XX
WPI; 2004-677519/66.
XX
DR
XX
PT  Recovering peptides such as colostrinin from mammalian colostrum, by
PT  mixing colostrum with alcohol to form alcohol phase containing peptides
PT  and precipitate, separating alcohol phase from precipitate, and
PT  recovering alcohol phase.
XX
PS  Disclosure; SEQ ID NO 17; 41pp; English.
XX
CC  The present sequence is that of a peptide that can be recovered from
CC  ovine colostrinin using the method of the invention. The invention
CC  provides a method for the recovery of peptides (especially colostrinin)
CC  from colostrum in substantially pure, biologically active form and in
CC  high yield. The method involves mixing the colostrum with an alcohol to
CC  form an alcohol phase containing the colostrinin and a precipitate
CC  containing higher molecular weight caseins and other proteins. Best
CC  results are obtained using methanol or ethanol of at least 80%, and
CC  preferably up to 100%, purity. The alcohol phase is then separated from
CC  the precipitate, and the colostrinin is separated from the alcohol,
CC  preferably by evaporation, to form a colostrinin-rich phase, which is
CC  recovered. A precipitation agent, such as ammonium sulfate, may be added
CC  either to the alcohol phase or, preferably, to the colostrinin-rich phase
CC  to induce precipitation of the colostrinin peptides. The method is
CC  generally applicable to the separation of peptides from fluids containing
CC  higher molecular weight proteins, lipids, carbohydrates and/or nucleic
CC  acids.
XX
SQ  Sequence 7 AA;
    Query Match      100.0%; Score 42; DB 8; Length 7;
    Best Local Similarity 100.0%; Pred. No. 1.8e+06;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 MQPPPLP 7
    |||||
DB  1 MQPPPLP 7

RESULT 10
AAB59354
ID  AAB59354 standard; peptide; 8 AA.
XX
AC  AAB59354;
XX
DT  21-MAR-2001 (first entry)
XX
DE  Ewe colostrinin peptide fragment derived sequence #14.
```

XX Sheep; colostrin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 OS Ovis sp.
 XX WO200075173-A2.
 XX
 XX PD 14-DEC-2000.
 XX
 XX PF 02-JUN-2000; 2000WO-GB002128.
 XX PR 02-JUN-1999; 99GB-00012852.
 XX
 XX PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 XX PI Georgiades JA;
 XX WI; 2001-071058/08.
 XX
 XX PT Peptides having an N-terminal amino acid sequence isolated from
 PT colostrin for treating e.g. disorders of the central nervous system and
 PT immune system, viral and bacterial infections, and diseases characterized
 PT by amyloid plaques.
 XX
 XX PS Claim 8; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques
 XX
 XX SQ Sequence 8 AA;

Query Match 100.0%; Score 42; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. NO. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
 Db 2 MQPPPLP 8

RESULT 11
 ADK10336
 ID ADK10336 standard; peptide; 9 AA.

XX AC ADK10336;
 XX
 XX DT 06-MAY-2004 (first entry)
 XX DE Human papillomavirus peptide #2391.

XX pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; HPV.

XX OS Human papillomavirus.
 XX
 XX PN WO2004011650-A2.
 XX PD 05-FEB-2004.

XX PF 24-JUL-2003; 2003WO-EP008112.
 XX PR 24-JUL-2002; 2002AT-00001124.
 XX PR 11-JUL-2003; 2003EP-00450171.

XX PA (INTE-) INTERCELL AG.

PI Mattner F, Schmidt W, Habel A;
 XX
 XX DR WI; 2004-169243/16.
 XX
 XX PT New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.
 XX
 XX PS Claim 18; Page 199; 220pp; English.
 XX
 CC This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
 CC invention.

XX Sequence 9 AA;

Query Match 92.9%; Score 39; DB 8; Length 9;
 Best Local Similarity 85.7%; Pred. NO. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
 Db 1 LQPPPLP 7

RESULT 12
 ADK10337
 ID ADK10337 standard; peptide; 10 AA.

XX AC ADK10337;
 XX
 XX DT 06-MAY-2004 (first entry)
 XX DE Human papillomavirus peptide #2392.

XX pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; HPV.

XX OS Human papillomavirus.

XX PN WO2004011650-A2.
 XX PD 05-FEB-2004.

XX PF 24-JUL-2003; 2003WO-EP008112.

XX PR 24-JUL-2002; 2002AT-00001124.
 XX PR 11-JUL-2003; 2003EP-00450171.

XX PA (INTE-) INTERCELL AG.

XX PI Mattner F, Schmidt W, Habel A;

XX WI; 2004-169243/16.

XX New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.

XX Claim 18; Page 199; 220pp; English.

CC This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a

CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope-peptide of the
 CC invention.

XX Sequence 10 AA;

Query Match 92.9%; Score 39; DB 8; Length 10;
 Best Local Similarity 85.7%; Pred. No. 45;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
 :|||||
 Db 1 LQPPPLP 7

RESULT 13

ADK10338
 ID ADK10338 standard; peptide; 10 AA.

XX AC ADK10338;

XX DT 06-MAY-2004 (first entry)

XX DE Human papillomavirus peptide #2393.

XX pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; HPV.
 .XX Human papillomavirus.

OS WO2004011650-A2.

XX PN 05-FEB-2004.

XX PD 24-JUL-2003; 2003WO-EP008112.

XX PF 24-JUL-2002; 2002AT-00001124.

XX PR 11-JUL-2003; 2003EP-00450171.

XX PA (INTE-) INTERCELL AG.

XX PI Mattner F, Schmidt W, Habel A;

XX DR WPI; 2004-169243/16.

XX PT New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.

XX PS Claim 18; Page 199; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 .CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
 CC invention.

XX Sequence 10 AA;

Query Match 92.9%; Score 39; DB 8; Length 10;
 Best Local Similarity 85.7%; Pred. No. 45;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
 :|||||
 Db 1 LQPPPLP 7

RESULT 14

ADK10335
 ID ADK10335 standard; peptide; 8 AA.

XX AC ADK10335;

XX DT 06-MAY-2004 (first entry)

XX DE Human papillomavirus peptide #2390.

XX pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; HPV.
 XX Human papillomavirus.

XX OS WO2004011650-A2.

XX PN 05-FEB-2004.

XX PF 24-JUL-2003; 2003WO-EP008112.

XX PR 24-JUL-2002; 2002AT-00001124.

XX PR 11-JUL-2003; 2003EP-00450171.

XX PA (INTE-) INTERCELL AG.

XX PI Mattner F, Schmidt W, Habel A;

XX DR WPI; 2004-169243/16.

XX PT New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.

XX PS Claim 18; Page 199; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
 CC invention.

XX Sequence 8 AA;

Query Match 88.1%; Score 37; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPLP 7
 :|||||
 Db 1 QPPPLP 6

RESULT 15

ADC36090
 ID ADC36090 standard; peptide; 12 AA.

XX AC ADC36090;

XX DT 18-DEC-2003 (first entry)

XX DE Chemokine binding peptide BKT-P4.

XX peptidic chemokine modulator; antiinflammatory; antiallergic;
 KW immunosuppressive; antidiabetic; antirheumatic; dermatological;
 KW antiarthritic; antibacterial; antipsoriatic; antiseborrheic;

KW antiarteriosclerotic; hypotensive; neuroprotective; virucide; vasotropic;
KW cytostatic; inflammation; allergy; immune response; autoimmune reaction;
KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
KW allograft rejection; diabetes; sepsis; cancer; malignant cell growth;
KW acne; infection; arthritis; colitis; psoriasis; atherosclerosis;
KW hypertension; reperfusion ischaemia.

XX Synthetic.

XX WO2003072599-A2.

XX PD 04-SEP-2003.

XX PF 27-FEB-2003; 2003WO-IL000155.

XX PR 28-FEB-2002; 2002US-0359999P.

XX PA (BIOK-) BIOKINE THERAPEUTICS LTD.

XX PI Peled A, Eizenberg O, Vaizel-Ohayon D;

XX DR WPI; 2003-671869/63.

XX New peptidic chemokine modulator, useful for preparing a composition for
PT treating a disease modulated through and/or caused by binding of a
PT chemokine to a chemokine receptor, e.g., inflammation, diabetes, sepsis
PT or cancer.

XX Example 1; Page 28; 43pp; English.

XX The present invention describes a peptidic chemokine modulator (I) for
CC modulating a biological effect of a chemokine. (I) comprises a molecule
CC consisting of: (a) the amino acids His, Ser, Ala, Leu, Ile, Lys, Arg, Thr
CC and Pro, and features at least 2 histidines spread along the molecule,
CC where the molecule features an overall positive charge (family 1); or (b)
CC the amino acids His, Pro, Thr, Leu, Arg and Trp and features at least two
CC neighbouring histidines, where the molecule features an overall positive
CC charge (family 2). Also described: (1) a composition for treating a
CC condition involving abnormal cell migration in a subject; (2) a method
CC for treating a disease modulated through and/or caused by binding of a
CC chemokine to a chemokine receptor in a subject; (3) an antibody for
CC binding to a chemokine-binding receptor that recognises at least a
CC portion of a chemokine-binding receptor or the peptide; (4) a vaccine
CC formed with the antibody; and (5) a method for producing an antibody. (I)
CC has antiinflammatory, anti-allergic, immunosuppressive, antidiabetic,
CC antirheumatic, dermatological, antiarthritic, antibacterial,
CC antipsoriatic, antiseborrheic, antiarteriosclerotic, hypotensive,
CC neuroprotective, virucide, vasotropic and cytostatic activities. The
CC peptidic chemokine modulator is useful for preparing a composition for
CC treating a disease modulated through and/or caused by binding of a
CC chemokine to a chemokine receptor, comprising inflammation (primary or
CC secondary), allergy, a non-optimal immune response, an autoimmune
CC reaction (including rheumatoid arthritis, systemic lupus erythematosus,
CC multiple sclerosis and others), allograft rejection, diabetes, sepsis,
CC cancer and any type of malignant cell growth, acne and chronic bacterial
CC and viral infections, arthritis, colitis, psoriasis, atherosclerosis,
CC hypertension or reperfusion ischaemia. The present sequence represents a
CC chemokine binding peptide, which is used in an example from the present
CC invention.

XX Sequence 12 AA;

Query Match 85.7%; Score 36; DB 7; Length 12;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MQPPPLP 7

Db 5 MQPPPRP 11

RESULT 16
ADR42838

ID ADR42838 standard; peptide; 12 AA.

XX ADR42838;

XX DT 18-NOV-2004 (first entry)

XX DE Modulatory chemokine-binding peptide BKT-P4.

XX Chemokine-binding peptide; MCP-1; SDF-1alpha; MIG; eotaxin;
KW interleukin-8; abnormal cell migration; vaccine; inflammation; allergy;
KW non-optimal immune response; autoimmune reaction; allograft rejection;
KW diabetes; sepsis; cancer; malignant cell growth; bacterial infection;
KW viral infection; arthritis; colitis; psoriasis; atherosclerosis;
KW hypertension; reperfusion ischaemia.

XX OS Synthetic.

XX XX US2004171552-A1.

XX PD 02-SEP-2004.

XX PF 28-AUG-2003; 2003US-00649873.

XX PR 27-FEB-2003; 2003WO-IL000155.

XX PA (BIOK-) BIOKINE THERAPEUTICS LTD.

XX PI Peled A, Eizenberg O, Vaizel-Ohayon D;

XX XX WPI; 2004-625117/60.

XX New peptidic chemokine modulators for modulating a biological effect of a
CC chemokine, useful for treating a condition involving abnormal cell
CC migration in a subject, e.g. inflammatory condition, or cancer
CC metastasis.

XX Claim 19; SEQ ID NO 112; 50pp; English.

XX The invention relates to peptidic chemokine modulators for modulating a
CC biological effect of a chemokine comprising a molecule composed of the
CC amino acids histidine (H), serine (S), alanine (A), leucine (L),
CC isoleucine (I), lysine (K), arginine (R), threonine (T), and proline (P),
CC and featuring at least 2 Histidines spread along said molecule, where the
CC molecule features an overall positive charge (family 1) or a molecule
CC composed of the amino acids H, P, T, L, R, Tryptophan (W), phenylalanine
CC (F), and featuring at least two neighbouring histidines, where the
CC molecule features an overall positive charge (family 2) and/or a molecule
CC comprising a peptide having an amino acid sequence from a list, given in
CC the specification. Also included are a composition for treating a
CC condition involving abnormal cell migration in a subject (comprising a
CC therapeutic agent for administering to the subject, where therapeutic
CC agent is any of the modulators cited above), a method for treating a
CC disease modulated through and/or caused by binding of a chemokine to a
CC chemokine receptor in a subject (by administering the therapeutic agent),
CC an antibody for binding a chemokine-binding receptor (comprising the
CC antibody capable of recognising at least a portion of a chemokine binding
CC receptor, where the antibody also recognises a peptide of the sequence of
CC the modulator), a vaccine formed with the antibody and a method for
CC producing an antibody (by inducing formation of antibody against a
CC peptide having the sequence of the chemokine modulator, where the
CC antibody is also capable of recognising a chemokine binding receptor).
CC The method, therapeutic agents and compositions are useful for treating a
CC disease modulated through and/or caused by binding of a chemokine to a
CC chemokine receptor, e.g. primary and secondary inflammation, allergy, non
CC -optimal immune response, autoimmune reaction, allograft rejection,
CC diabetes, sepsis, cancer, any type of malignant cell growth, acute and
CC chronic bacterial and viral infections, arthritis, colitis, psoriasis,
CC atherosclerosis, hypertension or reperfusion ischaemia. The present
CC sequence is a modulatory chemokine-binding peptide of the invention
CC binding chemokines MCP-1, SDF-1alpha, MIG, eotaxin and interleukin-8.

XX Sequence 12 AA;

```

Query Match      85.7%; Score 36; DB 8; Length 12;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPPLP 7
DB 5 MOPPPRP 11

RESULT 17
AAE32821
ID AAE32821 standard; peptide; 12 AA.
XX
AC AAE32821;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human CEA exon #24 encoded peptide.
XX
KW Human; carcinoembryonic antigen; CEA; cell adhesion-mediated disease;
KW prognosis; cancer; tumour; gene therapy; exon.
XX
OS Homo sapiens.
XX
PN WO200250508-A2.
XX
PD 14-NOV-2002.
XX
PF 07-MAY-2002; 2002WO-US014457.
XX
PR 07-MAY-2001; 2001US-0289179P.
PR 29-AUG-2001; 2001US-0315736P.
XX
PA (ALPH-) ALPHAGENE INC.
XX
PI Stark KA, Weaver A, Hoffmann HM, Krauss R, Valenzuela DB;
PI Saini KS;
XX
WPI; 2003-111965/10.
XX
New carcinoembryonic antigen and polynucleotides encoding them, useful
for treating and/or preventing cell adhesion-mediated disease (e.g.
PT cancers, solid tumors, tumor metastasis or benign tumors) symptoms.
XX
PS Claim 17; Page 130; 143pp; English.
XX
The invention relates to novel human carcinoembryonic antigen (CEA).
CC polypeptides and polynucleotides encoding such polypeptides. CEA genes
CC are useful as diagnostic and prognostic markers of colon, stomach and
CC breast cancers. Polypeptides of the invention can be used to diagnose,
CC treat and/or prevent cell adhesion-mediated disease (e.g. cancers, solid
CC tumours, tumour metastasis or benign tumours) and to modulate cell-cell
CC or cell-matrix adhesion in mammalian tissues. The invention is useful in
CC gene therapy. The present sequence is human CEA exon encoded peptide.
CC Note: This sequence is stated to be encoded by SEQ ID NO: 52 (AAD50572).
CC However this does not appear to be the case
XX
Sequence 12 AA;

Query Match      81.0%; Score 34; DB 6; Length 12;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPPLP 7
DB 1 MOPPDLP 7

RESULT 18
AAE32821
ID AAE32821 standard; peptide; 15 AA.
XX
AC AAE32821;
XX

Query Match      81.0%; Score 34; DB 3; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPLP 7
DB 6 QPPPPV 11

RESULT 19
AAE32821
ID AAE32821 standard; peptide; 16 AA.
XX
AC AAE32821;
XX
DT 03-JUL-2000 (first entry)
XX
DE Human ced-6 (hced-6) peptide epitope.
XX
KW ced-6; hced-6; h2ced-6; signal transduction pathway; phagocytosis;
KW cancer; autoimmune disease; neurodegenerative disease; stroke; AIDS;
KW Huntington's disease; myocardial infarction; cytostatic; neuroprotective;
KW cardiant; immunosuppressive; apoptosis modulator; epitope.
XX
OS Homo sapiens.
XX
PN WO9964586-A2.
XX
PD 16-DEC-1999.
XX
PF 10-JUN-1999; 99WO-EP004043.
XX
PR 11-JUN-1998; 98GB-00012660.
PR 24-SEP-1998; 98GB-00020816.
XX
PA (DEVG-) DEVGEN NV.
XX
PI Smits E, Van Crielinge WMR, Bogaert TRAE;
XX
WPI; 2000-246285/21.
XX
Assays for determining the phagocytosis of apoptotic cells useful for
identifying a compound which influences the phagocytic uptake of
PT apoptotic cells and treats cancers and neurodegenerative diseases.
XX
PS Claim 62; Page 56; 122pp; English.
XX
The invention relates to assays involving two human homologues of
CC Canorhabditis elegans ced-6 (hced-6 and h2ced-6) for identifying
CC compounds which function as an inhibitor or an enhancer of a signal
CC transduction pathway. The assays are carried out by measuring
CC phagocytosis of apoptotic cells. The methods are useful for identifying
CC compounds which can act as apoptotic modulators which are useful for
CC treating diseases such as cancer, autoimmune diseases, neurodegenerative
CC diseases such as Huntington's disease, stroke, myocardial infarction and
CC AIDS. The assays are well adapted for medium and high throughput
CC screening using a multi-well plate format. Sequences AAY85489-91
CC represent peptide epitopes of hced-6, used for generating antibodies
XX
Sequence 15 AA;

Query Match      81.0%; Score 34; DB 3; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPLP 7
DB 6 QPPPPV 11

RESULT 19
AAE32821
ID AAE32821 standard; peptide; 16 AA.
XX
AC AAE32821;
XX
DT 03-JUL-2000 (first entry)
XX
DE Human ced-6 (hced-6) peptide epitope.
XX
KW ced-6; hced-6; h2ced-6; signal transduction pathway; phagocytosis;
KW cancer; autoimmune disease; neurodegenerative disease; stroke; AIDS;
KW Huntington's disease; myocardial infarction; cytostatic; neuroprotective;
KW cardiant; immunosuppressive; apoptosis modulator; epitope.
XX
OS Homo sapiens.
XX
PN WO9964586-A2.
XX
PD 16-DEC-1999.
XX
PF 10-JUN-1999; 99WO-EP004043.
XX
PR 11-JUN-1998; 98GB-00012660.
PR 24-SEP-1998; 98GB-00020816.
XX
PA (DEVG-) DEVGEN NV.
XX
PI Smits E, Van Crielinge WMR, Bogaert TRAE;
XX
WPI; 2000-246285/21.
XX
Assays for determining the phagocytosis of apoptotic cells useful for
identifying a compound which influences the phagocytic uptake of
PT apoptotic cells and treats cancers and neurodegenerative diseases.
XX
PS Claim 62; Page 56; 122pp; English.
XX
The invention relates to assays involving two human homologues of
CC Canorhabditis elegans ced-6 (hced-6 and h2ced-6) for identifying
CC compounds which function as an inhibitor or an enhancer of a signal
CC transduction pathway. The assays are carried out by measuring
CC phagocytosis of apoptotic cells. The methods are useful for identifying
CC compounds which can act as apoptotic modulators which are useful for
CC treating diseases such as cancer, autoimmune diseases, neurodegenerative
CC diseases such as Huntington's disease, stroke, myocardial infarction and
CC AIDS. The assays are well adapted for medium and high throughput
CC screening using a multi-well plate format. Sequences AAY85489-91
CC represent peptide epitopes of hced-6, used for generating antibodies
XX
Sequence 15 AA;

```

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PN WO9964586-A2.
XX 16-DEC-1999.
XX 10-JUN-1999; 99WO-EP004043.
XX 11-JUN-1998; 98GB-00012660.
XX 24-SEP-1998; 98GB-00020816.
XX (DEVG-) DEVGEN NV.
XX
XX Smits E, Van Crieckinge WMR, Bogaert TAOE;
PI WPI; 2000-246285/21.
DR
XX Assays for determining the phagocytosis of apoptotic cells useful for
XX identifying a compound which influences the phagocytic uptake of
XX apoptotic cells and treats cancers and neurodegenerative diseases.
XX
XX Example 6; Page 35; 122pp; English.
XX
XX The invention relates to assays involving two human homologues of
XX Caenorhabditis elegans ced-6 (hced-6 and hced-6) for identifying
XX compounds which function as an inhibitor or an enhancer of a signal
XX transduction pathway. The assays are carried out by measuring
XX phagocytosis of apoptotic cells. The methods are useful for identifying
XX compounds which can act as apoptotic modulators which are useful for
XX treating diseases such as cancer, autoimmune diseases, neurodegenerative
XX diseases such as Huntington's disease, stroke, myocardial infarction and
XX AIDS. The assays are well adapted for medium and high throughput
XX screening using a multi-well plate format. Sequences AAY85492-94
XX represent peptide epitopes of hced-6, used for generating polyclonal
XX antibodies
XX
XX Sequence 16 AA;
SQ
    Query Match      81.0%; Score 34; DB 3; Length 16;
    Best Local Similarity 83.3%; Pred. No. 3.1e+02;
    Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPLP 7
Db 7 QPPVPV 12

RESULT 20
AAM46973
ID AAM46973 standard; peptide; 7 AA.
XX
XX AAM46973;
AC
XX 25-OCT-2001 (first entry)
DT
XX
XX H11 binding site consensus conforming peptide (CCP) #3244.
DE
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX CA2290722-A1.
PN
XX 08-JUN-2001.
PD
XX 08-DEC-1999; 99CA-02290722.
PF
XX 08-DEC-1999; 99CA-02290722.
PR
XX (NOVO-) NOVOPHARM BIOTECH INC.
PA

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, Macdonald GC;
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated antigen-
XX binding fragments of an antibody that binds specifically to the complex.
XX
XX Example 4; Page 112; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPPC) associated with tumours that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPPCs specific to target cancer (TC). Also described is an isolated
XX antigen-binding fragment of an antibody that binds specifically to SPPCs
XX or a population of different SPPCs consisting of immunogenic cancer cell
XX surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX used in vaccine production and as a tumour-specific immunogenic response
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention
XX
XX Sequence 7 AA;
SQ
    Query Match      78.6%; Score 33; DB 4; Length 7;
    Best Local Similarity 83.3%; Pred. No. 1.8e+06;
    Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPLP 7
Db 2 RPPPLP 7

RESULT 21
AAM06853
ID AAM06853 standard; peptide; 10 AA.
XX
XX AAM06853;
AC
XX 16-FEB-1997 (first entry)
DT
XX
XX Peptide binding the Crk-SH3 domain, used to treat cancer.
DE
XX
XX Peptide; binding; inhibition; binding domain; Crk-SH3; cancer; treatment;
XX diagnosis; antibody; signal transduction; disease; disorder;
XX intracellular signalling protein.
XX
XX Synthetic.
OS
XX
XX WO9621011-A2.
PN
XX 11-JUL-1996.
PD
XX 28-DEC-1995; 95WO-US016979.
PF
XX 30-DEC-1994; 94US-00367070.
PR
XX (UVRQ ) UNIV ROCKEFELLER.
PA
XX Hanafusa H, Knudsen BS, Feller SM, Kuriyan J, Wu X, Zheng J;
XX Cowburn D;
XX
XX WPI; 1996-333986/33.
XX
XX New peptide(s) which bind the Crk-SH3 domain - used to develop prods. for
XX the diagnosis and treatment of defects in intracellular signal
PT

```


PT transduction, partic. in cancer.
 XX Claim 3; Page 92; 120pp; English.
 XX

New peptides or proteins which comprise these peptides, bind to the Crk-SH3 domain and competitively inhibit the binding of intracellular signalling proteins. They can be used in the treatment of a disease or disorder associated with a defect in intracellular signal transduction, particularly cancer. They can also be used to diagnose such diseases and disorders. Antibodies raised against these proteins can be used for the same purposes. The peptides are derived from the Crk-SH3 binding domains of intracellular signalling proteins. Peptides related to the invention are described in AAW03149-63 and AAW06842-W06866

XX Sequence 10 AA;
 XX

Query Match 78.6%; Score 33; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPLP 7
 :|||||
 Db 1 KPPLP 6

RESULT 22
 AAB21127
 ID AAB21127 standard; peptide; 11 AA.
 AC AAB21127;
 XX

DT 19-JAN-2001 (first entry)
 XX

DE Src homology 3 domain binding peptide #4.
 XX

KW Src homology domain 3; SH3; protein-protein interaction; cancer;
 KW signal transduction inhibition; immune suppression-associated disease.
 XX

OS Synthetic.
 XX

XX WO200047607-A1.
 XX

PD 17-AUG-2000.
 XX

PF 12-FEB-2000; 2000WO-KR000107.
 XX

PR 12-FEB-1999; 99AU-00008643.
 PR 02-JUN-1999; 99KR-00020282.
 XX

XX (YOON/) YOON J H.
 PA (HANY/) HAN Y T.
 XX

PI Yoon JH, Han YT, Lee KY;
 XX

XX WPI; 2000-533010/48.
 DR

XX Synthetic peptides useful for treating cancers and immunosuppressive disorders by disrupting interactions of the SH (Src homology) 2 and SH3 motifs of Src family kinase proteins.
 PT

XX Claim 3; Page 33; 40pp; English.
 XX

The present sequence is a synthetic peptide which has a high affinity for the src homology 3 (SH3) domain of protein kinases. Protein kinases are involved in signal transduction pathways, and this peptide can be used to inhibit these, by disrupting protein-protein interactions, in the treatment of cancer, particularly hepatocellular carcinoma, cervical cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-associated diseases

XX Sequence 11 AA;
 XX

Query Match 78.6%; Score 33; DB 3; Length 11;
 Best Local Similarity 83.3%; Pred. No. 3.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPLP 7
 :|||||
 Db 2 KPPLP 7

RESULT 24
 AAW38072
 ID AAW38072 standard; peptide; 13 AA.
 XX
 AC AAW38072;
 XX

DT 23-APR-1998 (first entry)
 XX

Best Local Similarity 83.3%; Pred. No. 3.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPLP 7
 :|||||
 Db 3 RPPPLP 8

RESULT 23
 AAW06845
 ID AAW06845 standard; peptide; 12 AA.
 XX
 AC AAW06845;
 XX

DT 16-FEB-1997 (first entry)
 XX

DE Peptide binding the Crk-SH3 domain, used to treat cancer.
 XX

KW Peptide; binding; inhibition; binding domain; Crk-SH3; cancer; treatment;
 KW diagnosis; antibody; signal transduction; disease; disorder;
 KW intracellular signalling protein.
 XX

OS Synthetic.
 XX

XX WO9621011-A2.
 XX

PD 11-JUL-1996.
 XX

PF 28-DEC-1995; 95WO-US016979.
 XX

PR 30-DEC-1994; 94US-00367070.
 XX

XX (UYRQ) UNIV ROCKEFELLER.
 XX

PI Hanafusa H, Knudsen BS, Feller SM, Kuriyan J, Wu X, Zheng J;
 PI Cowburn D;
 XX

DR WPI; 1996-333986/33.
 XX

XX New peptide(s) which bind the Crk-SH3 domain - used to develop prods. for the diagnosis and treatment of defects in intracellular signal transduction, partic. in cancer.
 PT

XX Claim 3; Page 92; 120pp; English.
 XX

New peptides or proteins which comprise these peptides, bind to the Crk-SH3 domain and competitively inhibit the binding of intracellular signalling proteins. They can be used in the treatment of a disease or disorder associated with a defect in intracellular signal transduction, particularly cancer. They can also be used to diagnose such diseases and disorders. Antibodies raised against these proteins can be used for the same purposes. The peptides are derived from the Crk-SH3 binding domains of intracellular signalling proteins. Peptides related to the invention are described in AAW03149-63 and AAW06842-W06866

XX Sequence 12 AA;
 XX

Query Match 78.6%; Score 33; DB 2; Length 12;
 Best Local Similarity 83.3%; Pred. No. 3.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPLP 7
 :|||||
 Db 2 KPPLP 7

RESULT 24
 AAW38072
 ID AAW38072 standard; peptide; 13 AA.
 XX
 AC AAW38072;
 XX

DT 23-APR-1998 (first entry)
 XX

PD 05-MAR-1996.
 XX
 PF 09-MAR-1995; 95JP-00079661.
 XX
 PR 15-JUN-1994; 94JP-00158031.
 XX
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (NIHA-) NIPPON HAM KK.
 XX
 DR WPI; 1996-184809/19.
 XX
 PT Prolyl-endo:peptidase inhibitory peptide(s) - useful as additives for
 PT food and animal feed and to treat and prevent dementia.
 XX
 PS Claim 1; Page 11; 11pp; Japanese.
 XX
 CC AAR91746-R91753 represent prolyl endopeptidase (PEP) inhibitory peptides.
 CC These peptides are useful as PEP inhibitors in functional foods and in
 CC animal feeds. They are used to prepare oral and parenteral pharmaceutical
 CC preparations for the treatment and prevention of dementia of animals,
 CC including humans. The advantage with using these peptides, is that they
 CC are safe and easily absorbed
 XX
 SQ Sequence 6 AA;
 Query Match 76.2%; Score 32; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 .QY 3 PPPLP 7
 Db 2 PPPLP 6
 |||||
 . RESULT 27
 AAR60997
 ID AAR60997 standard; peptide; 7 AA.
 XX
 AC AAR60997;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-APR-1995 (first entry)
 XX
 DE Fragment of the 3BP1 protein that binds to SH3 of Ab1 kinase.
 XX
 KW CD4; T cell; surface antigen; receptor; MHC class II antigen;
 KW protein-tyrosine kinase; p56lck; TCR/CD3 complex; PI 3-kinase;
 KW PI 4-kinase; lipid kinase; T cell receptor complex; 3BP1; SH3;
 KW Ab1 kinase.
 XX
 OS Synthetic.
 XX
 EN WO9418832-A1.
 XX
 PD 01-SEP-1994.
 XX
 PF 25-FEB-1994; 94WO-US001840.
 .XX
 PR 26-FEB-1993; 93US-00023915.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 PI Rudd CB, Kanteti P, Cantley L;
 XX
 DR WPI; 1994-293868/36.
 XX
 PT Method for inhibiting or reducing signal transduction - utilises peptide
 PT or corresp. nucleic acid which decreases association of PI 3- or 4-
 PT kinase with CD4/p56lck.
 XX
 PS Example; Page 32; 46pp; English.
 XX
 CC In order for certain T cells to make an optimal response to antigen, it

CC is necessary for the T cell surface antigen CD4 to couple to the protein-
 CC tyrosine kinase p56lck. (CD4-p56lck is known to associate with and
 CC functionally synergise with the TcR/CD3 complex.) CD4-p56lck complex in T
 CC cells associates with two lipid kinases: PI 3-kinase and PI 4-kinase,
 CC which suggests that these lipid kinases are also involved in
 CC intracellular signalling via the T cell receptor complex. The interaction
 CC of a lipid kinase, such as PI 3-kinase or PI 4- kinase, with CD4-p56lck,
 CC may be blocked by administering a peptide. This peptide may be a fragment
 CC of the cytoplasmic domain of CD4 (eg AAR60987-R60991), a fragment of
 CC p56lck (eg AAR60992, AAR60993), a fragment of PI 3-kinase (eg AAR60994,
 CC AAR60995), or a fragment of PI 4-kinase. Other proline-rich peptides that
 CC bind to SH3 binding sequences can also be used, such as the fragment of
 CC 3BP1 protein that binds to the SH3 of the Ab1 kinase (AAR60997), or a
 CC sequence found in the SOS protein (AAR60999). (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 7 AA;
 Query Match 76.2%; Score 32; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 1 PPPLP 5
 |||||
 RESULT 28
 AAR91752
 ID AAR91752 standard; peptide; 7 AA.
 XX
 AC AAR91752;
 XX
 DT 14-AUG-1996 (first entry)
 XX
 DE Prolyl endopeptidase inhibitor peptide #7.
 XX
 KW Prolyl endopeptidase; PEP; inhibitory peptide; animal feed; therapy;
 KW prevention; dementia; human.
 XX
 OS Synthetic.
 XX
 EN JP08059697-A.
 XX
 PD 05-MAR-1996.
 XX
 PF 09-MAR-1995; 95JP-00079661.
 XX
 PR 15-JUN-1994; 94JP-00158031.
 XX
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (NIHA-) NIPPON HAM KK.
 XX
 DR WPI; 1996-184809/19.
 XX
 PT Prolyl-endo:peptidase inhibitory peptide(s) - useful as additives for
 PT food and animal feed and to treat and prevent dementia.
 XX
 PS Claim 1; Page 11; 11pp; Japanese.
 XX
 CC AAR91746-R91753 represent prolyl endopeptidase (PEP) inhibitory peptides.
 CC These peptides are useful as PEP inhibitors in functional foods and in
 CC animal feeds. They are used to prepare oral and parenteral pharmaceutical
 CC preparations for the treatment and prevention of dementia of animals,
 CC including humans. The advantage with using these peptides, is that they
 CC are safe and easily absorbed
 XX
 SQ Sequence 7 AA;
 Query Match 76.2%; Score 32; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 1 PPPLP 5
 |||||
 RESULT 28
 AAR91752
 ID AAR91752 standard; peptide; 7 AA.
 XX
 AC AAR91752;
 XX
 DT 14-AUG-1996 (first entry)
 XX
 DE Prolyl endopeptidase inhibitor peptide #7.
 XX
 KW Prolyl endopeptidase; PEP; inhibitory peptide; animal feed; therapy;
 KW prevention; dementia; human.
 XX
 OS Synthetic.
 XX
 EN JP08059697-A.
 XX
 PD 05-MAR-1996.
 XX
 PF 09-MAR-1995; 95JP-00079661.
 XX
 PR 15-JUN-1994; 94JP-00158031.
 XX
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (NIHA-) NIPPON HAM KK.
 XX
 DR WPI; 1996-184809/19.
 XX
 PT Prolyl-endo:peptidase inhibitory peptide(s) - useful as additives for
 PT food and animal feed and to treat and prevent dementia.
 XX
 PS Claim 1; Page 11; 11pp; Japanese.
 XX
 CC AAR91746-R91753 represent prolyl endopeptidase (PEP) inhibitory peptides.
 CC These peptides are useful as PEP inhibitors in functional foods and in
 CC animal feeds. They are used to prepare oral and parenteral pharmaceutical
 CC preparations for the treatment and prevention of dementia of animals,
 CC including humans. The advantage with using these peptides, is that they
 CC are safe and easily absorbed
 XX
 SQ Sequence 7 AA;
 Query Match 76.2%; Score 32; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 2 PPPLP 6

RESULT 29

AAW46827
 ID AAW46827 standard; peptide; 7 AA.

XX AC AAW46827;
 XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #3098.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.
 OS Synthetic.

XX PN CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-02290722.

XX PR 08-DEC-1999; 99CA-02290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, Macdonald GC;

XX DR WPI; 2001-425937/46.

XX PT Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated antigen-
 PT binding fragments of an antibody that binds specifically to the complex.

XX PS Example 4; Page 112; 154pp; English.

XX CC The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAW43707 to AAW47109 represent peptides
 CC which are used in the exemplification of the present invention

XX SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 3 PPPLP 7

RESULT 30

AAW46861
 ID AAW46861 standard; peptide; 7 AA.

XX AC AAW46861;
 XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #3132.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.
 OS Synthetic.

XX PN CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-02290722.

XX PR 08-DEC-1999; 99CA-02290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, Macdonald GC;

XX DR WPI; 2001-425937/46.

XX PT Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated antigen-
 PT binding fragments of an antibody that binds specifically to the complex.

XX PS Example 4; Page 112; 154pp; English.

XX CC The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAW43707 to AAW47109 represent peptides
 CC which are used in the exemplification of the present invention

XX SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 3 PPPLP 7

RESULT 31

AAW46876
 ID AAW46876 standard; peptide; 7 AA.

XX AC AAW46876;

XX 25-OCT-2001 (first entry)
 XX H11 binding site consensus conforming peptide (CCP) #3147.
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX Homo sapiens.
 OS Synthetic.
 XX CA2290722-Al.
 XX 08-JUN-2001.
 XX 08-DEC-1999; 99CA-02290722.
 XX 08-DEC-1999; 99CA-02290722.
 XX (NOVO-) NOVOPHARM BIOTECH INC.
 XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KB;
 PI Entwistle JM, Macdonald GC;
 XX WPI, 2001-425937/46.
 XX Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated antigen-
 PT binding fragments of an antibody that binds specifically to the complex.
 XX Example 4; Page 112; 154pp; English.
 XX The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention
 XX Sequence 7 AA;
 SQ
 Query Match 76.2%; Score 32; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db |||||
 3 PPPLP 7
 RESULT 32
 AAM47027
 ID AAM47027 standard; peptide; 7 AA.
 AC AAM47027;
 XX 25-OCT-2001 (first entry)
 XX H11 binding site consensus conforming peptide (CCP) #3298.
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX Homo sapiens.
 OS Synthetic.
 XX CA2290722-Al.
 XX 08-JUN-2001.
 XX 08-DEC-1999; 99CA-02290722.
 XX 08-DEC-1999; 99CA-02290722.
 XX (NOVO-) NOVOPHARM BIOTECH INC.
 XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KB;
 PI Entwistle JM, Macdonald GC;
 XX WPI, 2001-425937/46.
 XX Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated antigen-
 PT binding fragments of an antibody that binds specifically to the complex.
 XX Example 4; Page 112; 154pp; English.
 XX The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention
 XX Sequence 7 AA;
 SQ
 Query Match 76.2%; Score 32; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db |||||
 3 PPPLP 7
 RESULT 32
 AAM47027
 ID AAM47027 standard; peptide; 7 AA.
 AC AAM47027;
 XX 25-OCT-2001 (first entry)
 XX H11 binding site consensus conforming peptide (CCP) #3127.
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX Homo sapiens.
 OS Synthetic.
 XX CA2290722-Al.
 XX 08-JUN-2001.
 XX 08-DEC-1999; 99CA-02290722.
 XX 08-DEC-1999; 99CA-02290722.
 XX (NOVO-) NOVOPHARM BIOTECH INC.
 XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KB;
 PI Entwistle JM, Macdonald GC;
 XX WPI, 2001-425937/46.
 XX Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated antigen-
 PT binding fragments of an antibody that binds specifically to the complex.
 XX Example 4; Page 112; 154pp; English.
 XX The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention
 XX Sequence 7 AA;
 SQ
 Query Match 76.2%; Score 32; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db |||||
 3 PPPLP 7
 RESULT 33
 AAM46856
 ID AAM46856 standard; peptide; 7 AA.
 AC AAM46856;
 XX 25-OCT-2001 (first entry)
 XX H11 binding site consensus conforming peptide (CCP) #3127.
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

```

XX OS Homo sapiens.
XX OS Synthetic.
XX PN CA2290722-A1.
XX PD 08-JUN-2001.
XX PF 08-DEC-1999; 99CA-02290722.
XX PR 08-DEC-1999; 99CA-02290722.
XX PA (NOVO-) NOVOPHARM BIOTECH INC.
XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX PI Entwistle JM, Macdonald GC;
XX DR WPI; 2001-425937/46.
XX PT Composition useful for treating and diagnosing cancer, comprises stress
XX PT protein-peptide complexes associated with tumor, and isolated antigen-
XX PT binding fragments of an antibody that binds specifically to the complex.
XX PS Example 4; Page 112; 154pp; English.
XX CC The present invention describes a composition (I) comprising stress
XX CC protein-peptide complexes (SPPC) associated with tumours that is
XX CC specifically immunogenically cross-reactive with cell surface-associated
XX CC SPPCs specific to target cancer (TC). Also described is an isolated
XX CC antigen-binding fragment of an antibody that binds specifically to SPPCs
XX CC or a population of different SPPCs consisting of immunogenic cancer cell
XX CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX CC used in vaccine production and as a tumour-specific immunogenic response
XX CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX CC or imaging cancer cells, and to monitor the course of amelioration of
XX CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX CC which are used in the exemplification of the present invention
XX SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 3 PPPLP 7

RESULT 34
AAM46871
ID AAM46871 standard; peptide; 7 AA.
AC AAM46871;
XX 25-OCT-2001 (first entry)
XX H11 binding site consensus conforming peptide (CCP) #3142.
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX Homo sapiens.
XX OS Synthetic.
XX PN CA2290722-A1.

Query Match 76.2%; Score 32; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 3 PPPLP 7

RESULT 35
AAM46851
ID AAM46851 standard; peptide; 7 AA.
AC AAM46851;
XX 25-OCT-2001 (first entry)
XX H11 binding site consensus conforming peptide (CCP) #3122.
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX Homo sapiens.
XX OS Synthetic.
XX PN CA2290722-A1.
XX PD 08-JUN-2001.
XX PF 08-DEC-1999; 99CA-02290722.
XX PS Example 4; Page 112; 154pp; English.
XX CC The present invention describes a composition (I) comprising stress
XX CC protein-peptide complexes (SPPC) associated with tumours that is
XX CC specifically immunogenically cross-reactive with cell surface-associated
XX CC SPPCs specific to target cancer (TC). Also described is an isolated
XX CC antigen-binding fragment of an antibody that binds specifically to SPPCs
XX CC or a population of different SPPCs consisting of immunogenic cancer cell
XX CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX CC used in vaccine production and as a tumour-specific immunogenic response
XX CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX CC or imaging cancer cells, and to monitor the course of amelioration of
XX CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX CC which are used in the exemplification of the present invention
XX SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 3 PPPLP 7

RESULT 35
AAM46851
ID AAM46851 standard; peptide; 7 AA.
AC AAM46851;
XX 25-OCT-2001 (first entry)
XX H11 binding site consensus conforming peptide (CCP) #3122.
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX Homo sapiens.
XX OS Synthetic.
XX PN CA2290722-A1.

```


CC that the newly isolated human Grb3-3 protein was able to bind hSOS1, but
 CC not to the 3BP1 peptide, which corresponds to the SH3 domain of Abl and
 CC Src. A Grb3-3G162R mutant was unable to bind the hSOS1 peptide. (Updated
 CC on 25-MAR-2003 to correct PN field.)
 XX
 XX SQ Sequence 8 AA;

Query Match 76.2%; Score 32; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 PPPLP 7
 Db 1 PPPLP 5

RESULT 38
 ABW01573
 ID ABW01573 standard; peptide; 9 AA.
 XX
 XX AC ABW01573;
 XX
 XX DT 12-FEB-2004 (first entry)
 XX
 XX DE Mouse Fmn-2 FH1 domain proline repeat motif #4.
 XX
 XX KW Recurrent pregnancy loss; RPL; formin-2; Fmn-2; diagnosis; therapy;
 XX mouse.
 XX
 XX OS Mus musculus.
 XX
 XX PN US2003170683-A1.
 XX
 XX PD 11-SEP-2003.
 XX
 XX PF 03-DEC-2002; 2002US-00308485.
 XX
 XX PR 13-APR-2000; 2000US-0196811P.
 XX
 XX PR 12-APR-2001; 2001US-00835232.
 XX
 XX (LEDE/) LEADER P.
 XX
 XX PA (LEAD/) LEADER B.
 XX
 XX PI Leder P, Leader B;
 XX
 XX WPI; 2003-830607/77.
 XX

Diagnosing recurrent pregnancy loss comprises examining formin-2 gene for
 a mutation and measuring biological activity and expression of formin-2
 identified to play a role in oocyte development.
 XX
 XX Example 1; Page 7; Opp; English.
 XX
 XX The invention relates to a method of diagnosing recurrent pregnancy loss
 (RPL). The method involves examining formin (Fmn)-2 gene for a mutation
 CC and measuring biological activity and expression of Fmn-2, in which
 CC decreased levels indicates an increased risk for RPL; or examining the
 CC person's formin-2 gene for polymorphisms, in which the presence of a
 CC polymorphism indicates an altered risk for RPL. The method is used for
 CC diagnosing and treating RPL e.g. in humans. The present sequence is mouse
 CC Fmn-2 FH1 domain proline repeat motif
 XX
 XX Sequence 9 AA;

Query Match 76.2%; Score 32; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 PPPLP 7
 Db 4 PPPLP 8

RESULT 39
 AAR77371
 ID AAR77371 standard; peptide; 10 AA.
 XX
 XX AC AAR77371;
 XX
 XX DT 17-JAN-1996 (first entry)
 XX
 XX DE SH3 binding domain 3BP-1.
 XX
 XX KW Carboxyamido-triazole resistance; CAI; CAIR-1; cancer; gene therapy;
 XX Src homology 3; SH3 binding domain; 3BP-1.
 XX
 XX OS Homo sapiens.
 XX
 XX PN W09525125-A1.
 XX
 XX PD 21-SEP-1995.
 XX
 XX PF 14-MAR-1995; 95WO-US003610.
 XX
 XX PR 14-MAR-1994; 94US-00212190.
 XX
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX PI Kohn EC, Liotta LA, Kim YS;
 XX
 XX WPI; 1995-336944/43.
 XX
 XX DNA encoding CAI resistance proteins - used in gene therapy, and for
 XX detecting CAI resistance in biological samples.
 XX
 XX Example 4; Page 40; 56pp; English.

CAIR-1 protein (AAR77365), responsible for CAI resistance in A2058 human
 melanoma cells, contains a unique proline-rich sequence which fulfills
 the consensus definition for Src homology 3 (SH3) binding proteins
 (AAR77366). 4 Unique versions (AAR77367-70) are present that show
 homology to the known SH3 binding domains: 3BP-1, and the p85-alpha-1 and
 -2 subunits of phosphatidylinositol 3' kinase (AAR77371-73)
 XX
 XX SQ Sequence 10 AA;

Query Match 76.2%; Score 32; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 Db 5 PPPLP 9

RESULT 40
 AAW06861
 ID AAW06861 standard; peptide; 10 AA.
 XX
 XX AC AAW06861;
 XX
 XX DT 16-FEB-1997 (first entry)
 XX
 XX DE Peptide binding the Crk-SH3 domain, used to treat cancer.
 XX
 XX KW Peptide; binding; inhibition; binding domain; Crk-SH3; cancer; treatment;
 XX diagnosis; antibody; signal transduction; disease; disorder;
 XX intracellular signalling protein.
 XX
 XX OS Synthetic.
 XX
 XX PN W09621011-A2.
 XX
 XX PD 11-JUL-1996.
 XX
 XX PF 28-DEC-1995; 95WO-US016979.

XX 30-DEC-1994; 94US-00367070.
XX (UVRQ) UNIV ROCKEFELLER.
XX Hanafusa H, Knudsen BS, Feller SM, Kuriyan J, Wu X, Zheng J;
PI Cowburn D;
XX WPI; 1996-333986/33.
XX New peptide(s) which bind the Crk-SH3 domain - used to develop prods. for
PT the diagnosis and treatment of defects in intracellular signal
PT transduction, partic. in cancer.
XX
XX Claim 3; Page 93; 120pp; English.
XX
XX New peptides or proteins which comprise these peptides, bind to the Crk-
CC SH3 domain and competitively inhibit the binding of intracellular
CC signalling proteins. They can be used in the treatment of a disease or
CC disorder associated with a defect in intracellular signal transduction,
CC particularly cancer. They can also be used to diagnose such diseases and
CC disorders. Antibodies raised against these proteins can be used for the
CC same purposes. The peptides are derived from the Crk-SH3 binding domains
CC of intracellular signalling proteins. Peptides related to the invention
CC are described in AAW03149-63 and AAW06842-W06866
XX
SQ Sequence 10 AA;
Query Match 76.2%; Score 32; DB 2; Length 10;
Best Local Similarity 100.0%; Pred.No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 PPPLP 7
Db 2 PPPLP 6
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Job time : 42.6727 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:57:32 ; Search time 9.54545 Seconds
(without alignments)
54.743 Million cell updates/sec

Title: US-10-691-157-1

Perfect score: 42

Sequence: 1 MQPPPLP 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 183464

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.*

1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep.*
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3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	7	4	US-09-641-803-1
2	33	78.6	10	3	US-08-602-999A-278
3	33	78.6	10	4	US-09-500-124-278
4	32	76.2	7	1	US-08-230-047-40
5	32	76.2	7	5	PCT-US94-01840-11
6	32	76.2	8	1	US-09-641-640-8
7	32	76.2	8	2	US-08-612-857-8
8	32	76.2	10	1	US-08-230-047-12
9	32	76.2	10	1	US-08-230-047-14
10	32	76.2	10	1	US-08-212-190A-8
11	32	76.2	10	2	US-08-900-321-8
12	32	76.2	10	3	US-08-899-595-8
13	32	76.2	10	4	US-09-436-469-8
14	32	76.2	10	5	PCT-US95-03610-8
15	32	76.2	11	1	US-08-336-343A-25
16	32	76.2	11	3	US-08-652-877-22
17	32	76.2	11	3	US-08-652-877-32
18	32	76.2	11	3	US-08-476-515A-22
19	32	76.2	11	3	US-08-476-515A-32
20	32	76.2	12	1	US-08-230-047-17
21	32	76.2	12	3	US-08-602-999A-251
22	32	76.2	12	3	US-08-602-999A-267
23	32	76.2	12	4	US-09-500-124-251
24	32	76.2	12	4	US-09-500-124-267
25	32	76.2	13	4	US-09-485-529-103
26	32	76.2	14	1	US-08-185-432-12
27	32	76.2	14	3	US-08-630-916A-63

28	32	76.2	14	3	US-08-630-915A-186	Sequence 186, App
29	32	76.2	14	4	US-09-879-957-186	Sequence 186, App
30	32	76.2	15	1	US-08-185-432-10	Sequence 10, Appl
31	32	76.2	15	3	US-08-769-745-31	Sequence 31, Appl
32	32	76.2	15	3	US-08-602-999A-356	Sequence 356, App
33	32	76.2	15	3	US-08-602-999A-385	Sequence 385, App
34	32	76.2	15	3	US-08-602-999A-404	Sequence 404, App
35	32	76.2	15	3	US-08-602-999A-414	Sequence 414, App
36	32	76.2	15	3	US-08-602-999A-435	Sequence 435, App
37	32	76.2	15	3	US-08-602-999A-436	Sequence 436, App
38	32	76.2	15	3	US-08-602-999A-441	Sequence 441, App
39	32	76.2	15	3	US-08-602-999A-452	Sequence 452, App
40	32	76.2	15	4	US-09-500-124-356	Sequence 356, App
41	32	76.2	15	4	US-09-500-124-385	Sequence 385, App
42	32	76.2	15	4	US-09-500-124-404	Sequence 404, App
43	32	76.2	15	4	US-09-500-124-414	Sequence 414, App
44	32	76.2	15	4	US-09-500-124-435	Sequence 435, App
45	32	76.2	15	4	US-09-500-124-436	Sequence 436, App
46	32	76.2	15	4	US-09-500-124-441	Sequence 441, App
47	32	76.2	15	4	US-09-500-124-452	Sequence 452, App
48	32	76.2	16	1	US-08-185-432-9	Sequence 9, Appl
49	32	76.2	16	1	US-08-185-432-14	Sequence 14, Appl
50	32	76.2	16	3	US-08-602-999A-197	Sequence 197, App
51	32	76.2	16	4	US-09-500-124-197	Sequence 197, App
52	32	76.2	17	1	US-08-230-047-10	Sequence 10, Appl
53	32	76.2	17	3	US-08-602-999A-360	Sequence 360, App
54	32	76.2	17	3	US-08-602-999A-374	Sequence 374, App
55	32	76.2	17	4	US-09-500-124-360	Sequence 360, App
56	32	76.2	17	4	US-09-500-124-374	Sequence 374, App
57	32	76.2	18	3	US-08-602-999A-320	Sequence 320, App
58	32	76.2	18	3	US-08-602-999A-409	Sequence 409, App
59	32	76.2	18	4	US-09-500-124-320	Sequence 320, App
60	32	76.2	18	4	US-09-500-124-409	Sequence 409, App
61	31	73.8	12	4	US-09-315-926A-16	Sequence 16, Appl
62	31	73.8	13	3	US-08-630-916A-8	Sequence 8, Appl
63	31	73.8	13	3	US-08-630-916A-87	Sequence 87, Appl
64	31	73.8	13	3	US-08-630-915A-143	Sequence 143, App
65	31	73.8	13	4	US-09-879-957-143	Sequence 143, App
66	31	73.8	15	3	US-08-602-999A-301	Sequence 301, App
67	31	73.8	15	4	US-09-500-124-301	Sequence 301, App
68	31	73.8	16	3	US-08-602-999A-344	Sequence 344, App
69	31	73.8	16	4	US-09-500-124-344	Sequence 344, App
70	31	73.8	17	3	US-08-630-916A-10	Sequence 10, Appl
71	30	71.4	9	5	PCT-US94-01840-12	Sequence 12, Appl
72	30	71.4	10	3	US-08-348-518C-26	Sequence 26, Appl
73	30	71.4	10	3	US-08-476-509B-26	Sequence 26, Appl
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75	30	71.4	12	4	US-09-500-124-266	Sequence 266, App
76	30	71.4	12	4	US-09-428-082B-312	Sequence 312, App
77	30	71.4	15	3	US-08-602-999A-373	Sequence 373, App
78	30	71.4	15	3	US-08-602-999A-382	Sequence 382, App
79	30	71.4	15	3	US-08-602-999A-415	Sequence 415, App
80	30	71.4	15	3	US-08-602-999A-430	Sequence 430, App
81	30	71.4	15	3	US-08-602-999A-431	Sequence 431, App
82	30	71.4	15	4	US-09-500-124-373	Sequence 373, App
83	30	71.4	15	4	US-09-500-124-382	Sequence 382, App
84	30	71.4	15	4	US-09-500-124-415	Sequence 415, App
85	30	71.4	15	4	US-09-500-124-430	Sequence 430, App
86	30	71.4	15	4	US-09-500-124-431	Sequence 431, App
87	30	71.4	16	3	US-08-602-999A-174	Sequence 174, App
88	30	71.4	16	3	US-08-602-999A-199	Sequence 199, App
89	30	71.4	16	4	US-09-500-124-174	Sequence 174, App
90	30	71.4	16	4	US-09-500-124-199	Sequence 199, App
91	30	71.4	17	3	US-08-602-999A-413	Sequence 413, App
92	30	71.4	17	4	US-09-500-124-413	Sequence 413, App
93	29	69.0	8	3	US-08-246-441-8	Sequence 8, Appl
94	29	69.0	8	4	US-09-393-585-8	Sequence 8, Appl
95	29	69.0	10	1	US-08-230-047-11	Sequence 11, Appl
96	29	69.0	10	3	US-08-602-999A-5	Sequence 5, Appl
97	29	69.0	10	3	US-08-278-865-5	Sequence 5, Appl
98	29	69.0	10	4	US-09-500-124-5	Sequence 5, Appl
99	29	69.0	10	4	US-09-938-315-5	Sequence 5, Appl
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ALIGNMENTS

RESULT 1
US-09-641-803-1
; Sequence 1, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-1

Query Match 100.0%; Score 42; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
| | | | |
DB 1 MQPPPLP 7

RESULT 2
US-08-602-999A-278
; Sequence 278, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 278:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-278
Query Match 78.6%; Score 33; DB 3; Length 10;
Best Local Similarity 83.3%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 QPPPLP 7
| | | | |
DB 1 KPPPLP 6
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RESULT 3
US-09-500-124-278
; Sequence 278, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 278:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-278

Query Match 78.6%; Score 33; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPLP 7
Db 1 KPPLP 6

RESULT 4
US-08-230-047-40
; Sequence 40, Application US/08230047
; Patent No. 554109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashchenko, Yuri D.
; APPLICANT: Jave, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230.047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-230-047-40

Query Match 76.2%; Score 32; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 1 PPPLP 5

RESULT 5
PCT-US94-01840-11
; Sequence 11, Application PC/TUS9401840
; GENERAL INFORMATION:
; APPLICANT: Christopher E. Rudd
; APPLICANT: Prasad Kanteti
; APPLICANT: Lewis Cantley
; TITLE OF INVENTION: CD4 MEDIATED MODULATION OF
; TITLE OF INVENTION: LIPID KINASES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street

CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/023,915
; FILING DATE: February 26, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/063001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
PCT-US94-01840-11

Query Match 76.2%; Score 32; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 1 PPPLP 5

RESULT 6
US-09-641-640-8
; Sequence 8, Application US/09641640
; Patent No. RE37952
; GENERAL INFORMATION:
; APPLICANT: SCHWEIGHOFFER, Fabien
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/641,640
; FILING DATE: 15-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,857
; FILING DATE: <Unknown>
; APPLICATION NUMBER: WO PCT/FR94/00542
; FILING DATE: 09-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.

```
;
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST93044-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..8
; OTHER INFORMATION: /note= "3BP1 peptide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-641-640-8

Query Match          76.2%; Score 32; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPLP 7
Db      1 PPPLP 5

RESULT 7
US-08-612-857-8
; Sequence 8, Application US/08612857
; Patent No. 5831048
; GENERAL INFORMATION:
; APPLICANT: SCHWEIGHOFFER, Fabien
; APPLICANT: TOCQUE, Bruno
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,857
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: FR 93-10971
; FILING DATE: 15-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR94/00542
; FILING DATE: 09-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST93044-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..8
; OTHER INFORMATION: /note= "3BP1 peptide"
US-08-612-857-8

Query Match          76.2%; Score 32; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPLP 7
Db      1 PPPLP 5

RESULT 8
US-08-230-047-12
; Sequence 12, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashchenko, Yuri D.
; APPLICANT: Jaye, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-230-047-12

Query Match          76.2%; Score 32; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPLP 7
Db      5 PPPLP 9

RESULT 9
US-08-230-047-14
; Sequence 14, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
```

APPLICANT: Searfoss III, George H.
APPLICANT: Ivashchenko, Yuri D.
APPLICANT: Jaye, Michael C.
TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcoleta Road, 3043
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.0 (Patentin)
CURRENT APPLICATION DATA: US/08/230,047
FILING DATE: 19-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: A1465-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3817
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-230-047-14

Query Match 76.2%; Score 32; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 6 PPPLP 10

RESULT 10
US-08-212-190A-8
Sequence 8, Application US/08212190A
Patent No. 5652223
GENERAL INFORMATION:
APPLICANT: KOHN, Elise C.
APPLICANT: LIOTTA, Lance A.
APPLICANT: KIM, Young Sook
TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,190A
FILING DATE: 14-MAR-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15280-204US
REFERENCE/DOCKET NUMBER: DHHS Ref. No. 5652223 E-112-94/0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-212-190A-8

Query Match 76.2%; Score 32; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 11
US-08-900-321-8
Sequence 8, Application US/08900321
Patent No. 5981712
GENERAL INFORMATION:
APPLICANT: Kohn, Elise C.
APPLICANT: LIOTTA, Lance A.
APPLICANT: Kim, Young S.
TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,321
FILING DATE: 25-JUL-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,190
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-204100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-900-321-8

Query Match 76.2%; Score 32; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 5 PPPLP 9

RESULT 12
US-08-899-595-8
; Sequence 8, Application US/08899595
; Patent No. 6111072
; GENERAL INFORMATION:
; APPLICANT: Narumiya, Shuh
; APPLICANT: Takahashi, No. 6111072uaki
; TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,595
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-242701
; FILING DATE: 26-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 9-90170
; FILING DATE: 25-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen A. Bent
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 049441/0112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /product= "G/S/A/V"
US-08-899-595-8

Query Match 76.2%; Score 32; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 4 PPPLP 8

RESULT 13
US-09-436-469-8
; Sequence 8, Application US/09436469

; Patent No. 6790936
; GENERAL INFORMATION:
; APPLICANT: Kohn, Elise C.
; Liotta, Lance A.
; Kim, Young S.
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
; Uses Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/436,469
; FILING DATE: 08-NO. 6790936-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,321
; FILING DATE: 25-JUL-1997
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-204100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-436-469-8

Query Match 76.2%; Score 32; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 5 PPPLP 9

RESULT 14
PCT-US95-03610-8
; Sequence 8, Application PC/TUS9503610
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
; USES THEREOF
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03610
; FILING DATE: 14-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/212,190
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-204000PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-03610-8

Query Match 76.2%; Score 32; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 15

US-08-336-343A-25
Sequence 25, Application US/08336343A
Patent No. 5677144
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Alves, Frauke
TITLE OF INVENTION: CCK-2, A No. 5677144el Receptor Tyrosine Kinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336.343A
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742.
REFERENCE/DOCKET NUMBER: 7683-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-336-343A-25

Query Match 76.2%; Score 32; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 16

US-08-652-877-22
Sequence 22, Application US/08652877
Patent No. 6187548
GENERAL INFORMATION:
APPLICANT: Akerstrom, Goran
APPLICANT: Juhlin, Claes
APPLICANT: Rask, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
APPLICANT: Hjalrn, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd., 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652.877
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344.836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487.314
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355E-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-652-877-22

Query Match 76.2%; Score 32; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 17

US-08-652-877-32
; Sequence 32, Application US/08652877
; Patent No. 6187548

GENERAL INFORMATION:

APPLICANT: Akerstrom, Goran
APPLICANT: Juhlin, Claes
APPLICANT: Rask, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
APPLICANT: Hjaln, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd., 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A13555-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal

US-08-652-877-32

Query Match 76.2%; Score 32; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 18

US-08-476-515A-22
; Sequence 22, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes

APPLICANT: Rask, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
APPLICANT: Hjaln, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Martin Savitzky
STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
STREET: 3C43,
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Compaq PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 7.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00483
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A13555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal

US-08-476-515A-22

Query Match 76.2%; Score 32; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 19

US-08-476-515A-32
; Sequence 32, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjaln, Goran

;; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
;; TITLE OF INVENTION: Thereof and DNA Encoding Same
;; NUMBER OF SEQUENCES: 84
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Martin Savitzky
;; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
;; STREET: 3C43,
;; CITY: Collegeville
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19426-0107
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Compaq PC
;; OPERATING SYSTEM: Windows 95
;; SOFTWARE: Word 7.0 (Patentin)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/476.515A
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/344.836
;; FILING DATE: 23-NOV-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/SE94/00483
;; FILING DATE: 24-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: SE 9301764-8
;; FILING DATE: 24-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Savitzky, Martin
;; REGISTRATION NUMBER: 29,699
;; REFERENCE/DOCKET NUMBER: A135SD
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-454-3816
;; TELEFAX: 610-454-3808
;; INFORMATION FOR SEQ ID NO: 32:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; FRAGMENT TYPE: internal
US-08-476-515A-32

Query Match 76.2%; Score 32; DB 3; Length 11;
Best Local Similarity 100.0%; Pred.No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 20
US-08-230-047-17
; Sequence 17, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashchenko, Yuri D.
; APPLICANT: Jaye, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA

;; ZIP: 19426
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Macintosh
;; OPERATING SYSTEM: System 7.1
;; SOFTWARE: Word 5.0 (Patentin)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/230.047
;; FILING DATE: 19-APR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goodman, Rosanne
;; REGISTRATION NUMBER: 32,534
;; REFERENCE/DOCKET NUMBER: A1465-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (610) 454-3817
;; TELEFAX: (610) 454-3808
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-230-047-17

Query Match 76.2%; Score 32; DB 1; Length 12;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 21
US-08-602-999A-251
; Sequence 251, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602.999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-251

Query Match 76.2%; Score 32; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 6 PPPLP 10

RESULT 22
US-08-602-999A-267
Sequence 267, Application US/08602999A
Patent No. 6184205

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 267:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-267

Query Match 76.2%; Score 32; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 6 PPPLP 10

RESULT 23
US-09-500-124-251
Sequence 251, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-251

Query Match 76.2%; Score 32; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 6 PPPLP 10

RESULT 24
US-09-500-124-267
Sequence 267, Application US/09500124
Patent No. 6432920

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500.124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602.999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 267:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-267

Query Match 76.2%; Score 32; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 6 PPPLP 10

RESULT 25
US-09-485-529-103
Sequence 103, Application US/09485529
Patent No. 6762348
GENERAL INFORMATION:
APPLICANT: Harberd, Nicholas P
APPLICANT: Richards, Donald E
APPLICANT: Peng, Jinrong
TITLE OF INVENTION: Genetic Control of Plant Growth and Development
FILE REFERENCE: 620-91
CURRENT APPLICATION NUMBER: US/09/485.529
CURRENT FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/GB98/02383
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: GB 9717192.0
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 103
LENGTH: 13
TYPE: PRT
ORGANISM: Triticum aestivum
US-09-485-529-103

Query Match 76.2%; Score 32; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 26
US-08-185-432-12
Sequence 12, Application US/08185432
Patent No. 5750652
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Xu, Tian
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTEx PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185.432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-006
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-185-432-12

Query Match 76.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 27
US-08-630-916A-63
Sequence 63, Application US/08630916A
Patent No. 6011137
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: Kay, Brian K.
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas

;; CITY: New York
;; STATE: New York
;; COUNTRY: United States
;; ZIP: 10036-2711
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/630,916A
;; FILING DATE: 03-APR-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MISROCK, S. LESLIE
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-203
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 896-8864/9741
;;
;; INFORMATION FOR SEQ ID NO: 63:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;;
;; US-08-630-916A-63

Query Match 76.2%; Score 32; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 28
US-08-630-915A-186
; Sequence 186, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 186:
; US-09-879-957-186

Query Match 76.2%; Score 32; DB 4; Length 14;

;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-8864/9741
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 186:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;;
;; US-08-630-915A-186

Query Match 76.2%; Score 32; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 29
US-09-879-957-186
; Sequence 186, Application US/09879957
; Patent No. 6709821
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6709821h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 186:
; US-09-879-957-186

Query Match

Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 30

US-08-185-432-10
; Sequence 10, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Busseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-185-432-10

Query Match 76.2%; Score 32; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 31

US-08-769-745-31
; Sequence 31, Application US/08769745
; Patent No. 5952559
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; TITLE OF INVENTION: Channel Activity
; FILE REFERENCE: BRU96-02

; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-08-769-745-31

Query Match 76.2%; Score 32; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 32

US-08-602-999A-356
; Sequence 356, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 356:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-356

Query Match 76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 7 PPPLP 11

RESULT 33
US-08-602-999A-385
; Sequence 385, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-385

Query Match 76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 7 PPPLP 11

RESULT 34
US-08-602-999A-404
; Sequence 404, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 404:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-404

Query Match 76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 35
US-08-602-999A-414
; Sequence 414, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:


```

; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-414

Query Match 76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 36
US-08-602-999A-435
; Sequence 435, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 436:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-435

Query Match 76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 37
US-08-602-999A-436
; Sequence 436, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 436:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-436

Query Match 76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 57.1%; Pred. No. 78;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
Db 2 LSPPPIP 8

RESULT 38
US-08-602-999A-441
; Sequence 441, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
```

```

; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-414

Query Match 76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 36
US-08-602-999A-435
; Sequence 435, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-435

Query Match 76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
```

APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-441

Query Match 76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PPPLP 7
DB 5 PPPLP 9

RESULT 39
US-08-602-999A-452
Sequence 452, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 452:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-452

Query Match 76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PPPLP 7
DB 7 PPPLP 11

RESULT 40
US-09-500-124-356
Sequence 356, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 356:
SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-356

Query Match 76.2%; Score 32; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
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Db 7 PPPLP 11

Search completed: June 7, 2005, 23:23:09
Job time : 11.5455 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 23:00:52 ; Search time 31.5 Seconds
(without alignments)
85.185 Million cell updates/sec

Title: US-10-691-157-1

Perfect score: 42

Sequence: 1 MQPPLP 7

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Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 309695

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	42	100.0	7	16	US-10-691-157-1
3	42	100.0	7	17	US-10-691-330-1
4	36	85.7	12	16	US-10-649-873-112
5	34	81.0	12	16	US-10-704-363-53
6	33	78.6	10	14	US-10-161-791-278
7	33	78.6	13	14	US-10-185-050-139
8	32	76.2	9	9	US-09-835-232-11
9	32	76.2	9	14	US-10-308-485-11
10	32	76.2	10	14	US-10-185-050-141
11	32	76.2	10	14	US-10-185-050-178
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					Sequence 1, Appli
					Sequence 11, Appl
					Sequence 112, App
					Sequence 53, Appl
					Sequence 278, App
					Sequence 139, App
					Sequence 11, Appl
					Sequence 11, Appl
					Sequence 141, App
					Sequence 178, App

11	9	US-09-835-232-8	Sequence 8, Appli
11	9	US-09-835-232-9	Sequence 9, Appli
11	14	US-10-308-485-8	Sequence 8, Appli
11	14	US-10-308-485-9	Sequence 9, Appli
12	10	US-09-845-612B-9	Sequence 9, Appli
12	14	US-10-161-791-251	Sequence 251, App
12	14	US-10-161-791-267	Sequence 267, App
13	10	US-09-945-917-13	Sequence 13, Appl
13	10	US-09-945-917-14	Sequence 14, Appl
13	10	US-09-945-917-19	Sequence 19, Appl
13	10	US-09-945-917-21	Sequence 21, Appl
13	14	US-10-067-668-11	Sequence 11, Appl
13	14	US-10-175-696-11	Sequence 11, Appl
13	16	US-10-776-871-11	Sequence 11, Appl
13	17	US-10-809-945-103	Sequence 103, App
14	9	US-09-879-957-186	Sequence 186, App
14	14	US-10-185-050-63	Sequence 63, Appl
14	14	US-10-148-936-3	Sequence 3, Appli
14	16	US-10-807-856-186	Sequence 186, App
15	14	US-10-161-791-356	Sequence 356, App
15	14	US-10-161-791-385	Sequence 385, App
15	14	US-10-161-791-404	Sequence 404, App
15	14	US-10-161-791-414	Sequence 414, App
15	14	US-10-161-791-435	Sequence 435, App
15	14	US-10-161-791-436	Sequence 436, App
15	14	US-10-161-791-441	Sequence 441, App
15	14	US-10-161-791-452	Sequence 452, App
15	17	US-10-794-514A-80	Sequence 80, Appl
15	17	US-10-794-514A-81	Sequence 81, Appl
15	17	US-10-794-514A-82	Sequence 82, Appl
16	14	US-10-161-791-197	Sequence 197, App
16	14	US-10-161-791-360	Sequence 360, App
17	14	US-10-161-791-374	Sequence 374, App
18	14	US-10-161-791-320	Sequence 320, App
18	14	US-10-161-791-409	Sequence 409, App
12	14	US-10-235-175-16	Sequence 16, Appl
13	9	US-09-879-957-143	Sequence 143, App
13	14	US-10-185-050-8	Sequence 8, Appli
13	14	US-10-185-050-87	Sequence 87, Appl
13	16	US-10-807-856-143	Sequence 143, App
14	15	US-10-393-815-235	Sequence 235, App
15	14	US-10-161-791-301	Sequence 301, App
16	14	US-10-161-791-344	Sequence 344, App
17	14	US-10-185-050-10	Sequence 10, Appl
10	15	US-10-062-710-77	Sequence 77, Appl
10	15	US-10-285-394-212	Sequence 212, App
12	14	US-10-158-596A-25	Sequence 25, Appl
12	14	US-10-157-775B-25	Sequence 25, Appl
12	14	US-10-185-050-135	Sequence 135, App
12	14	US-10-254-446A-25	Sequence 25, Appl
12	14	US-10-155-883B-25	Sequence 25, Appl
12	14	US-10-161-791-266	Sequence 266, App
12	15	US-10-609-217-312	Sequence 312, App
12	15	US-10-832-388-312	Sequence 312, App
12	15	US-10-651-723-312	Sequence 312, App
12	15	US-10-645-761-312	Sequence 312, App
12	15	US-10-666-696-312	Sequence 312, App
12	15	US-10-653-048-312	Sequence 312, App
12	16	US-10-668-600-25	Sequence 25, Appl
13	14	US-10-156-932-75	Sequence 75, Appl
15	14	US-10-161-791-373	Sequence 373, App
15	14	US-10-161-791-382	Sequence 382, App
15	14	US-10-161-791-415	Sequence 415, App
15	14	US-10-161-791-430	Sequence 430, App
15	14	US-10-161-791-431	Sequence 431, App
15	15	US-10-328-916-58	Sequence 58, Appl
16	14	US-10-161-791-174	Sequence 174, App
16	14	US-10-161-791-199	Sequence 199, App
17	14	US-10-161-791-413	Sequence 413, App
8	14	US-10-193-709-8	Sequence 8, Appli
9	10	US-09-932-165-51	Sequence 51, Appl
9	10	US-09-932-165-1050	Sequence 1050, App
10	9	US-09-938-315-5	Sequence 5, Appli

85 29 69.0 10 10 US-09-932-165-152 Sequence 152, App
86 29 69.0 10 10 US-09-932-165-568 Sequence 568, App
87 29 69.0 10 14 US-10-161-791-5 Sequence 5, Appli
88 29 69.0 11 9 US-09-904-117-6 Sequence 6, Appli
89 29 69.0 11 14 US-10-161-791-261 Sequence 261, App
90 29 69.0 11 14 US-10-161-791-262 Sequence 262, App
91 29 69.0 11 14 US-10-161-791-290 Sequence 290, App
92 29 69.0 12 10 US-09-945-917-10 Sequence 10, Appl
93 29 69.0 12 10 US-09-945-917-22 Sequence 22, Appl
94 29 69.0 12 10 US-09-990-832C-84 Sequence 84, Appl
95 29 69.0 12 10 US-09-990-832C-96 Sequence 96, Appl
96 29 69.0 12 14 US-10-185-050-154 Sequence 154, App
97 29 69.0 12 14 US-10-161-791-268 Sequence 268, App
98 29 69.0 12 14 US-10-161-791-269 Sequence 269, App
99 29 69.0 12 15 US-10-418-751-47 Sequence 47, Appl
100 29 69.0 12 15 US-10-418-752-47 Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-1
; Sequence 1, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 1999-08-17
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-1

Query Match 100.0%; Score 42; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 MQPPPLP 7
Db 1 MQPPPLP 7

RESULT 2
US-10-691-157-1
; Sequence 1, Application US/10691157
; Publication No. US20040266681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265.00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-157-1

Query Match 100.0%; Score 42; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 MQPPPLP 7
Db 1 MQPPPLP 7

RESULT 3
US-10-691-330-1
; Sequence 1, Application US/10691330
; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: Boldogh, Istvan
; APPLICANT: Stanton, G. John
; APPLICANT: Georgiades, Jerzy A.
; APPLICANT: Hughes, Thomas K., Jr.
; APPLICANT: Kruzel, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265.00390101
; CURRENT APPLICATION NUMBER: US/10/691,330
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-330-1

Query Match 100.0%; Score 42; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 MQPPPLP 7
Db 1 MQPPPLP 7

RESULT 4
US-10-649-873-112
; Sequence 112, Application US/10649873
; Publication No. US20040171552A1
; GENERAL INFORMATION:
; APPLICANT: Biokine Therapeutics Ltd.
; APPLICANT: Peled, Amnon
; APPLICANT: Eizenberg, Orly
; APPLICANT: Vaisel-Ohayon, Dalit
; TITLE OF INVENTION: NOVEL CHEMOKINE BINDING PEPTIDES CAPABLE OF MODULATING THE

;; TITLE OF INVENTION: BIOLOGICAL ACTIVITY OF CHEMOKINES
;; FILE REFERENCE: 26732
;; CURRENT APPLICATION NUMBER: US/10/649,873
;; CURRENT FILING DATE: 2003-08-28
;; NUMBER OF SEQ ID NOS: 157
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 112
;; LENGTH: 12
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic peptide
US-10-649-873-112

Query Match 85.7%; Score 36; DB 16; Length 12;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
| | | | |
Db 5 MQPPRP 11

RESULT 5
US-10-704-363-53
;; Sequence 53, Application US/10704363
;; Publication No. US20040249145A1
;; GENERAL INFORMATION:
;; APPLICANT: Stark, Karen A.
;; APPLICANT: Weaver, Alix
;; APPLICANT: Hoffmann, Heidi M.
;; APPLICANT: Krauss, Raul
;; APPLICANT: Saini, Kulvinder S.
;; APPLICANT: Valenzuela, Dario B.
;; TITLE OF INVENTION: Cell Adhesion-Mediating Proteins and
;; FILE REFERENCE: 1966.1014003
;; CURRENT APPLICATION NUMBER: US/10/704,363
;; CURRENT FILING DATE: 2003-11-07
;; PRIOR APPLICATION NUMBER: PCT/US02/14457
;; PRIOR FILING DATE: 2002-05-07
;; PRIOR APPLICATION NUMBER: 60/289,179
;; PRIOR FILING DATE: 2001-05-07
;; PRIOR APPLICATION NUMBER: 60/315,736
;; PRIOR FILING DATE: 2001-08-29
;; NUMBER OF SEQ ID NOS: 88
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 53
;; LENGTH: 12
;; TYPE: PRT
;; ORGANISM: Homo Sapiens
US-10-704-363-53

Query Match 81.0%; Score 34; DB 16; Length 12;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
| | | | |
Db 1 MQPPDLP 7

RESULT 6
US-10-161-791-278
;; Sequence 278, Application US/10161791
;; Publication No. US20030186863A1
;; GENERAL INFORMATION:
;; APPLICANT: SPARKS, Andrew B.
;; APPLICANT: KAY, Brian K.
;; APPLICANT: THORN, Judith M.
;; APPLICANT: QUILLIAM, Lawrence A.
;; APPLICANT: DER, Channing J.
;; APPLICANT: FOWLKES, Dana M.

;; APPLICANT: RIDER, James E.
;; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;; ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/161,791
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Misrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 278:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-10-161-791-278

Query Match 78.6%; Score 33; DB 14; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPLP 7
: | | | |
Db 1 KPPPLP 6

RESULT 7
US-10-185-050-139
;; Sequence 139, Application US/10185050
;; Publication No. US20030077577A1
;; GENERAL INFORMATION:
;; APPLICANT: Pirozzi, Gregorio
;; Kay, Brian K.
;; Fowlkes, Dana M.
;; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
;; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
;; NUMBER OF SEQUENCES: 233
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: PENNIE & EDMONDS LLP
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036-2711
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/185,050

; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 139:
US-10-185-050-139

Query Match 78.6%; Score 33; DB 14; Length 13;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
Db 2 VQPPAP 8

RESULT 8

US-09-835-232-11
; Sequence 11, Application US/09835232
; Patent No. US20020098489A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leader, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/09/835,232
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-835-232-11

Query Match 76.2%; Score 32; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 9

US-10-308-485-11
; Sequence 11, Application US/10308485
; Publication No. US20030170683A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leader, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 00383/052002

; CURRENT APPLICATION NUMBER: US/10/308,485
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/835,232
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-308-485-11

Query Match 76.2%; Score 32; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 10

US-10-185-050-141
; Sequence 141, Application US/10185050
; Publication No. US20030077577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 141:
US-10-185-050-141

Query Match 76.2%; Score 32; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 11
US-10-185-050-178
; Sequence 178, Application US/10185050
; Publication No. US2003007577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/POCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 178:
US-10-185-050-178

Query Match 76.2%; Score 32; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 12
US-09-835-232-8
; Sequence 8, Application US/09835232
; Patent No. US20020098489A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/09/835,232
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Xaa=Met or Val
US-09-835-232-8

Query Match 76.2%; Score 32; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 6 PPPLP 10

RESULT 13
US-09-835-232-9
; Sequence 9, Application US/09835232
; Patent No. US20020098489A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/09/835,232
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-835-232-9

Query Match 76.2%; Score 32; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 7 PPPLP 11

RESULT 14
US-10-308-485-8
; Sequence 8, Application US/10308485
; Publication No. US20030170683A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/10/308,485
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/835,232
; PRIOR FILING DATE: 2001-04-12
; PRIOR FILING DATE: 2000-04-13

; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
; NAME/KEY: VARIANT
; FEATURE:
; LOCATION: 1
; OTHER INFORMATION: Xaa-Met or Val
US-10-308-485-8

Query Match 76.2%; Score 32; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 6 PPPLP 10

RESULT 15
US-10-308-485-9
; Sequence 9, Application US/10308485
; Publication No. US20030170683A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leder, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/10/308,485
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/835,232
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-308-485-9

Query Match 76.2%; Score 32; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 7 PPPLP 11

RESULT 16
US-09-845-612B-9
; Sequence 9, Application US/09845612B
; Publication No. US20030083261A1
; GENERAL INFORMATION:
; APPLICANT: YU, HONGTAO
; APPLICANT: TANG, ZHANYUN
; APPLICANT: LUO, XUELIAN
; APPLICANT: RIZO-REY, JOSE
; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MITOTIN
; FILE REFERENCE: UTSD:795
; CURRENT APPLICATION NUMBER: US/09/845,612B
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(12)
; OTHER INFORMATION: synthetic peptide
US-09-845-612B-9

Query Match 76.2%; Score 32; DB 10; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPL 6
Db 5 LQPPPL 10

RESULT 17
US-10-161-791-251
; Sequence 251, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-251

Query Match 76.2%; Score 32; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 6 PPPLP 10

RESULT 18
US-10-161-791-267
; Sequence 267, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TEL: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 267:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-267

Query Match 76.2%; Score 32; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 6 PPPLP 10

RESULT 19
US-09-945-917-13
; Sequence 13, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1

; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-13

Query Match 76.2%; Score 32; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 20
US-09-945-917-14
; Sequence 14, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-14

Query Match 76.2%; Score 32; DB 10; Length 13;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
Db 3 LSPPPIP 9

RESULT 21
US-09-945-917-19
; Sequence 19, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-19

Query Match 76.2%; Score 32; DB 10; Length 13;

Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
|
|
|
|
Db 6 PPPLP 10

RESULT 22

US-09-945-917-21
; Sequence 21, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-21

Query Match 76.2%; Score 32; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
|
|
|
|
Db 5 PPPLP 9

RESULT 23

US-10-067-668-11
; Sequence 11, Application US/10067668
; Publication No. US20030022334A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN
; TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-136001
; CURRENT APPLICATION NUMBER: US/10/067,668
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US-10-067-668-11

Query Match 76.2%; Score 32; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
|
|
|
|
Db 4 PPPLP 8

RESULT 24

US-10-175-696-11

; Sequence 11, Application US/10175696
; Publication No. US20030092658A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-193001
; CURRENT APPLICATION NUMBER: US/10/175,696
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/067,668
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19319
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,727
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-175-696-11

Query Match 76.2%; Score 32; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
|
|
|
|
Db 4 PPPLP 8

RESULT 25

US-10-776-871-11
; Sequence 11, Application US/10776871
; Publication No. US20040132087A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-193001
; CURRENT APPLICATION NUMBER: US/10/776,871
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/10/175,696
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/067,668
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720
; PRIOR FILING DATE: 2001-04-02

```
;
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-776-871-11

Query Match          76.2%; Score 32; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 26
US-10-809-945-103
; Sequence 103, Application US/10809945
; Publication No. US2005060773A1
; GENERAL INFORMATION:
; APPLICANT: Harberd, Nicholas P
; APPLICANT: Richards, Donald E
; APPLICANT: Peng, Jinrong
; TITLE OF INVENTION: Genetic Control of Plant Growth and Development
; FILE REFERENCE: 620-91
; CURRENT APPLICATION NUMBER: US/10/809,945
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/485,529
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/GB98/02383
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: GB 9717192.0
; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-809-945-103

Query Match          76.2%; Score 32; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 27
US-09-879-957-186
; Sequence 186, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.

;
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
;
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 186:
US-09-879-957-186

Query Match          76.2%; Score 32; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 28
US-10-185-050-63
; Sequence 63, Application US/10185050
; Publication No. US2003007757A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; KAY, Brian K.
; FOWLKES, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
;
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 63:
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-185-050-63

Query Match 76.2%; Score 32; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 29
US-10-148-936-3
; Sequence 3, Application US/10148936
; Publication No. US20030113819A1
; GENERAL INFORMATION:
; APPLICANT: Horton, Jeffrey
; APPLICANT: Smith, John
; APPLICANT: Teear, Michelle
; APPLICANT: Kendall, Jonathan
; APPLICANT: Michael, Nigel
; TITLE OF INVENTION: Reagent and Method for Delivery of Molecules into Cells
; FILE REFERENCE: PA9963
; CURRENT APPLICATION NUMBER: US/10/148,936
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04593
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: GB 9928674.2
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligomer
US-10-148-936-3

Query Match 76.2%; Score 32; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 30
US-10-807-856-186
; Sequence 186, Application US/10807856
; Publication No. US20040157216A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, Noah
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/807,856
; FILING DATE: 23-Mar-2004
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 186:
US-10-807-856-186

Query Match 76.2%; Score 32; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 31
US-10-161-791-356
; Sequence 356, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
```

;; TITLE OF INVENTION: ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/161,791
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mistrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 356:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-10-161-791-356

Query Match 76.2%; Score 32; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 7 PPPLP 11

RESULT 32
US-10-161-791-385
;; Sequence 385, Application US/10161791
;; Publication No. US20030186863A1
;; GENERAL INFORMATION:
;; APPLICANT: SPARKS, Andrew B.
;; APPLICANT: KAY, Brian K.
;; APPLICANT: THORN, Judith M.
;; APPLICANT: QUILLIAM, Lawrence A.
;; APPLICANT: DER, Channing J.
;; APPLICANT: FOWLKES, Dana M.
;; APPLICANT: RIDER, James E.
;; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;; ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/161,791
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mistrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 385:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-10-161-791-385

Query Match 76.2%; Score 32; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 7 PPPLP 11

RESULT 33
US-10-161-791-404
;; Sequence 404, Application US/10161791
;; Publication No. US20030186863A1
;; GENERAL INFORMATION:
;; APPLICANT: SPARKS, Andrew B.
;; APPLICANT: KAY, Brian K.
;; APPLICANT: THORN, Judith M.
;; APPLICANT: QUILLIAM, Lawrence A.
;; APPLICANT: DER, Channing J.
;; APPLICANT: FOWLKES, Dana M.
;; APPLICANT: RIDER, James E.
;; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;; ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/10/161,791
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mistrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 404:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-404

Query Match 76.2%; Score 32; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 4 PPPLP 8

RESULT 34
US-10-161-791-414
; Sequence 414, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-414

Query Match 76.2%; Score 32; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7

DB 4 PPPLP 8

RESULT 35
US-10-161-791-435
; Sequence 435, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-435

Query Match 76.2%; Score 32; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 4 PPPLP 8

RESULT 36
US-10-161-791-436
; Sequence 436, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.


```

; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 790-9090
; INFORMATION FOR SEQ ID NO: 436:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-436

```

```

Query Match 76.2%; Score 32; DB 14; Length 15;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MOPPPPLP 7
Db 2 LSPPPIP 8

```

```

RESULT 37
US-10-161-791-441
; Sequence 441, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 441:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-441

```

```

Query Match 76.2%; Score 32; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 3 PPPLP 7
Db 5 PPPLP 9

```

```

RESULT 38
US-10-161-791-452
; Sequence 452, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 452:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-452

Query Match 76.2%; Score 32; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 7 PPPLP 11

RESULT 39

US-10-794-514A-80
; Sequence 80, Application US/10794514A
; Publication No. US20050112134A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas
; APPLICANT: Laus, Reiner
; APPLICANT: Diegel, Michael
; APPLICANT: Vidovic, Damir
; TITLE OF INVENTION: Compositions and Methods Employing Alternative
; TITLE OF INVENTION: Reading Frame Polypeptides for the Treatment of
; TITLE OF INVENTION: Cancer and Infectious Disease
; FILE REFERENCE: 11311.1003U
; CURRENT APPLICATION NUMBER: US/10/794,514A
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 733
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab from synthetic material
US-10-794-514A-80

Query Match 76.2%; Score 32; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 10 PPPLP 14

RESULT 40

US-10-794-514A-81
; Sequence 81, Application US/10794514A
; Publication No. US20050112134A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas
; APPLICANT: Laus, Reiner
; APPLICANT: Diegel, Michael
; APPLICANT: Vidovic, Damir
; TITLE OF INVENTION: Compositions and Methods Employing Alternative
; TITLE OF INVENTION: Reading Frame Polypeptides for the Treatment of
; TITLE OF INVENTION: Cancer and Infectious Disease
; FILE REFERENCE: 11311.1003U
; CURRENT APPLICATION NUMBER: US/10/794,514A
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 733
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81

; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab from synthetic material
US-10-794-514A-81

Query Match 76.2%; Score 32; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 6 PPPLP 10

Search completed: June 7, 2005, 23:31:30
Job time : 33.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:56:36 ; Search time 6.49091 Seconds
(without alignments)
103.763 Million cell updates/sec

Title: US-10-691-157-1

Perfect score: 42

Sequence: 1 MQPPPLP 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 791*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	76.2	18	2	PC2280
2	27	64.3	15	2	hypothetical 1.5K
3	26	61.9	7	2	ICL2 protein - Par
4	25	59.5	10	2	A36454
5	25	59.5	13	2	A60856
6	25	59.5	13	2	S09716
7	25	59.5	14	2	S11129
8	25	59.5	15	2	PT0037
9	25	59.5	16	2	E58503
10	25	59.5	17	2	S57991
11	24	57.1	11	2	I33098
12	23	54.8	11	1	XAVI6B
13	23	54.8	13	2	S21152
14	23	54.8	13	2	A05174
15	23	54.8	17	2	S59481
16	22	52.4	12	2	PA0098
17	22	52.4	15	2	B35389
18	22	52.4	17	2	A49237
19	22	52.4	18	2	I52614
20	22	52.4	18	2	A54195
21	21	50.0	11	2	D45900
22	21	50.0	12	2	PN0663
23	21	50.0	12	2	B39690
24	21	50.0	13	2	B39690
25	21	50.0	14	2	S12904
26	21	50.0	15	2	P00545
27	21	50.0	16	2	JH0517
28	20	47.6	10	2	H28027
29	20	47.6	13	2	A40207

30	20	47.6	15	2	PA0002	photosystem II oxy
31	20	47.6	15	2	S67918	serine proteinase
32	19.5	46.4	14	2	H64008	hypothetical prote
33	19	45.2	7	2	PT0283	Ig heavy chain CRD
34	19	45.2	10	2	B59272	peptide-M4-(N-acet
35	19	45.2	11	1	XASNEA	bradykinin-potenti
36	19	45.2	11	2	C37196	bradykinin-potenti
37	19	45.2	11	2	D37196	bradykinin-potenti
38	19	45.2	11	2	YHHU	morphogenetic neur
39	19	45.2	11	2	YHBO	morphogenetic neur
40	19	45.2	11	2	YHJFHY	morphogenetic neur
41	19	45.2	11	2	YHXAE	morphogenetic neur
42	19	45.2	11	2	YHRT	morphogenetic neur
43	19	45.2	13	2	G61458	Ig lambda chain V-
44	19	45.2	13	2	A86126	hypothetical prote
45	19	45.2	15	2	PA0088	protein QP200051 -
46	19	45.2	15	2	A60221	apolipoprotein A-I
47	19	45.2	16	2	C49048	T-cell receptor be
48	19	45.2	17	2	I49593	cystic fibrosis tr
49	19	45.2	17	2	I84733	gene CFTR protein
50	19	45.2	17	2	PT0235	Ig heavy chain CRD
51	19	45.2	17	2	S05033	photosystem II pro
52	19	45.2	17	2	S10786	enamelin, 26K - bo
53	19	45.2	17	2	B25348	glycogen(starch) s
54	18	42.9	8	2	B39745	endoglycosylcerami
55	18	42.9	8	2	S10783	enamelin f - bovin
56	18	42.9	9	2	B41983	orf downstream to b
57	18	42.9	10	2	PC2171	triacylglycerol li
58	18	42.9	10	2	C39745	sphingomyelinase -
59	18	42.9	11	2	S07203	uperolein - frog (
60	18	42.9	13	2	I84603	deoxynucleotidyltr
61	18	42.9	14	2	B60683	malate dehydrogena
62	18	42.9	15	2	A32232	gentisate 1,2-diox
63	18	42.9	15	2	S27248	pseudogerm - whe
64	18	42.9	15	2	PA0060	protein QP200037 -
65	18	42.9	15	2	B61457	alpha-glucosidase
66	18	42.9	16	2	I57530	gene c-fms protein
67	18	42.9	16	2	PH1302	Ig heavy chain DJ
68	18	42.9	16	2	S57517	T cell receptor be
69	18	42.9	16	2	JT0609	leukocyte chemotact
70	18	42.9	17	2	S33609	extensin - maize (
71	18	42.9	17	2	A42920	fatty acid ethyl e
72	18	42.9	18	2	S04229	N4-(beta-N-acetyl
73	17	40.5	9	2	S26508	collagen alpha 2(V
74	17	40.5	10	2	H37196	bradykinin-potenti
75	17	40.5	11	2	D56979	collagen alpha 1(I
76	17	40.5	11	2	C60409	kassinin-like pept
77	17	40.5	11	2	B60409	substance P-like p
78	17	40.5	11	2	B60409	substance P-like p
79	17	40.5	11	2	D60409	kassinin-like pept
80	17	40.5	11	2	D60409	napiin small chain
81	17	40.5	12	2	S70337	tachykinin - Afric
82	17	40.5	12	2	S07436	seed storage prote
83	17	40.5	15	2	PA0014	seed storage prote
84	17	40.5	15	2	PN0173	seed storage prote
85	17	40.5	15	2	A60929	dichloromethane de
86	17	40.5	15	2	B60929	dichloromethane de
87	17	40.5	15	2	PA0071	superoxide dismuta
88	17	40.5	18	2	C56211	progesterone recep
89	17	40.5	18	2	A40760	basic fibroblast g
90	16	38.1	5	2	B37988	acid proteinase 11
91	16	38.1	8	2	PT0559	T-cell receptor be
92	16	38.1	10	1	XAVI6B	angiotensin-conver
93	16	38.1	10	2	B37196	bradykinin-potenti
94	16	38.1	11	2	PH1583	Ig H chain V-D-J r
95	16	38.1	11	2	I52304	gene rSSTR4 protei
96	16	38.1	11	2	C61497	seed protein ws-18
97	16	38.1	11	2	PN0042	scatamin - mouse (
98	16	38.1	12	2	E45691	probable minor cap
99	16	38.1	12	2	JU0356	cycloleominurin -
100	16	38.1	12	2	PQ0786	NADH2 dehydrogenas

ALIGNMENTS

```
RESULT 1
PC2280
A:Molecule type: protein
A:Residues: 1-7 <MAD>
A:Experimental source: strain d4-2
C:Genetics:
A:Genetic code: SGC5

Query Match          61.9%; Score 26; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPP 5
DB 2 QPPP 5

RESULT 4
A36454
trypsin-modulating oostatic factor - yellow fever mosquito
C:Species: Aedes aegypti (yellow fever mosquito)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
A:Accession: A36454; A61630
R:Bobrovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
FASEB J. 4, 3015-3020, 1990
A:Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi
A:Reference number: A36454; MUID:90367888; PMID:2394318
A:Molecule type: protein
A:Accession: A36454
A:Residues: 1-10 <BOR>
A:Cross-references: UNIPROT:P19425
R:Bobrovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
Insect Biochem. Mol. Biol. 23, 703-712, 1993
A:Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost
A:Reference number: A61630; MUID:93357794; PMID:8353526
A:Accession: A61630
A:Molecule type: protein
A:Residues: 1-10 <BO2>
A:Function:
C:Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ep
C:Keywords: hormone

Query Match          59.5%; Score 25; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPLP 7
DB 5 PPPPP 9

RESULT 5
A60856
inhibin alpha chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
A:Accession: A60856
R:Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wettenhall
J. Endocrinol. 113, 213-221, 1987
A:Title: Isolation of inhibin from ovine follicular fluid.
A:Reference number: A60856; MUID:87224684; PMID:3585232
A:Accession: A60856
A:Molecule type: protein
A:Residues: 1-13 <LEV>
C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.
C:Superfamily: inhibin
C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match          59.5%; Score 25; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
DB 5 PPPPP 7
```

```
RESULT 1
PC2280
A:Molecule type: protein
A:Residues: 1-7 <MAD>
A:Experimental source: strain d4-2
C:Genetics:
A:Genetic code: SGC5

Query Match          76.2%; Score 32; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPLP 7
DB 2 PPLP 6

RESULT 2
B39109
hypothetical 1.5K protein - hepatitis C virus
N:Alternate names: hypothetical protein 2
C:Species: hepatitis C virus
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
A:Accession: B39109; JQ1585
R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A:Reference number: A39109; MUID:91156678; PMID:1705704
A:Accession: B39109
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-15 <HAN>
A:Cross-references: GB:M59406
R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992
A:Title: Cloning and sequencing of the structural region and expression of putative core
A:Reference number: JQ1584; MUID:92300349; PMID:1318944
A:Accession: JQ1585
A:Molecule type: genomic RNA
A:Residues: 1-15 <KUM>
A:Experimental source: strain U.K.

Query Match          64.3%; Score 27; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MQP--PPLP 7
DB 4 VQPPGPPLP 12

RESULT 3
S71299
ICL2 protein - Paramecium tetraurelia (fragment)
C:Species: Paramecium tetraurelia
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
A:Accession: S71299
R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
Eur. J. Biochem. 238, 121-128, 1996
A:Title: Characterization of centrin genes in Paramecium.
A:Reference number: S71298; MUID:96248429; PMID:8665928
A:Accession: S71299
```

Db 3 PPLP 6

RESULT 6
S09716
2S albumin large chain (1 and 2) nII - rape (fragments)
N:Alternate names: 2S albumin large chain nIII
C:Species: Brassica napus (rape)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Aug-1998
C:Accession: S09716; S09718; S09717
R:Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263: 209-212, 1990
A:Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins
A:Reference number: S09720; PMID:90242974; PMID:2185951
A:Accession: S09716
A:Molecule type: protein
A:Residues: 1-9,10-13 <MON>
A:Experimental source: seed
A:Note: 3-Ser was also found
A:Accession: S09718
A:Molecule type: protein
A:Residues: 1-9,10-13 <MO2>
A:Experimental source: seed
A:Accession: S09717
A:Molecule type: protein
A:Residues: 1-9,10-13 <MO3>
A:Experimental source: seed

Query Match 59.5%; Score 25; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPLP 7
:|||||
7 RPPGCP 12

Db 7 RPPGCP 12

RESULT 7
S11129
phosphoprotein, bone - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 25-Oct-1996
C:Accession: S11129
R:Mikuni-Takagaki, Y.; Glimcher, M.J.
Biochem. J. 268, 585-591, 1990
A:Title: Post-translational processing of chicken bone phosphoproteins. Identification of
A:Reference number: S11127; PMID:90303246; PMID:2363696
A:Accession: S11129
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <MIK>
C:Keywords: phosphoprotein

Query Match 59.5%; Score 25; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPL 6
:|||||
5 PPPL 8

Db 5 PPPL 8

RESULT 8
PT0037
light harvesting complex chain III/b, photosystem I - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: PT0037; PS0205
R:Uchiyama, Y.; Teugita, A.
submitted to JIPID, June 1991
A:Reference number: PS0189
A:Accession: PT0037
A:Molecule type: protein

A:Residues: 1-15 <UCH>
A:Cross-references: UNIPROT:Q7M1V1

Query Match 59.5%; Score 25; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7
:|||||
8 PPPPP 12

Db 8 PPPPP 12

RESULT 9
E58503
superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)
N:Alternate names: 21.3K bladder and kidney stone protein
C:Species: unidentified bacterium
C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: E58503
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: E58503
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <BIN>
A:Cross-references: UNIPROT:Q7ML37
A:Experimental source: human bladder and kidney stones
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Keywords: metalloprotein; oxidoreductase

Query Match 59.5%; Score 25; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
:|||||
6 PPLP 9

Db 6 PPLP 9

RESULT 10
S57991
hydroxyproline-rich protein - Sesbania rostrata (fragment)
C:Species: Sesbania rostrata
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: S57991
R:Goormachtig, S.; Valerio-Lepiniec, M.; Szczyglowski, K.; van Montagu, M.; Holsters, M.
submitted to the EMBL Data Library, March 1995
A:Description: Use of differential display to identify novel Sesbania rostrata genes enh
A:Reference number: S57991
A:Accession: S57991
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <GOO>
A:Cross-references: UNIPROT:Q41400; EMBL:248673; NID:g899484; PID:g899485
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 59.5%; Score 25; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7
:|||||
10 PPPPP 14

Db 10 PPPPP 14

RESULT 11
I33098
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

C;Accession: I33098
 R;Nichols, J.H.; Hager, L.P.
 Submitted to the Protein Sequence Database, May 1990
 A;Reference number: A33098
 A;Accession: I33098
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-11 <NIC>

Query Match 57.1%; Score 24; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 3 PPPLP 7

RESULT 12
 XAVIDH
 bradykinin-potentiating peptide - halys viper
 N;Alternate names: BPP
 C;Species: Agkistrodon halys (halys viper)
 C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
 C;Accession: JCO002
 R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.
 Peptides 6, 339-342, 1985
 A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese
 A;Reference number: JCO002; MUID:86177022; PMID:3008123
 A;Accession: JCO002
 A;Molecule type: protein
 A;Residues: 1-11 <CHI>
 A;Cross-references: UNIPROT:P04562
 C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyrog
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 54.8%; Score 23; DB 1; Length 11;
 Best Local Similarity 75.0%; Pred. No. 4.1e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 |||||
 Db 7 PPIP 10

RESULT 13
 S21152
 tryptophyllin-related peptide - two-colored leaf frog
 C;Species: Phyllomedusa bicolor (two-colored leaf frog)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
 C;Accession: S21152
 R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
 FEBS Lett. 302, 151-154, 1992
 A;Title: Identification and characterization of two dermorphins from skin extracts of th
 A;Reference number: S21152; MUID:92339502; PMID:1633946
 A;Accession: S21152
 A;Molecule type: protein
 A;Residues: 1-13 <MIG>
 A;Cross-references: UNIPROT:Q7LZ51
 A;Experimental source: skin

Query Match 54.8%; Score 23; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 4.8e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 6
 |||||
 Db 7 PPPI 10

RESULT 14

A05174
 tryptophyllin-13 - Rohde's leaf frog
 C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
 C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
 C;Accession: A05174
 R;Montecucchi, P.C.; Gozzini, L.; Erspamer, V.
 Int. J. Pept. Protein Res. 27, 175-182, 1986
 A;Reference number: A05174
 A;Accession: A05174
 A;Molecule type: protein
 A;Residues: 1-13 <MON>
 A;Cross-references: UNIPROT:P04096
 C;Superfamily: unassigned animal peptides
 C;Keywords: pyroglutamic acid; skin
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 54.8%; Score 23; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 4.8e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 6
 |||||
 Db 7 PPPI 10

RESULT 15
 S59481
 hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)
 C;Species: Phaseolus vulgaris (kidney bean)
 C;Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C;Accession: S59481
 R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
 Plant Mol. Biol. 28, 1075-1087, 1995
 A;Title: Specificity in the immobilisation of cell wall proteins in response to differer
 A;Reference number: S59481; MUID:96011753; PMID:7548825
 A;Accession: S59481
 A;Molecule type: protein
 A;Residues: 1-17 <WOJ>
 A;Cross-references: UNIPROT:Q7MLI3
 C;Keywords: glycoprotein; hydroxyproline
 F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 54.8%; Score 23; DB 2; Length 17;
 Best Local Similarity 57.1%; Pred. No. 6.3e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
 |||||
 Db 2 MYLPVP 8

RESULT 16
 PA0098
 ribosomal protein S3 - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: PA0098
 R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
 A;Reference number: PA0051
 A;Accession: PA0098
 A;Molecule type: protein
 A;Residues: 1-12 <CHO>
 A;Cross-references: UNIPROT:Q7MAX9

Query Match 52.4%; Score 22; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 6.3e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 |||||
 Db 4 PPVP 7

RESULT 17
B35389
urease (EC 3.5.1.5) 15K chain - Morganella morganii (fragment)
C:Species: Morganella morganii
C>Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004
C:Accession: B35389
R:Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A:Title: Morganella morganii urease: purification, characterization, and isolation of gene
A:Reference number: A35389; MUID:90264298; PMID:2345135
A:Accession: B35389
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <HUA>
A:Cross-references: UNIPROT:P17338
C:Keywords: hydrolase

Query Match 52.4%; Score 22; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPL 6
|||
DB 5 QPTPL 9

RESULT 18
A49237
45/47K antigen - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A49237
R:Romain, F.; Laquerriere, A.; Milltzer, P.; Pescher, P.; Chavarot, P.; Lagranderie, M.;
Infect. Immun. 61, 742-750, 1993
A:Title: Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen complex, a
A:Reference number: A49237; MUID:93138802; PMID:8423100
A:Contents: BCG
A:Accession: A49237
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <ROM>
A:Cross-references: UNIPROT:P80069
A:Note: sequence extracted from NCBI backbone (NCBIP:123246)

Query Match 52.4%; Score 22; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 8.9e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
|||
DB 6 PPVP 9

RESULT 19
I52614
u-plasminogen activator receptor precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: I52614
R:Soravia, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blaszi, F.
Blood 86, 624-635, 1995
A:Title: A conserved TATA-less proximal promoter drives basal transcription from the urc
A:Reference number: I52614; MUID:95329719; PMID:7605992
A:Accession: I52614
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18 <RES>
A:Cross-references: UNIPROT:Q03405; GB:S78532; NID:9999307; PIDN:AA014289.1; PID:g426198
C:Genetics:
A:Gene: uPAR
C:Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 52.4%; Score 22; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPPLP 7
|||
DB 4 PPLLP 8

RESULT 20
A54195
Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)
C:Species: Squalus acanthias (spiny dogfish)
C>Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A54195
R:Esmann, M.; Karlish, S.J.; Sottrup-Jensen, L.; Marsh, D.
Biochemistry 33, 8044-8050, 1994
A:Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-AT
A:Reference number: A54195; MUID:94297020; PMID:8025109
A:Accession: A54195
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <ESM>
A:Cross-references: UNIPROT:Q9PSP6
A:Experimental source: rectal gland
A:Note: sequence extracted from NCBI backbone (NCBIP:149363)
C:Keywords: hydrolase

Query Match 52.4%; Score 22; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 9.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQPPP 5
:
DB 6 LTPPP 10

RESULT 21
D45900
complement C3b receptor type 2 - mouse (clone 12) (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: D45900
R:Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.
J. Immunol. 144, 3581-3591, 1990
A:Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2 gen
A:Reference number: A45900; MUID:90229754; PMID:2139460
A:Accession: D45900
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-11 <KUR>

Query Match 50.0%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
DB 9 PPP 11

RESULT 22
PN0663
dystrophin-associated glycoprotein A3a-II - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C:Accession: PN0663
R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
A:Reference number: PN0662; MUID:94156881; PMID:8113213
A:Accession: PN0663

A:Molecule type: protein
A:Residues: 1-12 <YOS>

C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C:Keywords: glycoprotein; skeletal muscle

Query Match 50.0%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 5 PPP 7

RESULT 23

B39690
neural cell adhesion molecule, cardiac splice form +,-,- - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)

C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999

C:Accession: B39690

R:Reyes, A.A.; Small, S.J.; Akesson, R.

Mol. Cell. Biol. 11, 1654-1661, 1991

A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
A:Reference number: A39690; MUID:91141516; PMID:1996115

C:Accession: B39690

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 1-12 <REY>

A:Cross-references: GB:M63970

C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 50.0%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 6 PPP 8

RESULT 24

B39690
neural cell adhesion molecule, cardiac splice form +,-,-,- - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)

C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999

C:Accession: B39690

R:Reyes, A.A.; Small, S.J.; Akesson, R.

Mol. Cell. Biol. 11, 1654-1661, 1991

A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
A:Reference number: A39690; MUID:91141516; PMID:1996115

C:Accession: B39690

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 1-13 <REY>

A:Cross-references: GB:M63970

C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like growth factor binding protein; thyroglobulin type I repeat

Query Match 50.0%; Score 21; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 6 PPP 8

RESULT 25

S12904
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)

C:Species: Pisaster ochraceus

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C:Accession: S12904

R:Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.
FEBS Lett. 273, 223-226, 1990
A:Title: Identification of the sites in myelin basic protein that are phosphorylated by protein kinase C

A:Reference number: S12904; MUID:91032186; PMID:1699809

A:Accession: S12904

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <SAN>

A:Cross-references: UNIPROT:Q7M3M4

C:Keywords: phosphotransferase

Query Match 50.0%; Score 21; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 8 PPP 10

RESULT 26

PQ0545
capsid protein VP19C - human herpesvirus 1 (fragment)

C:Species: human herpesvirus 1

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C:Accession: PQ0545

R:Davidson, M.D.; Rixon, F.J.; Davison, A.J.

J. Gen. Virol. 73, 2709-2713, 1992

A:Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes simplex virus type 1

A:Reference number: PQ0544; MUID:93019027; PMID:1328483

C:Accession: PQ0545

A:Molecule type: protein

A:Residues: 1-15 <DAV>

A:Cross-references: UNIPROT:Q7LZW6

A:Experimental source: strain 17

C:Genetics:

A:Gene: UL38

C:Keywords: capsid protein

Query Match 50.0%; Score 21; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
|:|:|
Db 1 MKTNPLP 7

RESULT 27

JH0517
insulin-like growth factor-binding protein 4 - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C:Accession: JH0517

R:Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.

Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991

A:Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth factor binding proteins

A:Reference number: JH0515; MUID:92109718; PMID:1722398

C:Accession: JH0517

A:Molecule type: protein

A:Residues: 1-16 <COL>

A:Cross-references: UNIPROT:P24854

A:Experimental source: serum

C:Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat

Query Match 50.0%; Score 21; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 7 PPP 9

RESULT 28

H28027
protein P11 - curled-leaved tobacco (fragment)
C:Species: Nicotiana glauca (curled-leaved tobacco)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993
C:Accession: H28027
R:Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A>Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-
A:Reference number: A94167
A:Accession: H28027
A:Molecule type: protein
A:Residues: 1-10 <BAU>
A>Note: 4-Val was also found

Query Match 47.6%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7
|||
Db 7 PPXP 10

RESULT 29

A40207
cell surface glycoprotein gp150 - slime mold (Dictyostelium discoideum) (fragment)
C:Species: Dictyostelium discoideum
C>Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
C:Accession: A40207
R:Gao, E.N.; Shier, P.; Siu, C.H.
J. Biol. Chem. 267, 9409-9415, 1992

A>Title: Purification and partial characterization of a cell adhesion molecule (gp150) i
A:Reference number: A40207; MUID:92250549; PMID:1577768
A:Accession: A40207
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-13 <GAO>
A:Cross-references: UNIPROT:Q7M370
C:Keywords: glycoprotein

Query Match 47.6%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7
|||
Db 3 PPTP 6

RESULT 30

PA0002
photosystem II oxygen-evolving complex protein 3 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Nov-1994 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C:Accession: PA0002
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Taugita, A.
submitted to JPIID, July 1994

A>Description: Separation and characterization of Arabidopsis proteins by two-dimensiona
A:Reference number: PA0001
A:Accession: PA0002
A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Experimental source: stem
C:Keywords: photosynthesis; photosystem II

Query Match 47.6%; Score 20; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7
|||

Db 10 PPXP 13

RESULT 31

S67918
serine proteinase laeD (EC 3.4.21.-), staphylytic - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S67918
R:Park, S.; Galloway, D.R.
Mol. Microbiol. 16, 263-270, 1995
A>Title: Purification and characterization of laeD: a second staphylytic proteinase p
A:Reference number: S67918; MUID:96015439; PMID:7565088
A:Accession: S67918
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-15 <PAR>
A:Cross-references: UNIPROT:Q9RMI4; UNIPROT:Q9I589
C:Genetics:
A:Gene: laeD
C:Keywords: hydrolase; serine proteinase

Query Match 47.6%; Score 20; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPP 5
|||
Db 4 METPP 8

RESULT 32

H64008
hypothetical protein HI0492 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998
C:Accession: H64008
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A>Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: H64008
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-14 <TIGR>
A:Cross-references: GB:U32731; GB:L42023; NID:G1573465; PID:G1573478; TIGR:HI0492

Query Match 46.4%; Score 19.5; DB 2; Length 14;
Best Local Similarity 41.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

Qy 1 MQP-----PPLP 7
|||
Db 1 MKPKYKMPKP 12

RESULT 33

PT0283
Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0283
R:Amada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0283
A:Molecule type: DNA
A:Residues: 1-7 <YAM>
A:Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 45.2%; Score 19; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
|||
DB 5 QPP 7

RESULT 34

B59272
peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain
N;Alternate names: peptide N-glycosidase
C;Species: Prunus dulcis var. saciva (sweet almond)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: B59272

R;Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.

A;Title: Characterisation of peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase A
A;Reference number: A59272; PMID:98181894; PMID:9523720

A;Accession: B59272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <ALT>

A;Cross-references: UNIPROT:P81898

C;Keywords: hydrolase

Query Match 45.2%; Score 19; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPL 6
: |||
DB 1 EPTPL 5

RESULT 35

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004

C;Accession: A01254

R;Kato, H.; Suzuki, T.

Proc. Jpn. Acad. 46, 176-181, 1970

A;Reference number: A01254

A;Accession: A01254

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Cross-references: UNIPROT:P01021

A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; vena
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
|||
DB 4 PPPP 7

RESULT 36

C37196

bradykinin-potentiating peptide 3 - island jararaca

C;Species: Bothrops insularis (island jararaca)

C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004

C;Accession: C37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides f
A;Reference number: A37196; PMID:90351557; PMID:2386615

A;Accession: C37196

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CIN>

A;Cross-references: UNIPROT:P30423

C;Keywords: pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.6e+03; Mismatches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PPLP 7
|||
DB 4 PPPP 7

RESULT 37

D37196

bradykinin-potentiating peptide 4 - island jararaca

C;Species: Bothrops insularis (island jararaca)

C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004

C;Accession: D37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides f

A;Reference number: A37196; PMID:90351557; PMID:2386615

A;Accession: D37196

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CIN>

A;Cross-references: UNIPROT:P30424

C;Keywords: pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.6e+03; Mismatches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PPLP 7
|||
DB 4 PPPP 7

RESULT 38

YHHU

morphogenetic neuropeptide - human

C;Species: Homo sapiens (man)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004

C;Accession: B01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coele

A;Reference number: A93266; PMID:82035850; PMID:7290191

A;Accession: B01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

A;Cross-references: UNIPROT:P01163

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; PMID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical struct

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head

malian intestine and hypothalamus.

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropep

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu

Query Match 45.2%; Score 19; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 1 QPP 3

QY 2 QPP 4
|||

Db 1 QPP 3

RESULT 39
YHBO
morphogenetic neuropeptide - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
C:Accession: C01427; A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelestis
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: C01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>
A:Cross-references: UNIPROT:P01163
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
PEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator
C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide
F:/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status

Query Match 45.2%; Score 19; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
|||

Db 1 QPP 3

RESULT 40
YHFBHY
morphogenetic neuropeptide - Hydra attenuata
N:Alternate names: head activator
C:Species: Hydra attenuata
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
C:Accession: B93900; A01427
R:Schaller, H.C.; Bodenmuller, H.
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
A:Reference number: A93900
A:Accession: B93900
A:Molecule type: protein
A:Residues: 1-11 <SCH>
A:Cross-references: UNIPROT:P01163
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
PEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator
C:Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
|||

Search completed: June 7, 2005, 23:20:34
Job time : 9.49091 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 30.8 Seconds
(without alignments)
116.382 Million cell updates/sec

Title: US-10-691-157-1

Perfect score: 42

Sequence: 1 MQPPPLP 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	26	61.9	17 1 APID_BOMPA	P81464 bombus pasc
2	26	61.9	18 2 Q9UCT9	Q9uct9 homo sapien
3	25	59.5	10 1 TMOF_AEDAE	P19425 aedes aegypt
4	25	59.5	15 2 P82439	P82439 nicotiana t
5	25	59.5	15 2 Q7M1V1	Q7mlv1 oryza sativ
6	25	59.5	16 2 Q7M137	Q7ml37 unidentified
7	25	59.5	17 2 Q41400	Q41400 sesbania ro
8	25	59.5	18 2 Q84129	Q84129 influenza a
9	24	57.1	9 2 Q9TWV0	Q9twv0 anthopleura
10	24	57.1	16 2 Q6W631	Q6w631 sphagnum cu
11	24	57.1	18 2 Q6W322	Q6w322 andreaea ro
12	24	57.1	18 2 Q6W619	Q6w619 sphagnum wu
13	24	57.1	18 2 Q6W622	Q6w622 sphagnum sq
14	24	57.1	18 2 Q6W628	Q6w628 sphagnum la
15	24	57.1	18 2 Q6W634	Q6w634 sphagnum se
16	24	57.1	18 2 Q6W637	Q6w637 sphagnum af
17	23	54.8	11 1 BPP_ACKHP	P04562 agkistrodon
18	23	54.8	13 1 TY13_PHYRO	P04096 phyllomedus
19	23	54.8	13 2 Q7LZ51	Q7l251 phyllomedus
20	23	54.8	14 1 TY13_BOMVA	P84215 bombina var
21	23	54.8	17 2 Q9NQY8	Q9nqy8 homo sapien
22	23	54.8	17 2 Q7M1I3	Q7ml13 phaseolus v
23	22	52.4	12 2 Q7M4X9	Q7m4x9 fusarium sp
24	22	52.4	15 1 URE2_MORMO	P17338 morganelia
25	22	52.4	16 2 Q9TRR1	Q9trr1 oryctolagus
26	22	52.4	17 1 A45K_MYCBO	P80069 mycobacteri
27	22	52.4	17 2 Q90XE2	Q90xe2 gallus gall
28	22	52.4	18 2 Q6DNI9	Q6dni9 oncorhynch
29	22	52.4	18 2 Q6WTX0	Q6wtx0 eleutheroda
30	22	52.4	18 2 Q6WTZ8	Q6wtz8 eleutheroda
31	22	52.4	18 2 Q6WU54	Q6wu54 eleutheroda

32	22	52.4	18	2	Q6WU67	Q6wu67 eleutheroda
33	21	50.0	10	2	Q8JV66	Q8jv66 polyomaviru
34	21	50.0	10	2	Q8JV68	Q8jv68 polyomaviru
35	21	50.0	10	2	Q8JV70	Q8jv70 polyomaviru
36	21	50.0	10	2	Q8JV72	Q8jv72 polyomaviru
37	21	50.0	10	2	Q8JV74	Q8jv74 polyomaviru
38	21	50.0	10	2	Q8JV76	Q8jv76 polyomaviru
39	21	50.0	10	2	Q8JV80	Q8jv80 polyomaviru
40	21	50.0	10	2	Q8JV82	Q8jv82 polyomaviru
41	21	50.0	10	2	Q8QV7	Q8qv7 polyomaviru
42	21	50.0	10	2	Q9QV9	Q9qv9 polyomaviru
43	21	50.0	10	2	Q9QW1	Q9qw1 polyomaviru
44	21	50.0	10	2	Q9QW3	Q9qw3 polyomaviru
45	21	50.0	10	2	Q9QW5	Q9qw5 polyomaviru
46	21	50.0	10	2	Q9QW7	Q9qw7 polyomaviru
47	21	50.0	10	2	Q9QW9	Q9qw9 polyomaviru
48	21	50.0	10	2	Q9QX1	Q9qx1 polyomaviru
49	21	50.0	10	2	Q9QX3	Q9qx3 polyomaviru
50	21	50.0	10	2	Q9QX5	Q9qx5 polyomaviru
51	21	50.0	10	2	Q9QX9	Q9qx9 polyomaviru
52	21	50.0	11	2	P82436	P82436 nicotiana t
53	21	50.0	11	2	Q8UUP1	Q8uup1 xenopus lae
54	21	50.0	12	2	Q9BZ49	Q9bz49 homo sapien
55	21	50.0	12	2	Q6X7V1	Q6x7v1 canis famil
56	21	50.0	12	2	Q93X21	Q93x21 zea mays (m
57	21	50.0	13	2	Q6LBR0	Q6lbr0 pseudomonas
58	21	50.0	14	2	Q7M3M4	Q7m3m4 pisaster oc
59	21	50.0	15	1	PRP_MYCBO	P80149 mycobacteri
60	21	50.0	15	1	UC25_MAIZE	P80635 zea mays (m
61	21	50.0	15	2	Q9UC2	Q9ucc2 homo sapien
62	21	50.0	15	2	Q9TR14	Q9tr14 bos taurus
63	21	50.0	15	2	Q9S8N8	Q9s8n8 hordeum vul
64	21	50.0	15	2	Q7LZM6	Q7lzm6 human herpe
65	21	50.0	15	2	Q6WFA4	Q6wfa4 sturnus vul
66	21	50.0	15	2	Q6WFA5	Q6wfa5 anas platyr
67	21	50.0	15	2	Q6WFA6	Q6wfa6 podager nac
68	21	50.0	15	2	Q6WFA7	Q6wfa7 falco pereg
69	21	50.0	15	2	Q6WFA8	Q6wfa8 strix urale
70	21	50.0	15	2	Q6WFA9	Q6wfa9 surina ulul
71	21	50.0	15	2	Q6WFB0	Q6wfb0 tyto alba (
72	21	50.0	16	1	IBP4_PIG	P24854 sus scrofa
73	21	50.0	17	2	Q14001	Q14001 homo sapien
74	21	50.0	17	2	Q9TR22	Q9tr22 bos taurus
75	21	50.0	17	2	O49225	O49225 glycine max
76	21	50.0	18	2	Q8NFB4	Q8nfb4 homo sapien
77	21	50.0	18	2	Q9H1I3	Q9h1i3 homo sapien
78	21	50.0	18	2	Q9JIE9	Q9jie9 mus musculu
79	21	50.0	18	2	Q8QFT3	Q8qft3 gallus gall
80	20	47.6	9	2	Q9UCS8	Q9ucs8 homo sapien
81	20	47.6	11	2	Q8IVG8	Q8ivg8 homo sapien
82	20	47.6	12	2	P82441	P82441 nicotiana t
83	20	47.6	13	2	Q7M3T0	Q7m3t0 dictyosteli
84	20	47.6	13	2	O67604	O67604 squash leaf
85	20	47.6	16	1	FOR2_MYRGU	P81437 myrmecia gu
86	20	47.6	16	2	Q8RVF4	Q8rvf4 zea mays (m
87	20	47.6	17	2	Q96P96	Q96p96 homo sapien
88	19.5	46.4	17	2	Q9TR78	Q9tr78 didelphis m
89	19	45.2	9	2	Q9UMF3	Q9umf3 homo sapien
90	19	45.2	9	2	P82429	P82429 nicotiana t
91	19	45.2	9	2	Q6QVK7	Q6qvk7 phaseolus v
92	19	45.2	10	1	PNAS_PRUDU	P81898 prunus dulc
93	19	45.2	10	2	Q6QVG6	Q6qvg6 phaseolus v
94	19	45.2	11	1	BPP3_BOTIN	P30423 bothrops in
95	19	45.2	11	1	BPP4_BOTIN	P30424 bothrops in
96	19	45.2	11	1	BPPB_AGKHA	P01021 agkistrodon
97	19	45.2	11	1	MORN_HUMAN	P01163 homo sapien
98	19	45.2	11	2	Q80W11	Q80w11 mus sp. nt-
99	19	45.2	12	1	FIF1_SARBU	P83349 sarcophaga
100	19	45.2	12	2	P82328	P82328 pisum sativ

ALIGNMENTS

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RESULT 1
APID_BOMPA
ID APID_BOMPA STANDARD; PRT; 17 AA.
AC P81464;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Apidaecin.
OS Bombus pascuorum (Brown bumble bee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=65598;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RX MEDLINE=97362903; PubMed=9219367; DOI=10.1016/S0965-1748(97)00013-1;
RA Rees J.A., Moniatte M., Bulet P.;
RT "Novel antibacterial peptides isolated from a European bumblebee,
RT Bombus pascuorum (Hymenoptera, Apoidea).";
RL Insect Biochem. Mol. Biol. 27:413-422(1997).
CC -!- FUNCTION: Antibacterial peptide active against Gram-negative
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By bacterial infection.
CC -!- SIMILARITY: Belongs to the apidaecin family.
DR InterPro; IPR004828; Apidaecin.
DR Pfam; PF00807; Apidaecin; 1.
KW Antibiotic; Direct protein sequencing; Hemolymph; Insect immunity.
SQ SEQUENCE 17 AA; 1963 MW; CD1DD02C8BC23D1 CRC64;

Query Match 61.9%; Score 26; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 8 PPRP 12

RESULT 2
Q9UCT9
ID Q9UCT9 PRELIMINARY; PRT; 18 AA.
AC Q9UCT9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE PRG=PROLINE-rich glycoprotein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=91373355; PubMed=1894623;
RA Gillette-Castro B.L., Prakobphol A., Burlingame A.L., Leffler H.,
RA Fisher S.J.;
RT "Structure and bacterial receptor activity of a human salivary
RT proline-rich glycoprotein.";
RL J. Biol. Chem. 266:17358-17368(1991).
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0008368; F:Gram-negative bacterial binding; NAS.
DR GO; GO:0009618; P:response to pathogenic bacteria; NAS.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1780 MW; 961F6FBOA83D2E40 CRC64;

Query Match 61.9%; Score 26; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPPLP 7

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Db 4 PPRP 8

RESULT 3
TMOF_AEDAE
ID TMOF_AEDAE STANDARD; PRT; 10 AA.
AC P19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like
RT enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=8353526; DOI=10.1016/0965-1748(93)90044-S;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
RT modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
CC in the midgut which indirectly reduces the vitellogenin
CC concentration in the hemolymph resulting in inhibition of oocyte
CC development.
CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular
CC epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs
CC and stops at 56 hrs.
DR PIR; A36454; A36454.
KW Direct protein sequencing; Hormone.
FT DOMAIN 3 10 Poly-Pro.
FT VARIANT 1 2 YD -> DY (in TMOF(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A777776DC7 CRC64;

Query Match 59.5%; Score 25; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 5 PPRP 9

RESULT 4
P82439
ID P82439 PRELIMINARY; PRT; 15 AA.
AC P82439;
DT 01-JUN-2000 (TRENBLrel. 14, Created)
DT 01-JUN-2000 (TRENBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE ~200 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed

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RT tobacco culture.";
 RL Planta 0:0-0(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 DR GO; GO:0005618; C:cell wall; IEA.
 KW Cell wall; Hydroxylation.
 FT MOD_RES 6
 FT NON_TER 15 15 HYDROXYLATION.
 SQ SEQUENCE 15 AA; 1870 MW; 3E1E05A20A3C5681 CRC64;
 Query Match 59.5%; Score 25; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 PPLP 7
 Db 6 PPLP 10

RESULT 5
 Q7M1V1
 ID Q7M1V1 PRELIMINARY; PRT; 15 AA.
 AC Q7M1V1
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Light harvesting complex chain III/b, photosystem I (Fragment).
 OS Oryza sativa (Rice).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Eriaraloideae; Oryzeae; Oryza.
 CC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE.
 RA Uchiyama Y., Tsugita A.;
 RL Submitted (JUN-1991) to the PIR data bank.
 DR PIR; P70037; P70037.
 DR Gramene; Q7M1V1; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1441 MW; 3D92222733333672 CRC64;
 Query Match 59.5%; Score 25; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 PPLP 7
 Db 8 PPLP 12

RESULT 6
 Q7M137
 ID Q7M137 PRELIMINARY; PRT; 16 AA.
 AC Q7M137;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Superoxide dismutase (EC 1.15.1.1) (Fragment).
 OS unidentified bacterium.
 CC Bacteria; environmental samples.
 CC NCBI_TaxID=2338;
 RN [1]
 RP SEQUENCE.
 RA Binette J.P., Binette M.B.;
 RL Submitted (OCT-1996) to the PIR data bank.
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems (By similarity).
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 CC family.
 DR PIR; E58503; E58503.
 DR GO; GO:0046872; P:metal ion binding; IEA.

DR GO; GO:0016491; P:oxidoreductase activity; IEA.
 DR GO; GO:0004784; P:superoxide dismutase activity; IEA.
 DR GO; GO:0006801; P:superoxide metabolism; IEA.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; Sod_Fe_N; 1.
 KW Oxidoreductase.
 FT NON_TER 16
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1828 MW; 12DE78949AC43609 CRC64;
 Query Match 59.5%; Score 25; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 PPLP 7
 Db 6 PPLP 9

RESULT 7
 Q41400
 ID Q41400 PRELIMINARY; PRT; 17 AA.
 AC Q41400;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Hydroxyproline-rich protein (Fragment).
 OS Sesbania rostrata.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.
 CC NCBI_TaxID=3895;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bacterial infected stem located root primordia;
 EX MEDLINE=96112737; PubMed=8664492;
 RA Coormachtig S., Valerio-Lepiniec M., Szczylowski K., Van Montagu M.,
 RA Holsters M., De Bruijn F.;
 RT "Use of differential display to identify novel Sesbania rostrata genes
 RT enhanced by Azorhizobium caulinodans infection.";
 RL Mol. Plant Microbe Interact. 8:816-824(1995).
 DR EMBL; Z48673; CAA88592.1; -.
 DR PIR; S57991; S57991.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;
 Query Match 59.5%; Score 25; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 PPLP 7
 Db 10 PPLP 14

RESULT 8
 Q84129
 ID Q84129 PRELIMINARY; PRT; 18 AA.
 AC Q84129;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Influenza A/Swine/Wisconsin/0W/2 (H1N1), non-structural protein (seg
 DE 8), COOH terminus of NS1. (Fragment).
 OS Influenza A virus.
 CC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 CC Influenzavirus A.
 CC NCBI_TaxID=11320;
 RN [1]
 RP SEQUENCE FROM N.A.
 EX MEDLINE=63303830; PubMed=6612993;
 RA Parvin J.D., Young J.P., Palese P.;
 RT "Nonsense mutations affecting the lengths of the NS1 nonstructural
 RT proteins of influenza A virus isolates.";

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RL Virology 128:512-517(1983).
DR EMBL; K00959; AAA43541.1; -.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu_NSI.
DR Pfam; PF00600; Flu_NSI; 1.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2105 MW; 87174BD420FEBEF CRC64;

Query Match 59.5%; Score 25; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 11 PPLP 14

RESULT 9
Q9TWV0 PRELIMINARY; PRT; 9 AA.
AC Q9TWV0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Antho-RPAMIDE-NEUROPEPTIDE.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actinilidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=93126143; PubMed=1480510; DOI=10.1016/0196-9781(92)90040-A;
RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPamide),
RT an N-terminally protected, biologically active neuropeptide from sea
RT anemones";
RL Peptides 13:851-857(1992).
SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 57.1%; Score 24; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MQPPLP 7
Db 1 LPPGFLP 7

RESULT 10
Q6W631 PRELIMINARY; PRT; 16 AA.
AC Q6W631;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Photosystem II subunit T (Fragment).
GN Name=psbt;
OS Sphagnum cuspidatum (Bog moss).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.
OX NCBI_TaxID=41840;
RN [1]
RP SEQUENCE FROM N.A.
RA Shaw A.J., Cox C.J., Boles S.B.;
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have
RT no roots?";
RL Am. J. Bot. 90:1777-1787(2003).
DR EMBL; AY309629; AAP70619.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1843 MW; 56167D25E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7
Db 6 EPPKIP 11

RESULT 11
Q6W322 PRELIMINARY; PRT; 18 AA.
AC Q6W322;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Photosystem II subunit T (Fragment).
GN Name=psbt;
OS Andreaea rothii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Andreaeopsida; Andreaeales; Andreaeaceae; Andreaea.
OX NCBI_TaxID=50745;
RN [1]
RP SEQUENCE FROM N.A.
RA Shaw A.J., Cox C.J., Boles S.B.;
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have
RT no roots?";
RL Am. J. Bot. 90:1777-1787(2003).
DR EMBL; AY312864; AAQ8205.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2143 MW; 2FA4E675E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7
Db 8 EPPKIP 13

RESULT 12
Q6W619 PRELIMINARY; PRT; 18 AA.
AC Q6W619;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Photosystem II subunit T (Fragment).
GN Name=psbt;
OS Sphagnum wulfianum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.
OX NCBI_TaxID=128256;
RN [1]
RP SEQUENCE FROM N.A.
RA Shaw A.J., Cox C.J., Boles S.B.;
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have
RT no roots?";
RL Am. J. Bot. 90:1777-1787(2003).
DR EMBL; AY309633; AAP70629.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2143 MW; 2FA4E675E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7
Db 8 EPPKIP 13

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Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7
:||:|
Db 8 EPPKIP 13

RESULT 13

Q6W622 PRELIMINARY; PRT; 18 AA.
AC Q6W622; (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Photosystem II subunit T (Fragment).
GN Name=p8bt;
OS Sphagnum squarrosum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.
OX NCBI_TaxID=128240;
RN [1]
RP SEQUENCE FROM N.A.
RA Shaw A.J., Cox C.J., Boles S.B.;
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have
no roots?";
RL Am. J. Bot. 90:1777-1787(2003).
DR EMBL; AY309632; AAP70626.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2143 MW; 2FA4B675E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7
:||:|
Db 8 EPPKIP 13

RESULT 14

Q6W628 PRELIMINARY; PRT; 18 AA.
AC Q6W628; (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Photosystem II subunit T (Fragment).
GN Name=p8bt;
OS Sphagnum lapazense.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.
OX NCBI_TaxID=231110;
RN [1]
RP SEQUENCE FROM N.A.
RA Shaw A.J., Cox C.J., Boles S.B.;
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have
no roots?";
RL Am. J. Bot. 90:1777-1787(2003).
DR EMBL; AY309630; AAP70621.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2143 MW; 2FA4B675E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7

Db :||:|
8 EPPKIP 13

RESULT 15

Q6W634 PRELIMINARY; PRT; 18 AA.
AC Q6W634; (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Photosystem II subunit T (Fragment).
GN Name=p8bt;
OS Sphagnum sericeum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.
OX NCBI_TaxID=128237;
RN [1]
RP SEQUENCE FROM N.A.
RA Shaw A.J., Cox C.J., Boles S.B.;
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have
no roots?";
RL Am. J. Bot. 90:1777-1787(2003).
DR EMBL; AY309628; AAP70616.1; -.
DR EMBL; AY309631; AAP70623.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2143 MW; 2FA4B675E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7
:||:|
Db 8 EPPKIP 13

RESULT 16

Q6W637 PRELIMINARY; PRT; 18 AA.
AC Q6W637; (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Photosystem II subunit T (Fragment).
GN Name=p8bt;
OS Sphagnum affine.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.
OX NCBI_TaxID=128174;
RN [1]
RP SEQUENCE FROM N.A.
RA Shaw A.J., Cox C.J., Boles S.B.;
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have
no roots?";
RL Am. J. Bot. 90:1777-1787(2003).
DR EMBL; AY309627; AAP70611.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2143 MW; 2FA4B675E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7
:||:|
Db 8 EPPKIP 13

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 17
BPP_AGRHP STANDARD; PRT; 11 AA.
ID P04562;
AC 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE Bradykinin-potentiating peptide (Angiotensin-converting enzyme
inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys
pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -|- FUNCTION: This peptide both inhibits the activity of the
angiotensin-converting enzyme and enhances the action of
bradykinin by inhibiting the kinases that inactivate it. It acts
as an indirect hypotensive agent.
DR PIR; JC0002; XAVIBH.
KW Direct protein sequencing; Hypotensive agent;
KW Pyrrolidone carboxylic acid. Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
SQ SEQUENCE 11 AA; 1112 MW; 30B8F127686777 CRC64;

Query Match 54.8%; Score 23; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
DB 7 PPPI 10

RESULT 18
TY13_PHYRO STANDARD; PRT; 13 AA.
ID P04096;
AC 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DE Tridecapeptide from Phyllomedusa rohdei".
RL Int. J. Pept. Protein Res. 27:175-182(1986).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
DR PIR; A05174; A05174.
KW Amphibian defense peptide; Direct protein sequencing;
KW Pyrrolidone carboxylic acid. Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
SQ SEQUENCE 13 AA; 1646 MW; 33BF3A212227773 CRC64;

Query Match 54.8%; Score 23; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY 3 PPPL 6
DB 7 PPPI 10

RESULT 19
Q7LZ51 PRELIMINARY; PRT; 13 AA.
ID Q7LZ51;
AC Q7LZ51;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Tryptophyllin-related peptide.
OS Phyllomedusa bicolor (Two-colored leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8393;
RN [1]
RP SEQUENCE.
RX MEDLINE=92339502; PubMed=1633846; DOI=10.1016/0014-5793(92)80427-I;
RA Mignogna G., Severini C., Simmaco M., Negri L.,
RA Falconieri Erspamer G., Kreil G., Barra D.;
RT "Identification and characterization of two dermorphins from skin
extracts of the Amazonian frog Phyllomedusa bicolor.";
RL FEBS Lett. 302:151-154(1992).
DR PIR; S21152; S21152.
SQ SEQUENCE 13 AA; 1575 MW; 094C33A21BC5777B CRC64;

Query Match 54.8%; Score 23; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 6
DB 7 PPPI 10

RESULT 20
TY13_BOMVA STANDARD; PRT; 14 AA.
ID TY13_BOMVA;
AC P84215;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DE Tryptophyllin-13.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
SPECTROMETRY.
RC TISSUE=Skin secretion;
RX PubMed=15134346;
RA Marenah L., Flatt P.R., Orr D.F., McClean S., Shaw C.,
RA Abdel-Wahab Y.H.;
RT "Skin secretion of the toad Bombina variegata contains multiple
insulin-releasing peptides including bombesin and entirely novel
insulinotropic structures.";
RL Biol. Chem. 395:315-321(2004).
CC -|- FUNCTION: Possesses insulin-releasing activity.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- MASS SPECTROMETRY: MW=1650.5; METHOD=Electrospray; RANGE=1-14;
NOTE=Ref.1.
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 14 AA; 1651 MW; 23C4809C33A0DC77 CRC64;

Query Match 54.8%; Score 23; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.1e+03;
```

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 6
Db 6 PPPI 9

RESULT 21

Q7M4X9 PRELIMINARY; PRT; 17 AA.
AC Q9NQY8
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Transcription factor 12 (Fragment).
GN Name=TCF12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gan T.-I., O'Sickey T., Zhang Y., Kim U.-J., Bina M.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF271610; AAF82574.1;
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1802 MW; E26E7FB1D7903679 CRC64;

Query Match 54.8%; Score 23; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 3.8e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 11 PPGLP 15

RESULT 22

Q7M1I3 PRELIMINARY; PRT; 17 AA.
AC Q7M1I3
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hydroxyproline-rich cell wall glycoprotein, 230K (Fragment).
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP SEQUENCE.
RX MEDLINE=96011753; PubMed=7548925;
RA Wojtaezek P., Trethowan J., Bolwell G.P.;
RT "Specificity in the immobilisation of cell wall proteins in response
RT to different elicitor molecules in suspension-cultured cells of French
RT bean (Phaseolus vulgaris L.).";
RL Plant Mol. Biol. 28:1075-1087(1995).
DR PIR; S59481; S59481.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1929 MW; 7C0525B0179CE555 CRC64;

Query Match 54.8%; Score 23; DB 2; Length 17;
Best Local Similarity 57.1%; Pred. No. 3.8e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
Db 2 MYLPVP 8

RESULT 23

Q7M4X9 PRELIMINARY; PRT; 12 AA.
AC Q7M4X9
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Ribosomal protein S3 (Fragment).
OS Fusarium sporotrichioides.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5514;
RN [1]
RP SEQUENCE.
RA Chow L.P., Fukaya N., Sugiyama Y., Ueno Y., Tabuchi K., Taugita A.;
RL Submitted (OCT-1994) to the PIR data bank.
DR PIR; PA0098; PA0098.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1242 MW; 227EFCBA7C2772D7 CRC64;

Query Match 52.4%; Score 22; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 3.7e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 4 PPVP 7

RESULT 24

URE2 MORMO STANDARD; PRT; 15 AA.
AC P17338;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Urease beta subunit (EC 3.5.1.5) (15 kDa subunit) (Urea
DE amidohydrolase) (Fragment).
GN Name=ureB;
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE.
RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -1- SUBUNIT: Alpha, beta, gamma(3) (By similarity).
CC -1- SIMILARITY: Belongs to the urease beta subunit family.
DR PIR; B35389; B35389.
KW Direct protein sequencing; Hydrolase.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1530 MW; 2D98944F2F20C7E8 CRC64;

Query Match 52.4%; Score 22; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPL 6
Db 5 QPTPL 9

RESULT 25

Q9TRR1 PRELIMINARY; PRT; 16 AA.
ID Q9TRR1
AC Q9TRR1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Fibronectin 47 kDa fragment (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=92283375; PubMed=1597256;
RA Lesot H., Fausser J.L., Akiyama S.K., Staub A., Black D., Kubler M.D.,
RA Ruch J.V.;
RT "The carboxy-terminal extension of the collagen binding domain of
RT fibronectin mediates interaction with a 165 kDa membrane protein
RT involved in odontoblast differentiation."
RL Differentiation 49:109-118(1992).
FT NON_TER 1
FT NON_TER 16
FT NON_TER 1
SQ SEQUENCE 16 AA; 1764 MW; B196CAAAC53F5739 CRC64;

Query Match 52.4%; Score 22; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPPLP 7
Db 1 QPQHP 6

RESULT 26
A45K MYCBO
ID A45K MYCBO STANDARD; PRT; 17 AA.
AC P80069;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 45/47 kDa antigen (Fragment).
OS Mycobacterium bovis
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE.
RC STRAIN=BCG / Paris 1173 P2;
RX MEDLINE=93138802; PubMed=8423100;
RA Romain F., Laqueyrie A., Miltzer P., Pescher P., Chavarot P.,
RA Lagranderie M., Auregan G., Gheorghiu M., Marchal G.A.;
RT "Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen
RT complex, an immunodominant target for antibody response after
RT immunization with living bacteria."
RL Infect. Immun. 61:742-750(1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: To M.leprae NL43, and M.tuberculosis MPT32.
DR PIR; A49237; A49237.
KW Antigen; Direct protein sequencing.
FT NON_TER 17
FT NON_TER 17
SQ SEQUENCE 17 AA; 1521 MW; 4492CC389D9D9893 CRC64;

Query Match 52.4%; Score 22; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 6 PPVP 9

RESULT 27
Q90XE2
ID Q90XE2 PRELIMINARY; PRT; 17 AA.
AC Q90XE2;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)

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DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Transforming growth factor beta 4 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22533207; PubMed=12646161; DOI=10.1016/S0006-291X(03)00300-0;
RA Pan H.J., Halper J.;
RT "Cloning, expression, and characterization of chicken transforming
RT growth factor beta 4."
RL Biochem. Biophys. Res. Commun. 303:24-30(2003).
DR EMBL; AF395834; AAL05481.1; -.
FT NON_TER 17
FT NON_TER 17
SQ SEQUENCE 17 AA; 1721 MW; 5080B3551E71BD63 CRC64;

Query Match 52.4%; Score 22; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 5.4e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQPPPL 6
Db 1 MDPSPL 6

RESULT 28
Q6DNI9
ID Q6DNI9 PRELIMINARY; PRT; 18 AA.
AC Q6DNI9;
DT 25-OCT-2004 (TremBLrel. 28, Created)
DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TremBLrel. 28, Last annotation update)
DE Urotensin I (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Bernier N.J., Craig P.M.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AY651778; AAT70095.1; -.
FT NON_TER 18
FT NON_TER 18
SQ SEQUENCE 18 AA; 1945 MW; ABC326A1540B8366 CRC64;

Query Match 52.4%; Score 22; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 5.7e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPL 6
Db 1 MKPVPL 6

RESULT 29
Q6WTX0
ID Q6WTX0 PRELIMINARY; PRT; 18 AA.
AC Q6WTX0;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Cellular myelocytomatosis (fragment).
GN Name=c-myc;
OS Eutherodactylus persimilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
OC Telmatobatinae; Eleutherodactylus.
OX NCBI_TaxID=228453;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=22850980; PubMed=12969459;
RA Crawford A.J.;
RT "Huge populations and old species of Costa Rican and Panamanian dirt
RT frogs inferred from mitochondrial and nuclear gene sequences.";
RL Mol. Ecol. 12:2525-2540(2003).
DR EMBL; AY269379; AAQ01124.1; -
DR EMBL; AY269380; AAQ01125.1; -
DR EMBL; AY269381; AAQ01126.1; -
DR EMBL; AY269382; AAQ01127.1; -
DR EMBL; AY269383; AAQ01128.1; -
DR EMBL; AY269384; AAQ01129.1; -
DR EMBL; AY269385; AAQ01130.1; -
DR EMBL; AY269386; AAQ01131.1; -
DR EMBL; AY269387; AAQ01132.1; -
DR EMBL; AY269388; AAQ01133.1; -
DR EMBL; AY269389; AAQ01134.1; -
DR EMBL; AY269390; AAQ01135.1; -
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1882 MW; 7F844740EE93A30 CRC64;

Query Match 52.4%; Score 22; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPL 6
Db 4 METPPI 9

RESULT 30
Q6WT28
ID Q6WT28 PRELIMINARY; PRT; 18 AA.
AC Q6WT28;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cellular myelocytomatosis (fragment).
GN Name=c-myc;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
OC Telmatobinae; Eleutherodactylus.
OX NCBI_TaxID=228451;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22850980; PubMed=12969459;
RA Crawford A.J.;
RT "Huge populations and old species of Costa Rican and Panamanian dirt
RT frogs inferred from mitochondrial and nuclear gene sequences.";
RL Mol. Ecol. 12:2525-2540(2003).
DR EMBL; AY269351; AAQ01096.1; -
DR EMBL; AY269352; AAQ01097.1; -
DR EMBL; AY269353; AAQ01098.1; -
DR EMBL; AY269354; AAQ01099.1; -
DR EMBL; AY269355; AAQ01100.1; -
DR EMBL; AY269356; AAQ01101.1; -
DR EMBL; AY269357; AAQ01102.1; -
DR EMBL; AY269358; AAQ01103.1; -
DR EMBL; AY269359; AAQ01104.1; -
DR EMBL; AY269360; AAQ01105.1; -
DR EMBL; AY269361; AAQ01106.1; -
DR EMBL; AY269362; AAQ01107.1; -
DR EMBL; AY269363; AAQ01108.1; -
DR EMBL; AY269364; AAQ01109.1; -
DR EMBL; AY269365; AAQ01110.1; -
DR EMBL; AY269366; AAQ01111.1; -
DR EMBL; AY269367; AAQ01112.1; -
DR EMBL; AY269368; AAQ01113.1; -
DR EMBL; AY269369; AAQ01114.1; -
DR EMBL; AY269370; AAQ01115.1; -
DR EMBL; AY269371; AAQ01116.1; -
DR EMBL; AY269372; AAQ01117.1; -

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DR EMBL; AY269373; AAQ01118.1; -
DR EMBL; AY269374; AAQ01119.1; -
DR EMBL; AY269375; AAQ01120.1; -
DR EMBL; AY269377; AAQ01122.1; -
DR EMBL; AY269378; AAQ01123.1; -
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1882 MW; 7F844740EE93A30 CRC64;

Query Match 52.4%; Score 22; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPL 6
Db 4 METPPI 9

RESULT 31
Q6WU54
ID Q6WU54 PRELIMINARY; PRT; 18 AA.
AC Q6WU54;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cellular myelocytomatosis (fragment).
GN Name=c-myc;
OS Eleutherodactylus stejnegerianus (Stejneger's rainfrog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
OC Telmatobinae; Eleutherodactylus.
OX NCBI_TaxID=228449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22850980; PubMed=12969459;
RA Crawford A.J.;
RT "Huge populations and old species of Costa Rican and Panamanian dirt
RT frogs inferred from mitochondrial and nuclear gene sequences.";
RL Mol. Ecol. 12:2525-2540(2003).
DR EMBL; AY269295; AAQ01040.1; -
DR EMBL; AY269296; AAQ01041.1; -
DR EMBL; AY269297; AAQ01042.1; -
DR EMBL; AY269298; AAQ01043.1; -
DR EMBL; AY269299; AAQ01044.1; -
DR EMBL; AY269300; AAQ01045.1; -
DR EMBL; AY269301; AAQ01046.1; -
DR EMBL; AY269302; AAQ01047.1; -
DR EMBL; AY269303; AAQ01048.1; -
DR EMBL; AY269304; AAQ01049.1; -
DR EMBL; AY269305; AAQ01050.1; -
DR EMBL; AY269306; AAQ01051.1; -
DR EMBL; AY269307; AAQ01052.1; -
DR EMBL; AY269308; AAQ01053.1; -
DR EMBL; AY269309; AAQ01054.1; -
DR EMBL; AY269310; AAQ01055.1; -
DR EMBL; AY269311; AAQ01056.1; -
DR EMBL; AY269312; AAQ01057.1; -
DR EMBL; AY269313; AAQ01058.1; -
DR EMBL; AY269314; AAQ01059.1; -
DR EMBL; AY269315; AAQ01060.1; -
DR EMBL; AY269316; AAQ01061.1; -
DR EMBL; AY269317; AAQ01062.1; -
DR EMBL; AY269318; AAQ01063.1; -
DR EMBL; AY269319; AAQ01064.1; -
DR EMBL; AY269320; AAQ01065.1; -
DR EMBL; AY269321; AAQ01066.1; -
DR EMBL; AY269322; AAQ01067.1; -
DR EMBL; AY269323; AAQ01068.1; -
DR EMBL; AY269324; AAQ01069.1; -
DR EMBL; AY269325; AAQ01070.1; -
DR EMBL; AY269326; AAQ01071.1; -
DR EMBL; AY269327; AAQ01072.1; -
DR EMBL; AY269328; AAQ01073.1; -

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DR EMBL; AY269329; AAQ01074.1; -
 DR EMBL; AY269330; AAQ01075.1; -
 DR EMBL; AY269331; AAQ01076.1; -
 DR EMBL; AY269332; AAQ01077.1; -
 DR EMBL; AY269333; AAQ01078.1; -
 DR EMBL; AY269334; AAQ01079.1; -
 DR EMBL; AY269335; AAQ01080.1; -
 DR EMBL; AY269336; AAQ01081.1; -
 DR EMBL; AY269337; AAQ01082.1; -
 DR EMBL; AY269338; AAQ01083.1; -
 DR EMBL; AY269339; AAQ01084.1; -
 DR EMBL; AY269340; AAQ01085.1; -
 DR EMBL; AY269341; AAQ01086.1; -
 DR EMBL; AY269342; AAQ01087.1; -
 DR EMBL; AY269343; AAQ01088.1; -
 DR EMBL; AY269344; AAQ01089.1; -
 DR EMBL; AY269345; AAQ01090.1; -
 DR EMBL; AY269346; AAQ01091.1; -
 DR EMBL; AY269347; AAQ01092.1; -
 DR EMBL; AY269348; AAQ01093.1; -
 DR EMBL; AY269349; AAQ01094.1; -
 DR EMBL; AY269350; AAQ01095.1; -
 FT NON_TER 1
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1882 MW; 7F844740EE93A30 CRC64;

Query Match 52.4%; Score 22; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 5.7e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPPP 6
 | : |||
 Db 4 METPPI 9

RESULT 32
 Q6WU67 PRELIMINARY; PRT; 18 AA.
 ID Q6WU67;
 AC Q6WU67;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Cellular myelocytomatosis (Fragment).
 GN Name=c-myc;
 OS Eleutherodactylus bransfordii (Bransford's litter frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
 OC Telmatobiinae; Eleutherodactylus.
 OC NCBI_TaxID=228452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22850980; PubMed=12969459;
 RA Crawford A.J.;
 RT "Huge populations and old species of Costa Rican and Panamanian dirt
 RT frogs inferred from mitochondrial and nuclear gene sequences.";
 RL Mol. Ecol. 12:2525-2540(2003).
 DR EMBL; AY269282; AAQ01027.1; -
 DR EMBL; AY269283; AAQ01028.1; -
 DR EMBL; AY269284; AAQ01029.1; -
 DR EMBL; AY269285; AAQ01030.1; -
 DR EMBL; AY269286; AAQ01031.1; -
 DR EMBL; AY269287; AAQ01032.1; -
 DR EMBL; AY269288; AAQ01033.1; -
 DR EMBL; AY269289; AAQ01034.1; -
 DR EMBL; AY269290; AAQ01035.1; -
 DR EMBL; AY269292; AAQ01037.1; -
 DR EMBL; AY269293; AAQ01038.1; -
 DR EMBL; AY269294; AAQ01039.1; -
 DR EMBL; AY269281; AAQ01026.1; -
 FT NON_TER 1
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1882 MW; 7F844740EE93A30 CRC64;

Query Match 52.4%; Score 22; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 5.7e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPPP 6
 | : |||
 Db 4 METPPI 9

RESULT 33
 Q8JUV66 PRELIMINARY; PRT; 10 AA.
 ID Q8JUV66;
 AC Q8JUV66;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OC NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21465052; PubMed=11581397;
 RX DOI=10.1128/JVI.75.21.10290-10299.2001;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL; AF304389; AAM97808.1; -
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 |||
 Db 7 PPP 9

RESULT 34
 Q8JUV68 PRELIMINARY; PRT; 10 AA.
 ID Q8JUV68;
 AC Q8JUV68;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OC NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21465052; PubMed=11581397;
 RX DOI=10.1128/JVI.75.21.10290-10299.2001;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL; AF304388; AAM97806.1; -
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 |||
 Db 7 PPP 9

```

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304387; AAM97804.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 35
Q8JV70 PRELIMINARY; PRT; 10 AA.
AC Q8JV70;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304387; AAM97804.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 36
Q8JV72 PRELIMINARY; PRT; 10 AA.
AC Q8JV72;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304386; AAM97802.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 37
Q8JV74 PRELIMINARY; PRT; 10 AA.
ID Q8JV74
AC Q8JV74;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

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DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303948; AAM97800.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 38
Q8JV76 PRELIMINARY; PRT; 10 AA.
ID Q8JV76
AC Q8JV76;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303947; AAM97798.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 39
Q8JV80 PRELIMINARY; PRT; 10 AA.
ID Q8JV80
AC Q8JV80;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
RA DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell P.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303945; AAM97794.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 40
Q8JV82
ID Q8JV82 PRELIMINARY; PRT; 10 AA.
AC Q8JV82;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
RA DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell P.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303944; AAM97792.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

Search completed: June 7, 2005, 23:18:47
Job time : 34.8 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 91.4909 Seconds
(without alignments)
71.864 Million cell updates/sec

Title: US-10-691-157-2

Perfect score: 89
Sequence: 1 LQTFQPLLQVMEPQGD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	17	4	AAB72501 Colostrin
2	89	100.0	17	4	AAB59310 Ewe colos
3	89	100.0	17	4	AAB72247 Colostrin
4	89	100.0	17	4	AAB72533 Colostrin
5	89	100.0	17	5	AAO14578 Neural ce
6	89	100.0	17	5	AAW51037 Colostrin
7	89	100.0	17	5	AAE20229 Colostrin
8	89	100.0	17	8	ADN60296 Constitue
9	89	100.0	17	8	ADS74386 Ovine col
10	89	100.0	18	4	AAB59341 Ewe colos
11	56	62.9	11	4	AAE07185 Colostrin
12	56	62.9	12	4	AAE07195 Modified
13	39	43.8	13	7	ADG73339 Enterococ
14	34.5	38.8	15	8	ADN17037 Gi-alpha
15	34	38.2	15	5	ABN99038 Carbamyla
16	33	37.1	12	7	ADC44467 Endotheli
17	33	37.1	15	4	AAE72531 Colostrin
18	33	37.1	15	4	AAB59334 Ewe colos
19	33	37.1	15	4	AAE72279 Colostrin
20	33	37.1	15	4	AAE72563 Colostrin
21	33	37.1	15	5	AAO14610 Neural ce
22	33	37.1	15	5	AAW51066 Colostrin
23	33	37.1	15	5	AAE20261 Colostrin
24	33	37.1	15	8	ADN60328 Constitue
25	33	37.1	15	8	ADS74410 Ovine col

26	32	36.0	8	2	AAR21055	Gamma-car
27	32	36.0	15	6	ABR31148	Human can
28	32	36.0	15	6	ABR31149	Human can
29	32	36.0	15	6	ABR30440	Human can
30	32	36.0	15	6	ABR31517	Human can
31	32	36.0	15	6	ABR30536	Human can
32	32	36.0	15	6	ABR30847	Human can
33	32	36.0	18	8	ADH14837	Glialin r
34	31	34.8	12	3	AAE23189	Hsp47-bin
35	31	34.8	14	4	AAW97279	Human pep
36	31	34.8	14	7	ADP71116	Saccharom
37	31	34.8	15	2	AAW56352	LO-CD2a 1
38	31	34.8	15	2	AAU30191	Framework
39	31	34.8	15	5	AAU74511	Human ATP
40	31	34.8	15	6	ABR38577	Human can
41	31	34.8	15	6	ABR38568	Human can
42	31	34.8	15	6	ABR38729	Human can
43	30	33.7	10	7	ADD15523	Predicted
44	30	33.7	12	8	ADJ57286	Provasopr
45	30	33.7	14	4	AAW96749	Human pep
46	30	33.7	15	5	AAW47320	Human zin
47	30	33.7	15	6	ABR30169	Human can
48	30	33.7	15	6	ABR30262	Human can
49	30	33.7	15	6	ABR30274	Human can
50	30	33.7	15	6	ABR30229	Human can
51	30	33.7	15	6	ABR30154	Human can
52	30	33.7	15	6	ABR31758	Human can
53	30	33.7	15	6	ABR30297	Human can
54	30	33.7	16	3	AAV65560	Oestrogen
55	30	33.7	16	5	AAU86297	Oestrogen
56	30	33.7	16	8	ADM79008	Oestrogen
57	30	33.7	17	4	AAU01845	Wheat pep
58	30	33.7	17	4	AAU01825	Wheat Gli
59	30	33.7	17	8	ADH16206	Glialin r
60	30	33.7	17	8	ADH14681	Glialin r
61	30	33.7	17	8	ADH14675	Glialin r
62	30	33.7	17	8	ADH14695	Glialin r
63	30	33.7	17	8	ADH14646	Glialin r
64	30	33.7	17	8	ADH14646	Glialin r
65	30	33.7	17	8	ADH14602	Glialin r
66	29	32.6	8	6	ABP73085	Amino aci
67	29	32.6	9	5	ABB08361	Synthetic
68	29	32.6	9	7	ABR82213	Human ant
69	29	32.6	10	2	RAY05729	Human G p
70	29	32.6	10	6	ABR05972	Human can
71	29	32.6	10	6	ABR05795	Human can
72	29	32.6	10	6	ABR05791	Human can
73	29	32.6	10	6	ADA14236	Human GPR
74	29	32.6	12	3	AAV92994	Transform
75	29	32.6	12	6	ABU07930	Neisseria
76	29	32.6	13	6	ABP81099	Human TPO
77	29	32.6	15	3	AAV93031	Transform
78	29	32.6	15	3	AAV93032	Transform
79	29	32.6	15	5	ABB09888	N-termina
80	29	32.6	15	6	ABR31395	Human can
81	29	32.6	15	6	ABR30682	Human can
82	29	32.6	15	6	ABR31783	Human can
83	29	32.6	15	6	ABR31394	Human can
84	29	32.6	18	2	AAW66658	HSV-2 gly
85	29	32.6	18	4	AAW20225	Peptide #
86	29	32.6	18	4	ABB40529	Peptide #
87	29	32.6	18	4	AAW34255	Peptide #
88	29	32.6	18	4	ABB24849	Protein #
89	29	32.6	18	4	AAW74093	Human bon
90	29	32.6	18	4	AAW61355	Human bra
91	29	32.6	18	4	ABG55849	Human liv
92	29	32.6	18	5	ABG43991	Human pep
93	29	32.6	18	8	ADH14842	Glialin r
94	28	31.5	7	2	AAW17515	Protein k
95	28	31.5	9	7	ADD99989	Human 193
96	28	31.5	9	7	ADD99556	Human 193
97	28	31.5	9	7	ADD99875	Human 193
98	28	31.5	9	7	ADD99363	Human 193

DR WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for

PT treating central nervous system diseases and bacterial and viral

PT infections, comprises administering colostrinin as an immunological

PT regulator.

XX

XX

PS Claim 1; Page 34; 50pp; English.

XX

CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,

CC a proline rich polypeptide aggregate contained in colostrum. The peptides

CC have immune response modulatory activity, and are capable of inducing

CC cytokines. Colostrinin and its derived peptides are useful for inducing

CC cytokine production, for modulating an immunological response and for

CC inducing blood cell proliferation. The peptides are useful in the

CC treatment of disorders of the central nervous system, neurological

CC disorders, mental disorders, dementia, neurodegenerative diseases,

CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic

CC disorders of the immune system, bacterial and viral infections and

CC acquired immunological deficiencies

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.2e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQLLQVWMEPQGD 17

Db 1 LQTPQLLQVWMEPQGD 17

RESULT 4

AAB72533

ID AAB72533 standard; peptide; 17 AA.

XX

AC AAB72533;

XX

XX 09-MAY-2001 (first entry)

XX

XX Colostrinin peptide #2.

XX

XX Neuroprotective; neural cell differentiation regulator; colostrinin;

KW colostrum.

XX

XX Unidentified.

XX

XX WO200112651-A2.

XX

XX 22-FEB-2001.

XX

XX 17-AUG-2000; 2000WO-US022774.

XX

XX 17-AUG-1999; 99US-0149633P.

XX

XX (TEXA) UNIV TEXAS SYSTEM.

XX

XX Boldogh I;

XX

XX WPI; 2001-226545/23.

XX

XX Use of colostrinin, its constituent peptide or analog as a neural cell

PT regulator, for promoting neural cell differentiation and treating damaged

PT neural cells in a patient.

XX

XX Claim 6; Page 21; 35pp; English.

XX

XX The present invention relates to a method for promoting neural cell

CC differentiation and treating damaged neural cells, using colostrinin and

CC colostrinin constituent peptides (e.g. the present peptide) as a neural

CC cell regulator. Colostrinin is a polypeptide complex found in colostrum

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.2e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQLLQVWMEPQGD 17

Db 1 LQTPQLLQVWMEPQGD 17

RESULT 5

RAO14578

ID AAO14578 standard; peptide; 17 AA.

XX

XX AAO14578;

XX

XX 27-MAY-2002 (first entry)

XX

XX Neural cell regulatory colostrinin peptide 2.

DE

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX

XX Unidentified.

OS

XX

XX Key Location/Qualifiers

FH Modified-site 17

FT /note= "Optional C-terminal amide"

FT

XX

XX WO200213851-A1.

XX

XX 21-FEB-2002.

XX

XX 17-AUG-2000; 2000WO-US022777.

XX

XX 17-AUG-2000; 2000WO-US022777.

PR

XX (TEXA) UNIV TEXAS SYSTEM.

XX

XX Boldogh I, Stanton JG, Hughes TK;

XX

XX WPI; 2002-269152/31.

DR

XX Promoting cell differentiation in a patient involves use of blood cell

PT regulator selected from colostrinin, its constituent peptide and/or

PT analog.

XX

XX Claim 7; Page 21; 37pp; English.

PS

XX The invention comprises a method for promoting cell differentiation (e.g.

CC neural cell differentiation). The method involves contacting cells with a

CC neural cell regulator (i.e. a colostrinin peptide) in order to change the

CC cells in morphology to form neural cells. Colostrinin is a proline-rich

CC polypeptide aggregate that is present in colostrum. The method of the

CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.2e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQLLQVWMEPQGD 17

Db 1 LQTPQLLQVWMEPQGD 17

RESULT 6

AAMS1037

ID AAM51037 standard; peptide; 17 AA.
XX AC AAM51037;
XX 30-MAY-2002 (first entry)
XX DE Colostrinin constituent peptide.
XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;
XX KW blood cell regulator; cytokine inducer; human.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Modified-site 17 /note= "optional C-terminal amidation"
XX FT

XX PN WO200213849-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US022775.

XX PR 17-AUG-2000; 2000WO-US022775.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PA (REGE-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX PI WPI; 2002-269150/31.

XX DR Modulation of blood cell proliferation in a patient involves use of blood
XX PT cell regulator selected from colostrinin, its constituent peptide and/or
XX PT analog.

XX PS Claim 1; Page 34; 54pp; English.

XX CC The present sequence is that of a colostrinin constituent peptide that is
XX CC preferred for use as an immunological regulator and as a blood cell
XX CC regulator in claimed methods of the invention. Methods are claimed for:
XX CC inducing a cytokine in a cell by contact with an immunological regulator,
XX CC where the cell is present in a cell culture, a tissue, an organ or an
XX CC organism, and the cell is mammalian, including human; modulating an
XX CC immune response in a cell by contact with the immunological regulator
XX CC under conditions effective to induce a cytokine; modulating an immune
XX CC response in a patient by administering an immunological regulator under
XX CC conditions effective to induce a cytokine, where the immunological
XX CC regulator is administered topically or as part of a dietary supplement,
XX CC and where the immune response is specific or non specific, an interferon
XX CC response or an antibody response; modulating blood cell proliferation by
XX CC contacting blood cells with a blood cell regulator, where the blood cells
XX CC are present in a cell culture or an organism, are mammalian or human, and
XX CC where the blood cells are increased in number or differentiated; and a
XX CC method for modulating blood cell proliferation in a patent. A claimed
XX CC cytokine-inducing composition comprises a pharmaceutical carrier and an
XX CC active agent such as the present peptide. Cytokines induced by this
XX CC peptide in human leucocyte cultures include interferon-gamma, tumour
XX CC necrosis factor-alpha, interleukin-4, interleukin-6, interleukin-10 and
XX CC interleukin-12. It was one of the best overall inducers in almost all
XX CC cytokine and blood cell proliferation experiments conducted

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQLQVWMEPQGD 17
|||||

DB 1 LQTPQLQVWMEPQGD 17
|||||

RESULT 7
AAE20229
ID AAE20229 standard; peptide; 17 AA.
XX AC AAE20229;

XX DT 18-JUN-2002 (first entry)

XX DE Colostrinin constituent peptide #2.

XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
XX KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
XX KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
XX KW transplantation; implantation; dermatological; vulnetary.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Modified-site 17 /note= "Optionally C-terminal amide"

XX PN WO200213850-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US022776.

XX PR 17-AUG-2000; 2000WO-US022776.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;

XX PI WPI; 2002-269151/31.

XX DR Composition useful for the modulation of blood cell proliferation in a
XX PT patient comprises a blood cell regulator selected from colostrinin, its
XX PT constituent peptide and/or analog.

XX PS Claim 6; Page 25; 51pp; English.

XX CC The invention relates to a composition which comprises a blood cell
XX CC regulator selected from colostrinin, its constituent peptide and/or
XX CC analogue. The invention is used for modulating the oxidative stress level
XX CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
XX CC organ, or organism; or for treating oxidative damage to the skin of a
XX CC patient e.g. animal or human; to modulate oxidative stress during/ after
XX CC a premature birth or normal birth, preventing/delaying aging in a
XX CC patient, enhancing wound healing, and the reduction of side effects of
XX CC cosmetic procedures. The method changes the level of an oxidising species
XX CC in the cell, such as decreases or prevents increase in the level of
XX CC damage to a biomolecule of the patient selected from DNA, protein and/or
XX CC lipid, compared to the same conditions when the oxidative stress
XX CC regulator is not present. The modulation of oxidative stress results in
XX CC enhanced repair, regeneration, and replacement of cells, tissues and
XX CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
XX CC external organs), as well as enhanced preservation of such organs for
XX CC transplantation, implantation, or scientific research. The present
XX CC sequence is a colostrinin constituent peptide

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQLQVWMEPQGD 17
|||||

DB 1 LQTPQLQVWMEPQGD 17
|||||

RESULT 8
ADN60296

ID ADN60296 standard; peptide; 17 AA.
XX AC ADN60296;
XX DT 29-JUL-2004 (first entry)
XX DE Constituent peptide of colostrinin SEQ ID NO:2.
XX KW modulator; colostrinin; intracellular signaling molecule modulator;
KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;
KW DNA damage; beta-amyloid; retinoic acid; cytosolic; 4HNE inhibitor;
KW 4HNE-protein adduct formation reduction;
KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;
KW c-Jun NH2-terminal kinase inhibition.
XX OS Synthetic.
XX PN WO2004037851-A2.
XX PD 06-MAY-2004.
XX PF 22-OCT-2003; 2003WO-US033423.
XX PR 22-OCT-2002; 2002US-0420369P.
XX PA (TEXA) UNIV TEXAS SYSTEM.
PA (BOLD) BOLDOGH I.
PA (STAN) STANTON J G.
PA (GEOR) GEORGIADIS J A.
PA (HUGH) HUGHES T K.
PA (KRUZ) KRUZEL M.
XX PI Bolldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;
XX WPI; 2004-365494/34.
XX DR Use of colostrinin for e.g. modulating an intracellular signaling
XX PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a
XX FT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
XX PT a cell.
XX PA Claim 6; SEQ ID NO 2; 46pp; English.
XX PS The present invention describes the use of a modulator selected from
XX CC colostrinin, its constituent peptide, its active analogue, and a
XX CC combination of these, for modulating an intracellular signaling molecule
XX CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,
XX CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
XX CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
XX CC The modulator has cytostatic activity, and can be used as a 4HNE
XX CC inhibitor. The modulator is useful in the manufacture of a medicament for
XX CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated
XX CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,
XX CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.
XX CC Colostrinin, or its constituent peptide or active analogue is useful for
XX CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
XX CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
XX CC The present sequence represents a synthetic constituent peptide of
XX CC colostrinin, which can be used as a modulator in the present invention.
XX SQ Sequence 17 AA;
Query Match 100.0%; Score 89; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQTPQLLVNMEPQGD 17
Db 1 LQTPQLLVNMEPQGD 17
RESULT 9
ADS74386

ID ADS74386 standard; peptide; 17 AA.
XX AC ADS74386;
XX DT 16-DEC-2004 (first entry)
XX DE Ovine colostrinin peptide.
XX KW Colostrum; colostrinin; sheep; peptide purification.
XX OS Ovis aries.
XX PN WO2004081038-A1.
XX PD 23-SEP-2004.
XX PF 10-MAR-2004; 2004WO-GB001014.
XX PR 11-MAR-2003; 2003GB-00005552.
XX PR 08-MAR-2004; 2004GB-00005190.
XX PA (REGE) REGEN THERAPEUTICS PLC.
XX PI Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;
XX WPI; 2004-677519/66.
XX DR Recovering peptides such as colostrinin from mammalian colostrum, by
XX PT mixing colostrum with alcohol to form alcohol phase containing peptides
XX FT and precipitate, separating alcohol phase from precipitate, and
XX FT recovering alcohol phase.
XX PS Example; SEQ ID NO 1; 41pp; English.
XX CC The present sequence is that of a peptide that can be recovered from
XX CC ovine colostrinin using the method of the invention. The invention
XX CC provides a method for the recovery of peptides (especially colostrinin)
XX CC from colostrum in substantially pure, biologically active form and in
XX CC high yield. The method involves mixing the colostrum with an alcohol to
XX CC form an alcohol phase containing the colostrinin and a precipitate
XX CC containing higher molecular weight caseins and other proteins. Best
XX CC results are obtained using methanol or ethanol of at least 80%, and
XX CC preferably up to 100%, purity. The alcohol phase is then separated from
XX CC the precipitate, and the colostrinin is separated from the alcohol,
XX CC preferably by evaporation, to form a colostrinin-rich phase, which is
XX CC recovered. A precipitation agent, such as ammonium sulfate, may be added
XX CC either to the alcohol phase or, preferably, to the colostrinin-rich phase
XX CC to induce precipitation of the colostrinin peptides. The method is
XX CC generally applicable to the separation of peptides from fluids containing
XX CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic
XX CC acids. In an example from the invention, the antigenic profile of
XX CC peptides recovered from sheep colostrum using the alcohol precipitation
XX CC methods was determined by ELISA using antibodies prepared against 9
XX CC synthetic peptides, including a peptide having the present sequence
XX CC (denoted antigen class A-1).
XX SQ Sequence 17 AA;
Query Match 100.0%; Score 89; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQTPQLLVNMEPQGD 17
Db 1 LQTPQLLVNMEPQGD 17
RESULT 10
AAB59341
ID AAB59341 standard; peptide; 18 AA.
XX AC AAB59341;
XX AC AAB59341;

DT 21-MAR-2001 (first entry)
 XX Ewe colostrinin peptide fragment derived sequence #1.
 DE
 XX
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 OS Ovis sp.
 XX
 PN WO200075173-A2.
 XX
 PD 14-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-GB002128.
 XX
 PR 02-JUN-1999; 99GB-00012852.
 XX
 PA (REGE-) REGEN THERAPEUTICS PLC.
 PI Georgiades JA;
 XX
 DR WPI; 2001-071058/08.
 XX
 XX Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system and
 PT immune system, viral and bacterial infections, and diseases characterized
 PT by amyloid plaques.
 XX
 PS Claim 8; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques
 XX
 XX Sequence 18 AA;
 SQ
 Query Match 100.0%; Score 89; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQTPQPLQLQVMPEQGD 17
 DB 2 LQTPQPLQLQVMPEQGD 18
 RESULT 11
 AAE07185
 ID AAE07185 standard; peptide; 11 AA.
 XX
 AC AAE07185;
 XX
 XX 06-NOV-2001 (first entry)
 DE
 XX
 DE Colostrinin peptide 1.
 KW
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral.
 XX
 OS Unidentified.
 XX
 XX WO200155199-A1.
 PN
 XX 02-AUG-2001.
 PD
 XX

PF 26-JAN-2001; 2001WO-GB000329.
 XX
 PR 26-JAN-2000; 2000GB-00001825.
 XX
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Georgiades JA;
 XX
 DR WPI; 2001-488775/53.
 XX
 XX Peptide useful as an interalia in the treatment of e.g. disorders of the
 PT immune system and the central nervous system comprises ten amino-terminal
 PT amino acid sequence derived from peptides present in colostrinin.
 XX
 PS Claim 1; Page 15; 40pp; English.
 XX
 CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child. The
 CC present sequence is colostrinin peptide 1 related to the invention
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 62.9%; Score 56; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.039;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPLLQVMPEQ 15
 DB 1 QPLLQVMPEQ 11
 RESULT 12
 AAE07195
 ID AAE07195 standard; peptide; 12 AA.
 XX
 AC AAE07195;
 XX
 XX 06-NOV-2001 (first entry)
 DE
 XX
 DE Modified colostrinin cyclic peptide #1.
 KW
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral; cyclic.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 XX
 FT Modified-site 1
 FT /note= "N-terminal acetyl; this residue forms a cyclic
 FT linkage with Gln found at the C-terminal end"
 XX
 XX WO200155199-A1.
 PN
 XX

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PD 02-AUG-2001.
XX
XX
PF 26-JAN-2001; 2001WO-GB000329.
XX
XX
PR 26-JAN-2000; 2000GB-00001825.
XX
XX
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
XX
PI Georgiades JA;
XX
XX
DR WPI; 2001-488775/53.
XX
XX
PT Peptide useful as an interalia in the treatment of e.g. disorders of the
PT immune system and the central nervous system comprises ten amino-terminal
PT amino acid sequence derived from peptides present in colostrinin.
XX
XX
PS Example 2; Page 8; 40pp; English.
XX
XX
CC The invention relates to colostrinin peptide fragments which are useful,
CC inter alia, in the treatment of chronic disorders of the immune system
CC and the central nervous system. Colostrinin peptides are used as a
CC medicament in the treatment of neurological disorders e.g., dementia,
CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
CC neurosis, in acquired immunological deficiencies, chronic bacterial and
CC viral infections and diseases characterised by the presence of beta-
CC amyloid plaques and as a dietary supplement for babies, small children,
CC adults and senile persons, who have been subjected to chemotherapy or
CC have suffered from cachexia or weight loss due to the chronic disease.
CC Colostrinin peptides are also used as food additives and as an auxiliary
CC withdrawal treatment for drug addicts, after a period of detoxification
CC and in persons dependent on stimulants. Colostrinin peptides are used to
CC prepare antibodies and to treat emotional disturbances, e.g. emotional
CC disturbances of psychiatric patients in a state of depression. These
CC colostrinin peptides improves the development of immune system in a new
CC born child and to correct the immunological deficiencies in a child. The
CC present sequence is modified colostrinin cyclic peptide #1 related to the
CC invention
XX
XX
SQ Sequence 12 AA;
Query Match 62.9%; Score 56; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 QPLLQVMEPQ 15
Db 2 QPLLQVMEPQ 12
RESULT 13
ID ADG73339 standard; peptide; 13 AA.
XX
XX
AC ADG73339;
XX
XX
DT 11-MAR-2004 (first entry)
XX
XX
DE Enterococcus faecalis EFG (fusa) epitopic region peptide - SEQ ID 47.
XX
XX
KW (5-methylaminomethyl-2-thiouridylate)-methyltransferase; antibacterial;
KW bacterial infection; antimicrobial; disinfectant; soap; additive;
KW culture media; enzyme; epitopic region; translation elongation factor G;
KW EFG; fusa.
XX
XX
OS Enterococcus faecalis.
XX
XX
FN WO2003083099-A2.
XX
XX
PD 09-OCT-2003.
XX
XX
PF 02-APR-2003; 2003WO-CA000462.
XX
XX

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PR 02-APR-2002; 2002US-0369511P.
PR 31-MAY-2002; 2002US-0385089P.
PR 04-JUN-2002; 2002US-0385751P.
PR 05-JUN-2002; 2002US-0386367P.
PR 05-JUN-2002; 2002US-0386553P.
PR 05-JUN-2002; 2002US-0386566P.
PR 05-JUN-2002; 2002US-0386577P.
PR 06-JUN-2002; 2002US-0386390P.
PR 06-JUN-2002; 2002US-0386601P.
PR 31-JUL-2002; 2002US-0399972P.
PR 05-NOV-2002; 2002US-0424053P.
PR 27-DEC-2002; 2002US-0436804P.
PR 27-DEC-2002; 2002US-0436834P.
PR 27-DEC-2002; 2002US-0436861P.
PR 31-DEC-2002; 2002US-0437281P.
PR 31-DEC-2002; 2002US-0437527P.
XX
XX
PA (AFFI-) AFFINIUM PHARM INC.
XX
XX
PI Edwards A, Dharamsi A, Vedadi M, Alam MZ, Arrowsmith C, Awrey D;
PI Beattie B, Richards D, Canadien V, Domagala M, Houston S;
PI Mansoury K, Li Q, Nethery K, Virag C, Ng I, Ouyang H, Tai M;
PI Thalakada R, Kanagarajah D;
XX
XX
DR WPI; 2003-812543/76.
XX
XX
PS New isolated recombinant bacterial peptides, useful as targets for
PT antibacterial agents, also screening methods and host cells that express
PT them.
XX
XX
PS Disclosure; SEQ ID NO 47; 369pp; English.
XX
XX
CC The invention relates to a novel isolated recombinant polypeptide that
CC has at least one of the biological activities of (5-methylaminomethyl-2-
CC thiouridylate)-methyltransferase of Staphylococcus aureus. The
CC polypeptide of the invention demonstrates antibacterial activity and may
CC be useful for rational design of agents that may be utilised for treating
CC bacterial infections or as general antimicrobials, for example, as
CC disinfectants, soaps or additives for culture media. The current sequence
CC is that of the (5-methylaminomethyl-2-thiouridylate)-methyltransferase-
CC related protein epitopic region peptide of the invention.
XX
XX
SQ Sequence 13 AA;
Query Match 43.8%; Score 39; DB 7; Length 13;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 4 QPLLQVMEPQ 15
Db 2 PDPVIQVAEPK 13
RESULT 14
ADN17037
ID ADN17037 standard; peptide; 15 AA.
XX
XX
AC ADN17037;
XX
XX
DT 15-JUL-2004 (first entry)
XX
XX
DE Gi-alpha 1 GDP-specific phase D peptide motif, SEQ ID 46.
XX
XX
KW G alpha subunit; G protein; G protein coupled receptor; GPCR;
KW allosteric modulator; Gi-alpha 1; GDP-specific phase; D peptide.
XX
XX
OS Unidentified.
XX
XX
FN WO2004035614-A1.
XX
XX
PD 29-APR-2004.
XX
XX
PF 15-JAN-2003; 2003WO-EP000352.
XX
XX

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XX PR 18-OCT-2002; 2002US-0419143P.
XX PA (KARO-) KARO BIO AB.
XX Fowlkes DM, Christensen DJ, Hamilton PT, Blaesus R, Ramer JK;
XX PI Hyde-Deruysscher R, Duffin D, Fredericks Z;
XX WPI; 2004-365151/34.
XX New synthetic or partially purified peptides that can bind to specific
XX PT subunits of G proteins, useful for detecting the activation or
XX PT deactivation of a G protein-coupled receptor (GPCR) or for identifying
XX PT allosteric modulators of GPCR.
XX Example 300d; SEQ ID NO 46; 242pp; English.
XX The invention relates to a novel non-naturally occurring and/or at least
XX partially purified peptide, which does not comprise a V-H or V-L homology
XX unit of an antibody and specifically binds to an activated G alpha
XX subunit of a G protein. The invention further comprises: an assay kit for
XX the identification of the activation state of a G protein coupled
XX receptor (GPCR), the kit comprising a first peptide cited above labeled
XX with a first label; methods of identifying the activation state of a GPCR
XX; a method of identifying a modulator of a GPCR; a method of determining
XX the presence or amount of a modulator of a GPCR in a sample; methods of
XX identifying a substance as an agonist or antagonist of GPCR; and a method
XX of identifying a G-alpha subunit which interacts with a GPCR. The
XX composition and methods are useful in detecting the activation or
XX deactivation of a G protein-coupled receptor or in monitoring the
XX activation state of a GPCR within a cell. These may also be used for
XX identifying allosteric modulators of GPCRs. This sequence represents a Gi
XX -alpha 1 GDP-specific phase D peptide motif of the invention.
XX SQ Sequence 15 AA;
Query Match 38.8%; Score 34.5; DB 8; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 3; Gaps 1;
QY 4 PQLL---QVMMEP 14
||||| :|||
Db 1 PQLLHWMEWMEP 14
RESULT 15
ABB99038
ID ABB99038 standard; peptide; 15 AA.
XX AC ABB99038;
XX 24-JAN-2003 (first entry)
XX Carbamylaspartic dehydrase 9.68 N-terminal amino acid sequence.
XX Carbamylaspartic dehydrase 9.68; enzyme; malignant tumour; haemopathy;
XX development disorder; inflammation; human immunodeficiency virus; HIV;
XX infection; immunological disease.
XX Unidentified.
XX CN1352302-A.
XX 05-JUN-2002.
XX 02-NOV-2000; 2000CN-00127191.
XX 02-NOV-2000; 2000CN-00127191.
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX Mao Y, Xie Y;
XX

DR WPI; 2002-644474/70.
XX New polypeptide-carbamylaspartic dehydrase 9.68 and polynucleotide
XX PT encoding the polypeptide.
XX Example 5; Page 18 (disclosure); 31pp; Chinese.
XX The invention relates to the polypeptide carbamylaspartic dehydrase 9.68,
XX the polynucleotides encoding this polypeptide, and a DNA recombination
XX process for production of the polypeptide. Also disclosed is the method
XX of applying the polypeptide in the treatment of various diseases such as,
XX malignant tumours, haemopathy, development disorder, inflammations, human
XX immunodeficiency virus (HIV) infection, and immunological diseases. The
XX present invention also discloses the antagonist resisting the polypeptide
XX and its treatment effect, and the application of the polynucleotides for
XX encoding carbamylaspartic dehydrase 9.68. The current sequence represents
XX the carbamylaspartic dehydrase 9.68 N-terminal amino acid sequence
XX SQ Sequence 15 AA;
Query Match 38.2%; Score 34; DB 5; Length 15;
Best Local Similarity 41.7%; Pred. No. 1.8e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 TPQPLLQVMMEP 14
:|||| :|||
Db 4 SPQPLTGALLQP 15
RESULT 16
ADC44467
ID ADC44467 standard; peptide; 12 AA.
XX AC ADC44467;
XX 18-DEC-2003 (first entry)
XX Endothelial cell binding peptide SEQ ID NO:195.
XX Endothelial cell binding protein; ECRP; anti-tumour; cytostatic;
XX vasotropic; antipsoriatic; dermatological; ophthalmological;
XX antiidiabetic; antiarthritic; vulnery; antiulcer; antiinflammatory;
XX antibacterial; gynaecological; angiogenesis.
XX Synthetic.
XX WO2003037172-A2.
XX 08-MAY-2003.
XX 01-NOV-2002; 2002WO-US035258.
XX 01-NOV-2001; 2001US-0334822P.
XX (GPCB-) GPC BIOTECH INC.
XX Gyuris J, Lamphere L, Morris AJ, Tsaoun K;
XX WPI; 2003-482072/45.
XX Novel synthetic or recombinant polypeptide useful for promoting, reducing
XX proliferation and/or migration of endothelial cells, and for modulating
XX angiogenesis, has endothelial cell binding protein sequences.
XX Claim 3; SEQ ID NO 195; 126pp; English.
XX The invention relates to a novel isolated, synthetic or recombinant
XX peptide or polypeptide which includes one or more endothelial cell
XX binding protein (ECBP) sequences. A peptide of the invention has anti-
XX tumour, cytostatic, vasotropic, antipsoriatic, dermatological,
XX ophthalmological, antidiabetic, antiarthritic, vulnery, antiulcer,
XX antiinflammatory, antibacterial, and gynaecological activity. The peptide
XX is useful for promoting, reducing the proliferation and/or migration of

CC endothelial cells, by treating the cells with an ECPB agonist, which is
 CC preferably the peptide, to promote proliferation and/or migration of the
 CC treated cells, and for reducing or promoting angiogenesis, by treating
 CC the cells with an ECPB antagonist, which is preferably the peptide of the
 CC invention. A peptide of the invention is also useful for manufacturing a
 CC medicament for promoting angiogenesis, by admixing an ECPB agonist or
 CC ECPB antagonist to promote or reduce angiogenesis at one or more sites in
 CC a treated mammal. The medicament is useful for promoting or reducing
 CC angiogenesis. ECPB sequences are useful to alter the infectivity spectrum
 CC of a viral particle. The present sequence represents an ECPB of the
 CC invention.
 XX
 SQ Sequence 12 AA;

Query Match 37.1%; Score 33; DB 7; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQP 6
 |||||
 DB 2 LQTPQP 7

RESULT 17
 AAB72531
 ID AAB72531 standard; peptide; 15 AA.

XX AC AAB72531;
 XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #32.

XX KW Dermatological; oxidative stress regulator; colostrinin.

XX OS Unidentified.

XX PN WO200112650-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US022665.

XX PR 17-AUG-1999; 99US-0149310P.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;

XX DR WPI; 2001-218342/22.

XX PT Modulating oxidative stress level in a cell, involves contacting the cell
 with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations.

XX PS Claim 6; Page 26; 48pp; English.

XX CC The present invention relates to a method for modulating the oxidative
 stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient

XX SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 4; Length 15;
 Best Local Similarity 53.8%; Pred. No. 2.6e+02;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPQPLQVMMEP 14
 |||||

DB 3 QPPQPLPPTVMFP 15

RESULT 18

AAB59334

ID AAB59334 standard; peptide; 15 AA.

XX AC AAB59334;

XX DT 21-MAR-2001 (first entry)

XX DE Ewe colostrinin peptide fragment C-9.

XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX PN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB002128.

XX PR 02-JUN-1999; 99GB-00012852.

XX PA (REGG-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-071058/08.

XX PT Peptides having an N-terminal amino acid sequence isolated from
 colostrinin for treating e.g. disorders of the central nervous system and

XX PT immune system, viral and bacterial infections, and diseases characterized
 by amyloid plaques.

XX PS Claim 7; Page 27; 63pp; English.

XX CC The present invention provides the sequences of a number of peptides
 found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques

XX SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 4; Length 15;
 Best Local Similarity 53.8%; Pred. No. 2.6e+02;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPQPLQVMMEP 14
 |||||

DB 3 QPPQPLPPTVMFP 15

RESULT 19

AAB72279

ID AAB72279 standard; peptide; 15 AA.

XX AC AAB72279;

XX DT 14-MAY-2001 (first entry)

XX DE Colostrinin derived cytokine inducing peptide SEQ ID 34.

XX KW Colostrinin; immune response; cytokine; blood cell proliferation;
 central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 neurosis; infection.

```
XX OS Synthetic.
XX PN WO200111937-A2.
XX PD 22-FEB-2001.
XX PF 17-AUG-2000; 2000WO-US022818.
XX PR 17-AUG-1999; 99US-0149311P.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PA (REGE-) REGEN THERAPEUTICS PLC.
XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX WPI; 2001-202804/20.
XX DR Inducing a cytokine and modulating an immune response, useful for
XX PT treating central nervous system diseases and bacterial and viral
XX PT infections, comprises administering colostrinin as an immunological
XX PT regulator.
XX PS Claim 1; Page 34; 50pp; English.
XX SS Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The peptides
CC have immune response modulatory activity, and are capable of inducing
CC cytokines. Colostrinin and its derived peptides are useful for inducing
CC cytokine production, for modulating an immunological response and for
CC inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies
XX SQ Sequence 15 AA;
    Query Match      37.1%; Score 33; DB 4; Length 15;
    Best Local Similarity 53.8%; Pred. No. 2.6e+02;
    Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 2 QTPQPLQVMMEP 14
Db 3 QPPQPLPPTVMFP 15
RESULT 20
AAB72563
ID AAB72563 standard; peptide; 15 AA.
XX AC AAB72563;
XX DT 09-MAY-2001 (first entry)
XX DE Colostrinin peptide #32.
XX KW Neuroprotective; neural cell differentiation regulator; colostrinin;
XX KW colostrum.
XX OS Unidentified.
XX PN WO200112651-A2.
XX PD 22-FEB-2001.
XX PF 17-AUG-2000; 2000WO-US022774.
XX PR 17-AUG-1999; 99US-0149633P.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX
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```
PI Boldogh I;
XX WPI; 2001-226545/23.
XX Use of colostrinin, its constituent peptide or analog as a neural cell
XX PT regulator, for promoting neural cell differentiation and treating damaged
XX PT neural cells in a patient.
XX PS Claim 6; Page 22; 35pp; English.
XX CC The present invention relates to a method for promoting neural cell
XX CC differentiation and treating damaged neural cells, using colostrinin and
XX CC colostrinin constituent peptides (e.g. the present peptide) as a neural
XX CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
XX SQ Sequence 15 AA;
    Query Match      37.1%; Score 33; DB 4; Length 15;
    Best Local Similarity 53.8%; Pred. No. 2.6e+02;
    Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 2 QTPQPLQVMMEP 14
Db 3 QPPQPLPPTVMFP 15
RESULT 21
AAO14610
ID AAO14610 standard; peptide; 15 AA.
XX AC AAO14610;
XX DT 27-MAY-2002 (first entry)
XX DE Neural cell regulatory colostrinin peptide 32.
XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
XX KW neural cell treatment.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT Modified-site 15 /note= "Optional C-terminal amide"
XX PN WO200213851-A1.
XX PD 21-FEB-2002.
XX PF 17-AUG-2000; 2000WO-US022777.
XX PR 17-AUG-2000; 2000WO-US022777.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Boldogh I, Stanton JG, Hughes TK;
XX WPI; 2002-269152/31.
XX PT Promoting cell differentiation in a patient involves use of blood cell
XX PT regulator selected from colostrinin, its constituent peptide and/or
XX PT analog.
XX PS Claim 7; Page 22; 37pp; English.
XX CC The invention comprises a method for promoting cell differentiation (e.g.
XX CC neural cell differentiation). The method involves contacting cells with a
XX CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
XX CC cells in morphology to form neural cells. Colostrinin is a proline-rich
XX CC polypeptide aggregate that is present in colostrum. The method of the
XX CC invention is useful for promoting the differentiation of cells and for
XX CC treating damaged neural cells in a patient. The present amino acid
```

CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention
XX
SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 5; Length 15;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPQPLQLQVMMEP 14
| | | | | : | |
Db 3 QPPQPLPTVMFP 15

RESULT 22
AAM51066
ID AAM51066 standard; peptide; 15 AA.
XX
AC AAM51066;
XX
DT 30-MAY-2002 (first entry)
XX
DE Colostrinin constituent peptide (casein amino acids 159-173).
XX
KW Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; beta-casein; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 15 /note= "optional C-terminal amidation"
XX
PN WO200213849-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022775.
XX
PR 17-AUG-2000; 2000WO-US022775.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
PI WPI; 2002-269150/31.
XX
DR Modulation of blood cell proliferation in a patient involves use of blood
XX cell regulator selected from colostrinin, its constituent peptide and/or
XX analog.
XX
PS Claim 1; Page 34; 54pp; English.
XX

The present sequence is that of a colostrinin constituent peptide that is
used as an immunological regulator and as a blood cell regulator in
claimed methods of the invention. It is classified as having a beta-
casein homologue precursor, and corresponds to casein amino acids 159-
173. Methods are claimed for: inducing a cytokine in a cell by contact
with an immunological regulator, where the cell is present in a cell
culture, a tissue, an organ or an organism, and the cell is mammalian,
including human; modulating an immune response in a cell by contact with
the immunological regulator under conditions effective to induce a
cytokine; modulating an immune response in a patient by administering an
immunological regulator under conditions effective to induce a cytokine,
where the immunological regulator is administered topically or as part of
a dietary supplement, and where the immune response is specific or non
specific, an interferon response or an antibody response; modulating
blood cell proliferation by contacting blood cells with a blood cell
regulator, where the blood cells are present in a cell culture or an
organism, are mammalian or human, and where the blood cells are increased
in number or differentiated; and a method for modulating blood cell
proliferation in a patient. A claimed cytokine-inducing composition

CC comprises a pharmaceutical carrier and an active agent such as the
CC present peptide
XX
SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 5; Length 15;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPQPLQLQVMMEP 14
| | | | | : | |
Db 3 QPPQPLPTVMFP 15

RESULT 23
AAE20261
ID AAE20261 standard; peptide; 15 AA.
XX
AC AAE20261;
XX
DT 18-JUN-2002 (first entry)
XX
DE Colostrinin constituent peptide #32.
XX
KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnery.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 15 /note= "Optionally C-terminal amide"
XX
PN WO200213850-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022776.
XX
PR 17-AUG-2000; 2000WO-US022776.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA Stanton GJ, Hughes TK, Boldogh I;
PI WPI; 2002-269151/31.
XX
DR Composition useful for the modulation of blood cell proliferation in a
XX patient comprises a blood cell regulator selected from colostrinin, its
XX constituent peptide and/or analog.
XX
PS Claim 6; Page 26; 51pp; English.
XX

The invention relates to a composition which comprises a blood cell
regulator selected from colostrinin, its constituent peptide and/or
analog. The invention is used for modulating the oxidative stress level
in a cell e.g. mammalian or human cell present in a cell culture, tissue,
organ, or organism; or for treating oxidative damage to the skin of a
patient e.g. animal or human; to modulate oxidative stress during/ after
a premature birth or normal birth, preventing/delaying in a
patient, enhancing wound healing, and the reduction of side effects of
cosmetic procedures. The method changes the level of an oxidising species
in the cell, such as decreases or prevents increase in the level of
damage to a biomolecule of the patient selected from DNA, protein and/or
lipid, compared to the same conditions when the oxidative stress
regulator is not present. The modulation of oxidative stress results in
enhanced repair, regeneration, and replacement of cells, tissues and
organs (e.g. kidney, liver, pancreas, skin, and the other internal and
external organs), as well as enhanced preservation of such organs for
transplantation, implantation, or scientific research. The present
sequence is a colostrinin constituent peptide

XX SQ Sequence 15 AA;
Query Match 37.1%; Score 33; DB 5; Length 15;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPQPLQVMMEP 14
Db 3 QPPQPLPTVMFP 15

RESULT 24
ADN60328
ID ADN60328 standard; peptide; 15 AA.
XX
AC ADN60328;
XX
DT 29-JUL-2004 (first entry)
XX
DE Constituent peptide of colostrinin SEQ ID NO:34.
XX
KW modulator; colostrinin; intracellular signaling molecule modulator;
KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;
KW DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNE inhibitor;
KW 4HNE-protein adduct formation reduction;
KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;
KW c-Jun NH2-terminal kinase inhibition.
XX
OS Synthetic.
XX
FN WO2004037851-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003WO-US033423.
XX
PR 22-OCT-2002; 2002US-0420369P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (BOLD/) BOLDGOH I.
PA (STAN/) STANTON J G.
PA (GEOR/) GEORGIADIS J A.
PA (HUGH/) HUGHES T K.
PA (KRUZ/) KRUZEL M.
XX
PI Boldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;
XX
DR WPI; 2004-365494/34.
XX
PT Use of colostrinin for e.g. modulating an intracellular signaling
PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a
PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
PT a cell.
XX
PS Claim 6; SEQ ID NO 34; 46pp; English.
XX
CC The present invention describes the use of a modulator selected from
CC colostrinin, its constituent peptide, its active analogue, and a
CC combination of these, for modulating an intracellular signaling molecule
CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,
CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
CC The modulator has cytostatic activity, and can be used as a 4HNE
CC inhibitor. The modulator is useful in the manufacture of a medicament for
CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated
CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,
CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.
CC Colostrinin, or its constituent peptide or active analogue is useful for
CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
CC The present sequence represents a synthetic constituent peptide of
CC colostrinin, which can be used as a modulator in the present invention.

XX SQ Sequence 15 AA;
Query Match 37.1%; Score 33; DB 8; Length 15;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPQPLQVMMEP 14
Db 3 QPPQPLPTVMFP 15

RESULT 25
ADS74410
ID ADS74410 standard; peptide; 15 AA.
XX
AC ADS74410;
XX
DT 16-DEC-2004 (first entry)
XX
DE Ovine colostrinin peptide.
XX
KW Colostrum; colostrinin; sheep; peptide purification.
XX
OS Ovis aries.
XX
FN WO2004081038-A1.
XX
PD 23-SEP-2004.
XX
PF 10-MAR-2004; 2004WO-GB001014.
XX
PR 11-MAR-2003; 2003GB-00005552.
PR 08-MAR-2004; 2004GB-00005190.
XX
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;
XX
DR WPI; 2004-677519/66.
XX
PT Recovering peptides such as colostrinin from mammalian colostrum, by
PT mixing colostrum with alcohol to form alcohol phase containing peptides
PT and precipitate, separating alcohol phase from precipitate, and
PT recovering alcohol phase.
XX
PS Disclosure; SEQ ID NO 27; 41pp; English.
XX
CC The present sequence is that of a peptide that can be recovered from
CC ovine colostrinin using the method of the invention. The invention
CC provides a method for the recovery of peptides (especially colostrinin)
CC from colostrum in substantially pure, biologically active form and in
CC high yield. The method involves mixing the colostrum with an alcohol to
CC form an alcohol phase containing the colostrinin and a precipitate
CC containing higher molecular weight caseins and other proteins. Best
CC results are obtained using methanol or ethanol of at least 80%, and
CC preferably up to 100%, purity. The alcohol phase is then separated from
CC the precipitate, and the colostrinin is separated from the alcohol,
CC preferably by evaporation, to form a colostrinin-rich phase, which is
CC recovered. A precipitation agent, such as ammonium sulfate, may be added
CC either to the alcohol phase or, preferably, to the colostrinin-rich phase
CC to induce precipitation of the colostrinin peptides. The method is
CC generally applicable to the separation of peptides from fluids containing
CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic
CC acids.

XX SQ Sequence 15 AA;
Query Match 37.1%; Score 33; DB 8; Length 15;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPQPLQVMMEP 14

PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX Claim 13; Page 487; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC inhibiting the expression of the protein, as tools for modulating or
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 15 AA;
Query Match 36.0%; Score 32; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 LQTPQPLQLQVMM 12
|: ||||:|
Db 1 LKAVQPLLVKVM 12
|: ||||:|
RESULT 29
ABR30440
ID ABR30440 standard; peptide; 15 AA.
XX
AC ABR30440;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 83P4B8 HLA peptide #1502.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
FN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX Claim 13; Page 494; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC inhibiting the expression of the protein, as tools for modulating or
CC directing the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 15 AA;
Query Match 36.0%; Score 32; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 LQTPQPLQLQVMM 12
|: ||||:|
Db 1 LKAVQPLLVKVM 12
|: ||||:|
RESULT 30
ABR31517
ID ABR31517 standard; peptide; 15 AA.
XX
AC ABR31517;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 83P4B8 HLA peptide #2579.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
FN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX Claim 13; Page 494; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX

SQ Sequence 15 AA;

Query Match 36.0%; Score 32; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQLQVMM 12
|: ||||:|
Db 1 LKAVQLLKVSM 12

RESULT 31

ABR30536
ID ABR30536 standard; peptide; 15 AA.

XX ABR30536;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 83P4B8 HLA peptide #1598.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

XX 10-APR-2001; 2001US-0283112P.

XX 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of

XX proteins and polynucleotides, useful for therapeutic, prognostic and

XX diagnostic reagents for eliciting cellular or humoral immune response in

XX cancer patients.

XX Claim 13; Page 476; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention

XX

SQ Sequence 15 AA;

Query Match 36.0%; Score 32; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQLQVMM 12
|: ||||:|
Db 4 LKAVQLLKVSM 15

RESULT 32

ABR30847
ID ABR30847 standard; peptide; 15 AA.

XX ABR30847;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 83P4B8 HLA peptide #1909.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

XX 10-APR-2001; 2001US-0283112P.

XX 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of

XX proteins and polynucleotides, useful for therapeutic, prognostic and

XX diagnostic reagents for eliciting cellular or humoral immune response in

XX cancer patients.

XX Claim 13; Page 482; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention

SQ Sequence 15 AA;

Query Match 36.0%; Score 32; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQLQVMM 12
|: ||||:|
Db 1 LKAVQLLKVSM 12

RESULT 33
ADH14837
ID ADH14837 standard; peptide; 18 AA.
XX AC
XX ADH14837;
XX
DT 11-MAR-2004 (first entry)
XX
XX Gliadin related epitope peptide.
DE
XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
XX KW vaccine.
KW
XX Synthetic.
OS
XX WO2003104273-A2.
FN
XX 18-DEC-2003.
PD
XX 05-JUN-2003; 2003WO-GB002450.
XX PF
XX 05-JUN-2002; 2002GB-00012885.
XX PR
XX (ISIS-) ISIS INNOVATION LTD.
XX PA
XX Anderson RP, Hill AVS, Jewell DP;
XX PI
XX WPI; 2004-043640/04.
DR
XX Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognised by T
PT cell receptor.
PT
XX Example 13; Page 96; 177pp; English.
PS
XX The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 18 AA;
Query Match 36.0%; Score 32; DB 8; Length 18;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 4 PQLQLQVMEPEQ 15
||| : : :
DB 5 PQLQLQVMEPEQ 16
||| : : :
RESULT 34
AAB23189
ID AAB23189 standard; peptide; 12 AA.
XX AC
XX AAB23189;
XX
DT 29-JAN-2001 (first entry)
XX
XX Hsp47-binding hydrophobic phage display dodecapeptide, SEQ ID NO:11.
DE
XX Hsp47-binding hydrophobic dodecapeptide; phage display library;
KW Hsp47 external domain; carcinoma; cancer; targeting molecule; therapy;
KW

KW diagnosis; detection; imaging; drug delivery; invasion; migration;
KW metastasis; modulation; tumour; skin; basal cells; colon;
KW large intestine; lung; breast; bladder; oral cancer;
KW head and neck cancer; larynx; nasopharynx; adrenal cortex;
KW apocrine gland; kidney; liver; pancreas; prostate.
XX
OS Synthetic.
XX
XX WO200054805-A1.
FN
XX 21-SEP-2000.
PD
XX 15-MAR-2000; 2000WO-US006588.
XX PF
XX 15-MAR-1999; 99US-0124481P.
XX PR
XX (UYMA-) UNIV MARYLAND BALTIMORE.
XX PA
XX Sauk JU;
XX PI
XX WPI; 2000-655997/63.
DR
XX Treating, diagnosing or modulating a carcinoma cell, which expresses Heat
PT shock protein 47 on its surface, involves administering an agent
PT comprising targeting moiety which binds to Hsp47 external domain.
PT
XX Claim 6; Page 8; 87pp; English.
PS
XX The invention relates to methods of treating and diagnosing carcinomas in
CC which heat shock protein 47 (Hsp47) is expressed on the surface of the
CC carcinoma cells, involving administering an agent comprising a targeting
CC moiety which specifically binds to the external domain of Hsp47. The
CC invention also relates to peptides (AAB23181-B23203) which specifically
CC bind to external domains of such surface-localised Hsp47 molecules and
CC have sequences encompassed by the generic sequences XHxHYXXxXxHYHy or
CC HyXXxHYXXxXx where X, independently, can be any amino acid and Hy,
CC independently, can be any hydrophobic amino acid. The invention also
CC encompasses methods of screening for agents which bind Hsp47 external
CC domains. Hsp47-binding agents can be used to treat Hsp47-
CC expressing carcinomas, and for modulating the activity of a tumour cell
CC with respect to invasion, migration, motility or metastasis, or to its
CC interaction with the extracellular matrix. The targeting moiety (such as
CC an Hsp47-binding peptide, a toxin or an antibody) may be coupled with a
CC therapeutic moiety (such as a cytotoxic agent or a therapeutic gene) for
CC cancer treatment, or with a detectable moiety for imaging. Carcinomas
CC which may be treated or diagnosed according to methods of the invention
CC include those of the skin, basal cells, large intestine, lung, colon,
CC breast, bladder, oral, head and neck, larynx, nasopharynx, adrenal
CC cortex, apocrine glands, kidney, liver, pancreas, or prostate. Targeting
CC carcinoma cells with Hsp47-binding agents results in efficient delivery
CC of therapeutic agents, reduced doses, reduced side effects and sensitive
CC detection or imaging of carcinoma cells. Sequences AAB23181-B23191
CC represent predominantly hydrophobic phage display library dodecapeptides
CC identified as being able to bind Hsp47 in an exemplification of the
CC invention
XX
SQ Sequence 12 AA;
Query Match 34.8%; Score 31; DB 3; Length 12;
Best Local Similarity 41.7%; Pred. No. 4.3e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 3 TPQLQLQVMEPE 14
||| : : :
DB 1 TPQPNMLRLRSP 12
||| : : :
RESULT 35
AAM97279
ID AAM97279 standard; peptide; 14 AA.
XX
XX AAM97279;
AC
XX

DT	24-JAN-2002	(first entry)	
XX	Human peptide #554	encoded by a SNP oligonucleotide.	
XX	Immunosuppressive;	immunostimulatory; antiinflammatory; cytostatic;	
XX	neuroprotective;	antimicrobial; gene therapy; vaccine; amylase; cancer;	
XX	amyloid protein;	angiopoietin; apoptosis related protein; cadherin;	
XX	cyclin; polymerase;	oncogene; histone; kinase; colony stimulating factor;	
XX	complement related protein;	cytochrome; kinesin; cytokine; interferon;	
XX	interleukin; G-protein coupled receptor;	thioesterase; inflammation;	
XX	multifactorial disease;	autoimmune disease; infection;	
XX	nervous system disease.		
OS	Homo sapiens.		
XX	WO200147944-A2.		
XX	05-JUL-2001.		
XX	28-DEC-2000;	2000WO-US035498.	
XX	28-DEC-1999;	99US-0173419P.	
XX	27-DEC-2000;	2000US-00173419.	
XX	(CURA-) CURAGEN CORP.		
XX	Shimkets RA, Leach M;		
XX	WPI; 2001-465210/50.		
XX	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,		
XX	oncogenes and histones, useful for diagnosing and treating, e.g. cancer,		
XX	autoimmune diseases and infections.		
XX	Disclosure; Page 3789; 4143pp; English.		
XX	The present invention relates to oligonucleotides (see AAL26793-AAL34659)		
XX	encoding polymorphic variants of proteins related to amylases, amyloid		
XX	proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,		
XX	polymerase, oncogenes, histones, kinases, colony stimulating factors,		
XX	complement related proteins, cytochromes, kinesins, cytokines,		
XX	interferons, interleukins, G-protein coupled receptors and thioesterases.		
XX	The present sequence is a peptide encoded by one such oligonucleotide.		
XX	The oligonucleotides and the peptides encoded by them may be used in the		
XX	prevention, diagnosis and treatment of diseases associated with		
XX	inappropriate expression of the proteins listed above. Disorders that may		
XX	be prevented, diagnosed and/or treated include multifactorial diseases		
XX	with a genetic component, such as autoimmune diseases (e.g. rheumatoid		
XX	arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus		
XX	and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,		
XX	brain, breast, colon and kidney, leukaemia), diseases of the nervous		
XX	system and an infection of pathogenic organisms		
XX	Sequence 14 AA;		
XX	Query Match	34.8%; Score 31; DB 4; Length 14;	
XX	Best Local Similarity	75.0%; Pred. No. 5e+02;	
XX	Matches	6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	6	PLIQVME 13	
DB	1	PLIQVME 8	
RESULT 36			
ADF71116			
ID	ADF71116	standard; peptide; 14 AA.	
XX	ADF71116;		
XX	12-FEB-2004	(first entry)	
XX	Saccharomyces cerevisiae phosphopeptide, SEQ ID NO 132.		
XX	phosphopeptide; peptidomimetics; phosphorylation; dephosphorylation;		
XX	protein kinase inhibitor; protein phosphatase inhibitor; cytotoxic;		
XX	antiproliferative.		
XX	Saccharomyces cerevisiae.		
XX	WO2003074992-A2.		
XX	12-SEP-2003.		
XX	03-MAR-2003;	2003WO-US006553.	
XX	01-MAR-2002;	2002US-0360787P.	
XX	(MDS-) MDS PROTEOMICS INC.		
XX	(UVVI-) UNIV VIRGINIA PATENT FOUND.		
XX	Burke DJ, Ross MM, Stukenberg PT, White FM;		
XX	WPI; 2003-767383/72.		
XX	New phosphorylated peptides, polypeptides and peptidomimetics useful for		
XX	drug screening and producing antibodies and conjugates.		
XX	Disclosure; SEQ ID NO 132; 67pp; English.		
XX	The invention relates to novel peptides of 4-20 amino acids comprising		
XX	any of hundreds of Saccharomyces cerevisiae phosphopeptide sequences		
XX	fully defined in the specification (or a related sequence from a		
XX	homologous mammalian protein) and isolated or recombinant polypeptides or		
XX	peptidomimetics including any of the defined phosphopeptide sequences.		
XX	The phosphopeptide sequences have the following properties: modulator of		
XX	protein phosphorylation, modulator of protein dephosphorylation, protein		
XX	kinase inhibitor, and protein phosphatase inhibitor. The peptides, in		
XX	polypeptides or peptidomimetics and associated methods are useful in		
XX	screening for modulators of protein phosphorylation potentially useful as		
XX	drugs, for producing antibodies, for detecting phosphorylated proteins,		
XX	and for producing conjugates with cytotoxic or antiproliferative agents,		
XX	labels or polymers. This sequence represents a Saccharomyces cerevisiae		
XX	phosphopeptide of the invention.		
XX	Sequence 14 AA;		
XX	Query Match	34.8%; Score 31; DB 7; Length 14;	
XX	Best Local Similarity	85.7%; Pred. No. 5e+02;	
XX	Matches	6; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
QY	3	TPQPLQ 9	
DB	4	TPQPLQ 10	
RESULT 37			
AAW56352			
ID	AAW56352	standard; peptide; 15 AA.	
XX	AAW56352;		
XX	17-AUG-1998	(first entry)	
XX	LO-CD2a	light chain framework region 2.	
XX	LO-CD2a;	monoclonal antibody; CD2; rat; chimeric antibody;	
XX	humanised antibody; antibody engineering; graft rejection;		
XX	graft versus host disease; autoimmune disease; therapy.		
XX	Rattus sp.		
XX	Key	Location/Qualifiers	
XX	Misc-difference 2	/note= "retained in humanised antibody"	
XX	Misc-difference 3		

FT	/note= "retained in humanised antibody"
FT	Misc-difference 11
FT	/note= "retained in humanised antibody"
FT	Misc-difference 12
FT	/note= "retained in humanised antibody"
XX	
FN	W09807444-A1.
XX	
PD	26-FEB-1998.
XX	
PF	16-AUG-1996; 96WO-US013281.
XX	
PR	16-AUG-1996; 96WO-US013281.
XX	
PA	(BIOT-) BIOTRANSPLANT INC.
PA	(UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX	
Bazin H, Latinne D, Kaplan R, Kieber-Emmons T, Postema CE;	
White-Scharf ME;	
WPI; 1998-168898/15.	
XX	
DR	Humanised antibody - comprises complementarity determining region from LO
PT	-CD2a, useful to prevent or inhibit graft versus host or auto-immune
PT	disease.
PS	Example 7; Page 58; 133pp; English.
XX	
CC	This peptide comprises framework region 2 (FR 2) of the light chain (see
CC	AAW56347) of rat anti-CD2 monoclonal antibody LO-CD2a. FRs 1-4 (see
CC	AAW56351-54) were compared with FRs 1-4 of the human HUM5400 light chain.
CC	A novel humanized LO-CD2a light chain (see AAW56349) comprises rat LO-
CC	CD2a complementarity determining regions and HUM5400 constant regions,
CC	but with amino acids 9, 12, 41, 42, 50, 51 and 82 of the rat framework
CC	retained to maintain binding specificity. The chimeric antibody can be
CC	used to inhibit an immune response, specifically human T cell activation
CC	and proliferation, in a patient, and to inhibit rejection of a graft in a
CC	patient (claimed), useful for preventing or inhibiting graft versus host
CC	or autoimmune disease
XX	
SQ	Sequence 15 AA;
	Query Match 34.8%; Score 31; DB 2; Length 15;
	Best Local Similarity 71.4%; Pred. No. 5.4e+02;
	Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY	2 QTPQPPLL 8
	: :
Db	8 QSPQPLI 14
	RESULT 38
	AAV30191
ID	AAV30191 standard; peptide; 15 AA.
XX	
AC	AAV30191;
XX	
DT	29-OCT-1999 (first entry)
XX	
DE	Framework 2 region of rat monoclonal antibody LO-CD2a light chain.
XX	
KW	Antibody LO-CD2a; CD2 antigen; T-lymphocyte; humanised antibody;
KW	T-cell-mediated immune response; graft rejection; autoimmune disease;
KW	graft-versus-host disease; T cell; natural killer cell.
XX	
OS	Rattus sp.
XX	
PN	US5951983-A.
XX	
PD	14-SEP-1999.
XX	
Pf	07-JUN-1995; 95US-00477989.
XX	
	05-MAR-1993; 93US-00027008.
PR	09-SEP-1993; 93US-00119032.
PR	29-MAR-1993; 95US-00407009.
XX	
PA	(BIOT-) BIO TRANSPLANT INC.
PA	(UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX	
PI	White-Scharf ME, Postema CE, Kaplan R, Latinne D, Bazin H;
PI	Kieber-Emmons T;
XX	
DR	WPI; 1999-526991/44.
XX	
PT	Antibody mediated inhibition of T cell immune response.
XX	
PS	Example 7; Col 33-34; 104pp; English.
XX	
CC	The present sequence represent a framework region of rat monoclonal
CC	antibody LO-CD2a. LO-CD2a binds to an epitope of a CD2 antigen T-
CC	lymphocytes. The present sequence is compared to the corresponding region
CC	from a human V kappa gene, and used to design humanised sequences. The
CC	humanized LO-CD2a antibody comprises the human constant regions, a light
CC	chain framework region derived from a human antibody, a heavy chain
CC	framework region derived from a human antibody, heavy and light chain
CC	complementarity determining regions (CDRs) of the non-human monoclonal
CC	antibody produced by the cell line deposited as ATCC HB11423. The
CC	humanised antibodies are used in a method for treating a patient to
CC	inhibit a T-cell-mediated immune response. The method is useful for the
CC	treatment or prevention of graft rejection and graft-versus-host disease,
CC	as well as in the treatment of autoimmune diseases which are mediated by
CC	the activation and proliferation of T cells or natural killer cells
XX	
SQ	Sequence 15 AA;
	Query Match 34.8%; Score 31; DB 2; Length 15;
	Best Local Similarity 71.4%; Pred. No. 5.4e+02; Indels 0; Gaps 0;
	Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY	2 QTPQPPLL 8
	: :
Db	8 QSPQPLI 14
	RESULT 39
	AAU74511
ID	AAU74511 standard; peptide; 15 AA.
XX	
AC	AAU74511;
XX	
DT	09-APR-2002 (first entry)
XX	
DE	Human ATP dependent serine proteinase 21 N-terminal peptide.
XX	
KW	Human; ATP dependent serine protease 21; malignant tumour; HIV;
KW	haemopathy; human immunodeficiency virus; immunological disease;
KW	inflammation; cytostatic; haemostatic; virucide; immunomodulatory;
KW	antiinflammatory; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO200194529-A2.
XX	
PD	13-DEC-2001.
XX	
Pf	28-APR-2001; 2001WO-CN000658.
XX	
PR	29-APR-2000; 2000CN-00115512.
XX	
PA	(SHAN-) SHANGHAI BLOWINDOW GENE DEV INC.
XX	
Pf	Mao Y, Xie Y;
XX	
DR	WPI; 2002-090143/12.
XX	

PT Human ATP dependent serien proteinase 21 and encoding polynucleotide,
 PT used in diagnosis and treatment of malignant tumors, hemopathy, human
 PT immunodeficiency virus infection, immunological diseases and
 PT inflammation.

XX Example 5; Page 18; 32pp; Chinese.

XX The invention relates to an isolated polypeptide of human ATP dependent
 CC serine proteinase 21. The protein of the invention and its associated
 CC cDNA sequence are used in the treatment of various diseases including
 CC malignant tumors, haemopathy, human immunodeficiency virus (HIV)
 CC infection, immunological diseases and various inflammations. This
 CC sequence represents the N-terminal peptide of ATP dependent serine
 CC proteinase 21, used in ELISA

XX Sequence 15 AA;

Query Match 34.8%; Score 31; DB 5; Length 15;
 Best Local Similarity 46.2%; Pred. No. 5.4e+02;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 QPLQVMMPEQGD 17
 | | : : : : :
 Db 3 QLESTVIQPGD 15

RESULT 40

ABR38577
 ID ABR38577 standard; peptide; 15 AA.

XX ABR38577;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 192P2G7 HLA peptide #1437.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

XX 10-APR-2001; 2001US-0283112P.

XX 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;

XX Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

XX Claim 13; Page 622; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX Sequence 15 AA;

Query Match 34.8%; Score 31; DB 6; Length 15;
 Best Local Similarity 46.2%; Pred. No. 5.4e+02;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LQTPQPLQVMM 13
 | : : : : :
 Db 2 LEYFPQGLDIKE 14

Search completed: June 7, 2005, 23:10:42
 Job time : 95.4909 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:57:32 ; Search time 23.1818 Seconds
(without alignments)
54.743 Million cell updates/sec

Title: US-10-691-157-2

Perfect score: 89

Sequence: 1 LQTPQLQVMFPGD 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 183464

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.*

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2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	17	4	US-09-641-803-2
2	33	37.1	15	4	US-09-641-803-34
3	32	36.0	8	5	PCT-US91-05177-19
4	31	34.8	13	2	US-08-162-081B-5
5	31	34.8	13	2	US-08-780-872-5
6	31	34.8	13	3	US-09-085-957-5
7	31	34.8	15	1	US-08-477-877B-30
8	31	34.8	15	2	US-08-472-281A-30
9	31	34.8	15	2	US-08-477-989B-30
10	29	32.6	18	2	US-09-017-205-35
11	28	31.5	7	1	US-08-594-447-74
12	28	31.5	7	1	US-08-541-964-73
13	28	31.5	7	2	US-08-665-647-88
14	28	31.5	10	3	US-09-981-392-53
15	28	31.5	10	4	US-09-908-322-53
16	28	31.5	15	2	US-08-553-257A-21
17	28	31.5	15	4	US-09-441-992-21
18	28	31.5	16	3	US-08-602-999A-195
19	28	31.5	16	4	US-09-500-124-195
20	27	30.3	15	3	US-08-646-285A-125
21	27	30.3	15	4	US-09-947-372A-27
22	27	30.3	16	3	US-08-837-226-2
23	27	30.3	16	4	US-09-537-226-2
24	26.5	29.8	18	4	US-09-829-855-240
25	26	29.2	8	4	US-08-475-955-182
26	26	29.2	8	4	US-08-475-955-185
27	26	29.2	9	3	US-08-159-339A-1062

28	26	29.2	9	4	US-08-737-109-5	Sequence 5, Appli
29	26	29.2	9	6	5204326-100	Patent No. 5204326
30	26	29.2	9	6	5204326-100	Patent No. 5204326
31	26	29.2	10	3	US-08-159-339A-971	Sequence 971, App
32	26	29.2	10	3	US-08-159-339A-1070	Sequence 1070, App
33	26	29.2	13	3	US-09-023-173-9	Sequence 9, Appli
34	26	29.2	13	3	US-09-023-339-7	Sequence 7, Appli
35	26	29.2	14	4	US-08-855-744-2	Sequence 2, Appli
36	26	29.2	14	6	5204326-36	Patent No. 5204326
37	26	29.2	14	6	5204326-95	Patent No. 5204326
38	26	29.2	14	6	5204326-36	Patent No. 5204326
39	26	29.2	14	6	5204326-95	Patent No. 5204326
40	26	29.2	15	3	US-08-096-044C-14	Sequence 14, Appli
41	26	29.2	15	6	US-09-514-245-121	Sequence 121, App
42	26	29.2	15	6	5204326-37	Patent No. 5204326
43	26	29.2	15	6	5204326-40	Patent No. 5204326
44	26	29.2	15	6	5204326-71	Patent No. 5204326
45	26	29.2	15	6	5204326-74	Patent No. 5204326
46	26	29.2	15	6	5204326-37	Patent No. 5204326
47	26	29.2	15	6	5204326-40	Patent No. 5204326
48	26	29.2	15	6	5204326-71	Patent No. 5204326
49	26	29.2	15	6	5204326-74	Patent No. 5204326
50	26	29.2	16	1	US-07-700-526-8	Sequence 8, Appli
51	26	29.2	16	3	US-08-096-044C-13	Sequence 13, Appli
52	26	29.2	16	3	US-08-096-044C-15	Sequence 15, Appli
53	26	29.2	16	5	PCT-US92-03132-8	Sequence 8, Appli
54	26	29.2	16	6	5204326-96	Patent No. 5204326
55	26	29.2	16	6	5204326-96	Patent No. 5204326
56	26	29.2	17	2	US-08-675-921B-7	Sequence 7, Appli
57	26	29.2	17	6	5204326-97	Patent No. 5204326
58	26	29.2	17	6	5204326-97	Patent No. 5204326
59	26	29.2	18	4	US-08-945-038-12	Sequence 12, Appli
60	26	29.2	18	6	5204326-38	Patent No. 5204326
61	26	29.2	18	6	5204326-41	Patent No. 5204326
62	26	29.2	18	6	5204326-98	Patent No. 5204326
63	26	29.2	18	6	5204326-101	Patent No. 5204326
64	26	29.2	18	6	5204326-38	Patent No. 5204326
65	26	29.2	18	6	5204326-41	Patent No. 5204326
66	26	29.2	18	6	5204326-98	Patent No. 5204326
67	26	29.2	18	6	5204326-101	Patent No. 5204326
68	25	28.1	6	3	US-09-467-423-1	Sequence 1, Appli
69	25	28.1	6	3	US-09-467-423-5	Sequence 5, Appli
70	25	28.1	7	1	US-08-594-447-75	Sequence 75, Appli
71	25	28.1	7	1	US-08-541-964-74	Sequence 74, Appli
72	25	28.1	7	2	US-08-665-647-89	Sequence 89, Appli
73	25	28.1	7	3	US-09-467-423-80	Sequence 80, Appli
74	25	28.1	7	3	US-09-467-423-94	Sequence 94, Appli
75	25	28.1	7	3	US-09-467-423-166	Sequence 166, App
76	25	28.1	7	3	US-09-467-423-180	Sequence 180, App
77	25	28.1	8	3	US-09-467-423-65	Sequence 65, Appli
78	25	28.1	8	3	US-09-467-423-79	Sequence 79, Appli
79	25	28.1	8	3	US-09-467-423-93	Sequence 93, Appli
80	25	28.1	8	3	US-09-467-423-151	Sequence 151, App
81	25	28.1	8	3	US-09-467-423-165	Sequence 165, App
82	25	28.1	8	3	US-09-467-423-179	Sequence 179, App
83	25	28.1	9	1	US-08-421-702A-113	Sequence 113, App
84	25	28.1	9	1	US-08-421-702A-116	Sequence 116, App
85	25	28.1	9	1	US-08-421-702A-19	Sequence 19, Appli
86	25	28.1	9	1	US-08-303-052A-55	Sequence 55, Appli
87	25	28.1	9	1	US-08-303-052A-113	Sequence 113, App
88	25	28.1	9	1	US-08-421-696A-19	Sequence 19, Appli
89	25	28.1	9	1	US-08-421-696A-113	Sequence 113, App
90	25	28.1	9	1	US-08-421-696A-116	Sequence 116, App
91	25	28.1	9	1	US-08-421-697A-19	Sequence 19, Appli
92	25	28.1	9	1	US-08-421-697A-113	Sequence 113, App
93	25	28.1	9	1	US-08-421-698A-19	Sequence 19, Appli
94	25	28.1	9	1	US-08-421-698A-113	Sequence 113, App
95	25	28.1	9	1	US-08-421-698A-116	Sequence 116, App
96	25	28.1	9	2	US-08-421-695A-19	Sequence 19, Appli
97	25	28.1	9	2	US-08-421-695A-55	Sequence 55, Appli
98	25	28.1	9	2	US-08-421-695A-114	Sequence 114, App
99	25	28.1	9	2		
100	25	28.1	9	2		

ALIGNMENTS

RESULT 1
US-09-641-803-2
; Sequence 2, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-2

Query Match 100.0%; Score 89; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTQPQLLQVMMPEQGD 17
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Db 1 LQTQPQLLQVMMPEQGD 17

RESULT 2
US-09-641-803-34
; Sequence 34, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-34

Query Match 37.1%; Score 33; DB 4; Length 15;
Best Local Similarity 53.8%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLQVMMPEP 14
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Db 3 QPPQLPPTVMEFP 15

RESULT 3
PCT-US91-05177-19
; Sequence 19, Application PC/TUS9105177
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathy L
; TITLE OF INVENTION: GAMMA-CARBOXYLASE AND METHODS OF USE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05177
; FILING DATE: 19910722
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/557,220
; FILING DATE: 23-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.544PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; FRAGMENT TYPE: internal
PCT-US91-05177-19

Query Match 36.0%; Score 32; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPQPLL 8
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Db 1 TPQPLL 6

RESULT 4
US-08-162-081B-5
; Sequence 5, Application US/08162081B
; Patent No. 5824492
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-162-081B-5

Query Match 34.8%; Score 31; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQLLQVME 13
| | | : | | :
Db 4 PDLPLVEMLK 13

RESULT 5
US-08-780-872-5
; Sequence 5, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-780-872-5

TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-780-872-5

Query Match 34.8%; Score 31; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQLLQVME 13
| | | : | | :
Db 4 PDLPLVEMLK 13

RESULT 6
US-09-085-957-5
; Sequence 5, Application US/09085957
; Patent No. 6274327
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,957
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/780,872
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-085-957-5

Query Match 34.8%; Score 31; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQLLQVME 13

Db 4 PDPLVVMLK 13
| | | | |

RESULT 7
US-08-477-877B-30
; Sequence 30, Application US/08477877B
; Patent No. 5730979
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,877B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1744
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-477-877B-30

Query Match 34.8%; Score 31; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8
| | | | |

Db 8 QSPQPLI 14

RESULT 8
US-08-472-281A-30
; Sequence 30, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette

; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,281A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-472-281A-30

Query Match 34.8%; Score 31; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8
| | | | |

Db 8 QSPQPLI 14

RESULT 9
US-08-477-989B-30
; Sequence 30, Application US/08477989B
; Patent No. 5951983
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette


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;
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,989B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-147
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-477-989B-30

Query Match 34.8%; Score 31; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8
Db 8 QSPQPLI 14

RESULT 10
US-09-017-205-35
; Sequence 35, Application US/09017205
; Patent No. 5965357
; GENERAL INFORMATION:
; APPLICANT: Marsden, Howard S
; TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 5965357th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,205
; FILING DATE: 02-FEB-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-436
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
```

```
;
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide from HSV-2 glycoprotein G
; FRAGMENT TYPE: internal
US-09-017-205-35

Query Match 32.6%; Score 29; DB 2; Length 18;
Best Local Similarity 37.5%; Pred. No. 3e+02;
Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMPEQGD 17
Db 1 KTLPLVVSATAMAPSVD 16

RESULT 11
US-08-594-447-74
; Sequence 74, Application US/08594447
; Patent No. 5776716
; GENERAL INFORMATION:
; APPLICANT: Ron, Dorit
; APPLICANT: Napolitano, Eugene W.
; APPLICANT: Voronova, Anna F.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH
; TITLE OF INVENTION: BLOCKTHE INTERACTION OF FYN WITH PKC-THETA, AND USES
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,447
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.24
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /label= PRK1-3
US-08-594-447-74

Query Match 31.5%; Score 28; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MEPOG 16
Db 1 MEPOG 5
```

RESULT 12
US-08-541-964-73
; Sequence 73, Application US/08541964
; Patent No. 5783405
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; APPLICANT: Kauvar, Lawrence W.
; APPLICANT: Napolitano, Eugene W.
; TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS
; TITLE OF INVENTION: OF SIGNAL TRANSDUCTION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW-STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,964
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.23
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /label= PRK1-3
US-08-541-964-73
Query Match 31.5%; Score 28; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 MEPOG 16
Db 1 MEPOG 5
RESULT 13
US-08-665-647-88
; Sequence 88, Application US/08665647
; Patent No. 5935803
; GENERAL INFORMATION:
; APPLICANT: Dasquez, Nicki J.
; APPLICANT: Ron, Dorit
; APPLICANT: Voronova, Anna F.
; APPLICANT: Napolitano, Eugene W.
; TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS
; TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,647
; FILING DATE: 18-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /label= PRK1-3
US-08-665-647-88
Query Match 31.5%; Score 28; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 MEPOG 16
Db 1 MEPOG 5
RESULT 14
US-08-981-392-53
; Sequence 53, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-981-392-53

Query Match      31.5%; Score 28; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      4 PQLPLQVWME 13
      |||||:
Db      1 PQLPLVTRTEQ 10

RESULT 15
US-09-908-322-53
; Sequence 53, Application US/09908322
; Patent No. 6783956
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
;             Henrique, Domingos Manuel Pinto
;             Lewis, Julian Hart
;             Artavanis-Tsakonas, Spyridon
;             Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
;                     VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-908-322-53

Query Match      31.5%; Score 28; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      4 PQLPLQVWME 13
      |||||:
Db      1 PQLPLVTRTEQ 10

RESULT 16
US-08-553-257A-21
; Sequence 21, Application US/08553257A
; Patent No. 5994083
; GENERAL INFORMATION:
; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA
; APPLICANT: MOLECOLARE P. ANGELETTI S.p.A.
; APPLICANT: FELICI, Franco
; APPLICANT: LUZZAGO, Alessandra
; APPLICANT: NICOSIA, Alfredo
; APPLICANT: MONACI, Paolo
; APPLICANT: CORTESE, Riccardo
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
; TITLE OF INVENTION: OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
; TITLE OF INVENTION: DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,257A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IT94/00054
; FILING DATE: 05-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: RM93A000301
; FILING DATE: 11-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: recombinant protein
; HYPOTHETICAL: yes
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; LIBRARY: of recombinant peptides on phage
; CLONE: phagic
; FEATURE:
; NAME/KEY: polypeptide
; IDENTIFICATION METHOD: selection with specific antibodies
US-08-553-257A-21
```

Query Match 31.5%; Score 28; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

Qy 2 QTPQLQVMMEPGD 17
Db 4 QVPQSRL---EPWGD 15

RESULT 17

US-09-441-992-21
; Sequence 21, Application US/09441992
; Patent No. 6541210
; GENERAL INFORMATION:
; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA
; MOLECOLARE P. ANGELETTI S.p.A.
; FELICI, Franco
; LUZZAGO, Alessandra
; NICOSIA, Alfredo
; MONACI, Paolo
; CORTESE, Riccardo
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
; OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
; DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/441,992
FILING DATE: 18-NO. 6541210-1999
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: RM93A000301
FILING DATE: <Unknown>
FILING DATE: 11-MAY-1993
NAME: Browdy, Roger L.
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: recombinant protein
HYPOTHETICAL: yes
FRAGMENT TYPE: internal
IMMEDIATE SOURCE:
LIBRARY: of recombinant peptides on phage
CLONE: phagic
(ix) FEATURE
(A) NAME: polypeptide

SEQUENCE DESCRIPTION: SEQ ID NO: 21:
(ix) FEATURE
(A) NAME: polypeptide

US-09-441-992-21
Query Match 31.5%; Score 28; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;

Qy 2 QTPQLQVMMEPGD 17
Db 4 QVPQSRL---EPWGD 15

US-08-602-999A-195
; Sequence 195, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 195:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-195

Query Match 31.5%; Score 28; DB 3; Length 16;
Best Local Similarity 41.7%; Pred. No. 3.8e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TPQPLQVMMEP 14
Db 4 TPRPAVQRMNP 15

RESULT 19

US-09-500-124-195
; Sequence 195, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.

;; APPLICANT: FOWLKES, Dana M.
;; APPLICANT: RIDER, James E.
;; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;; TITLE OF INVENTION: ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/500,124
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mirostock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 195:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-09-500-124-195

Query Match 31.5%; Score 28; DB 4; Length 16;
Best Local Similarity 41.7%; Pred. No. 3.8e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TPQPLLQVMPEP 14
|||:|:
Db 4 TPRPVPQRMWP 15

RESULT 20
US-08-646-265A-125
; Sequence 125, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/646,265A
;; FILING DATE: 09-SEP-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/JP94/01763
;; FILING DATE: 19-OCT-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 5-291078
;; FILING DATE: 19-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WEGNER, Harold C.
;; REGISTRATION NUMBER: 25,258
;; REFERENCE/DOCKET NUMBER: 53466/184
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 672-5300
;; TELEFAX: (202) 672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 125:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-646-265A-125

Query Match 30.3%; Score 27; DB 3; Length 15;
Best Local Similarity 57.1%; Pred. No. 5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTQPPLL 8
||:|:
Db 8 QSPKPLI 14

RESULT 21
US-09-947-372A-27
; Sequence 27, Application US/09947372A
; Patent No. 6613557
; GENERAL INFORMATION:
; APPLICANT: FRAZER, IAN
; APPLICANT: ZHOU, JIAN
; TITLE OF INVENTION: PAPILLOMAVIRUS VACCINE
; FILE REFERENCE: 065064/0137
; CURRENT APPLICATION NUMBER: US/09/947,372A
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 08/185,928
; PRIOR FILING DATE: 1994-01-19
; PRIOR APPLICATION NUMBER: PCT/AU92/02184
; PRIOR FILING DATE: 1992-07-20
; PRIOR APPLICATION NUMBER: AU PK7322
; PRIOR FILING DATE: 1991-07-19
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-947-372A-27

Query Match 30.3%; Score 27; DB 4; Length 15;
Best Local Similarity 40.0%; Pred. No. 5e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 8 LQVMMEPOGD 17
:::|:
Db 1 IKMVSEPIGD 10

RESULT 22
US-08-837-226-2
; Sequence 2, Application US/08837226
; Patent No. 6043216
; GENERAL INFORMATION:

APPLICANT: Toback, F. Gary
APPLICANT: Lieske, John C.
TITLE OF INVENTION: METHODS AND COMPOSITION FOR DETECTING
AND TREATING KIDNEY DISEASES ASSOCIATED WITH ADHESION OF
CRYSTALS TO KIDNEY CELLS
TITLE OF INVENTION: CRYSTALS TO KIDNEY CELLS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,226
FILING DATE: 08-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/389,005
FILING DATE: 15-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-837-226-2

Query Match 30.3%; Score 27; DB 3; Length 16;
Best Local Similarity 83.3%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQLLQ 9
Db 10 PQLYQ 15

RESULT 23
US-09-537-226-2
Sequence 2, Application US/09537226
Patent No. 6482934
GENERAL INFORMATION:
APPLICANT: TOBACK, F. GARY
APPLICANT: LIESKE, JOHN C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
AND TREATING KIDNEY DISEASES ASSOCIATED WITH ADHESION OF CRYSTALS TO
CRYSTALS TO KIDNEY CELLS
TITLE OF INVENTION: KIDNEY CELLS
FILE REFERENCE: 21459/90606
CURRENT APPLICATION NUMBER: US/09/537,226
CURRENT FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: 08/389,005
PRIOR FILING DATE: 1995-02-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
US-09-537-226-2

Query Match 30.3%; Score 27; DB 4; Length 16;
Best Local Similarity 83.3%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQLLQ 9
Db 10 PQLYQ 15

RESULT 24
US-09-829-855-240
Sequence 240, Application US/09829855
Patent No. 6613520
GENERAL INFORMATION:
APPLICANT: Matthew, Ashby N.
TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations
FILE REFERENCE: ASHY-1
CURRENT APPLICATION NUMBER: US/09/829,855
CURRENT FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/196063
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/196258
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 244
SOFTWARE: PatentIn version 3.1
SEQ ID NO 240
LENGTH: 18
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Uncultured Acidobacterium Sub.Div-2
US-09-829-855-240

Query Match 29.8%; Score 26.5; DB 4; Length 18;
Best Local Similarity 58.3%; Pred. No. 7.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 5 QPLQVMMEPQ 16
Db 3 QP-LHVATPQ 13

RESULT 25
US-08-475-955-182
Sequence 182, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
City: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819

; FILING DATE: April 13, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; INFORMATION FOR SEQ ID NO: 182:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-475-955-182

Query Match 29.2%; Score 26; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 QVWMEPOG 16
Db 1 QQVWTPQG 8

RESULT 26
US-08-475-955-185
; Sequence 185, Application US/08475955
; Patent No. 6641813
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,955
; FILING DATE: June 7, 1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-475-955-185

Query Match 29.2%; Score 26; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 MEPOGD 17
Db 1 MTPQGB 6

RESULT 27
US-08-159-339A-1062
; Sequence 1062, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1062:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1062

Query Match 29.2%; Score 26; DB 3; Length 9;

Best Local Similarity 80.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

Qy 13 EPQGD 17
:||||
Db 1 QPQGD 5

RESULT 28
US-08-737-109-5
; Sequence 5, Application US/08737109
; Patent No. 6455688
; GENERAL INFORMATION:
; APPLICANT: SIABAS, Antoni Ryszard
; APPLICANT: ELBOROUGH, Kieran Michael
; APPLICANT: BRIGHT, Simon William Jonathan
; APPLICANT: FENTIM, Philip Anthony
; TITLE OF INVENTION: Plant Gene Specifying Acetyl Coenzyme A
; TITLE OF INVENTION: Carboxylase and Transformed Plants Containing Same
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,109
; FILING DATE: 21-OCT-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/00846
; FILING DATE: 02-MAY-1994
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Avena sativa
US-08-737-109-5

Query Match 29.2%; Score 26; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0;

Qy 11 MNEPQ 16
:||||
Db 2 VLEPQ 7

RESULT 29
5204326-100
; Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHIRO;SHIMIZU, FUMIO
; FINAL, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:100:
; LENGTH: 9

5204326-100

Query Match 29.2%; Score 26; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 LQTPQ 5
:||||
Db 3 LQTPQ 7

RESULT 30
5204326-100
; Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHIRO;SHIMIZU, FUMIO
; FINAL, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:100:
; LENGTH: 9
5204326-100

Query Match 29.2%; Score 26; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 LQTPQ 5
:||||
Db 3 LQTPQ 7

RESULT 31
US-08-159-339A-971
; Sequence 971, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver

; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of '1-Antitrypsin
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,339
; FILING DATE: 13-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,991
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 0665-0003.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: N-terminal sequence of plant-produced mature AAT
; US-09-023-339-7

Query Match 29.2%; Score 26; DB 3; Length 13;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPQGD 17
Db 2 DPQGD 6

RESULT 35
US-08-855-744-2
; Sequence 2, Application US/08855744
; Patent No. 6685930
; GENERAL INFORMATION:
; APPLICANT: Chang, Tse Wen
; TITLE OF INVENTION: METHODS AND SUBSTANCES FOR RECRUITING
; TITLE OF INVENTION: THERAPEUTIC AGENTS TO SOLID TISSUES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Hi Density Diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS, Version 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,744
; FILING DATE: 08-May-1997

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,649
; FILING DATE:
; APPLICATION NUMBER: US/07/675,654
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
; REFERENCE/DOCKET NUMBER: TNX91-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-664-2288
; TELEFAX: 713-664-8914
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; US-08-855-744-2

Query Match 29.2%; Score 26; DB 4; Length 14;
Best Local Similarity 62.5%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TPQPLLQV 10
Db 4 TPSPGIQV 11

RESULT 36
5204326-36
; Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:36:
; LENGTH: 14
; 5204326-36

Query Match 29.2%; Score 26; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5
Db 2 LQTPQ 6

RESULT 37
5204326-95
; Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:95:
; LENGTH: 14
; 5204326-95

Query Match 29.2%; Score 26; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5
|
|
|
|
Db 2 LQTPQ 6

RESULT 38
5204326-36
;PATENT NO. 5204326
;APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
;MITSURU;SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
;TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
;METABOLISM IMPROVING AGENT
;NUMBER OF SEQUENCES: 147
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/493,359
;FILING DATE: 14-MAR-1990
;SEQ ID NO:36:
;LENGTH: 14
5204326-36

Query Match 29.2%; Score 26; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5
|
|
|
|
Db 2 LQTPQ 6

RESULT 39
5204326-95
;PATENT NO. 5204326
;APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
;MITSURU;SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
;TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
;METABOLISM IMPROVING AGENT
;NUMBER OF SEQUENCES: 147
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/493,359
;FILING DATE: 14-MAR-1990
;SEQ ID NO:95:
;LENGTH: 14
5204326-95

Query Match 29.2%; Score 26; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5
|
|
|
|
Db 2 LQTPQ 6

RESULT 40
US-08-096-044C-14
;Sequence 14, Application US/08096044C
;Patent No. 6153192
;GENERAL INFORMATION:
;APPLICANT: Kopetzki, Erhard, Klein, Christian
;TITLE OF INVENTION: PEPTIDES WITH CHARACTERISTIC
;TITLE OF INVENTION: ANTIGENIC DETERMINANTS FOR
;TITLE OF INVENTION: 1-MICROGLOBULIN
;NUMBER OF SEQUENCES: 18
;CORRESPONDENCE ADDRESS:
;ADDRESSEE: Felfe & Lynch
;STREET: 805 Third Avenue
;CITY: New York
;STATE: New York
;COUNTRY: USA
;ZIP: 10022

;COMPUTER READABLE FORM:
;MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
;COMPUTER: IBM PS/2
;OPERATING SYSTEM: PC-DOS
;SOFTWARE: Wordperfect
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/08/096,044C
;FILING DATE: July 22, 1993
;CLASSIFICATION: 424
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: DE 40 24 919
;FILING DATE: August 6, 1990
;ATTORNEY/AGENT INFORMATION:
;NAME: Bauer, John A.
;REGISTRATION NUMBER: 32,554
;REFERENCE/DOCKET NUMBER: HUBR 1000.1-PFF/JAB
;TELECOMMUNICATION INFORMATION:
;TELEPHONE: (212) 688-9200
;TELEFAX: (212) 838-3884
;INFORMATION FOR SEQ ID NO: 14:
;SEQUENCE CHARACTERISTICS:
;LENGTH: 15
;TYPE: amino acid
;STRANDEDNESS: single
;TOPOLOGY: linear
US-08-096-044C-14

Query Match 29.2%; Score 26; DB 3; Length 15;
Best Local Similarity 57.1%; Pred. No. 7.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8
|
|
|
|
Db 6 QEPEPIL 12

Search completed: June 7, 2005, 23:23:11
Job time : 25.1818 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 23:00:52 ; Search time 76.5 Seconds
(without alignments)
85.185 Million cell updates/sec

Title: US-10-691-157-2

Perfect score: 89

Sequence: 1 LQTPQLQVMMPEQGD 17

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 309695

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	17	14	US-10-381-652-2
2	89	100.0	17	16	US-10-691-157-2
3	89	100.0	17	17	US-10-691-330-2
4	56	62.9	11	16	US-10-182-110-1
5	33	37.1	12	14	US-10-286-457-195
6	33	37.1	15	14	US-10-381-652-34
7	33	37.1	15	16	US-10-691-157-34
8	33	37.1	15	17	US-10-691-330-34
9	30	33.7	16	15	US-10-346-162-130
10	29	32.6	9	11	US-09-870-216C-3
11	29	32.6	9	13	US-10-017-327-3
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 195, App
					Sequence 34, Appl
					Sequence 34, Appl
					Sequence 34, Appl
					Sequence 130, App
					Sequence 3, Appli
					Sequence 3, Appli

12	29	32.6	10	14	US-10-073-054-20	Sequence 20, Appl
13	29	32.6	13	15	US-10-469-101-53	Sequence 53, Appl
14	29	32.6	18	9	US-09-864-761-40147	Sequence 40147, A
15	28	31.5	9	15	US-10-013-312-33	Sequence 33, Appl
16	28	31.5	9	15	US-10-013-312-412	Sequence 412, App
17	28	31.5	9	15	US-10-013-312-502	Sequence 502, App
18	28	31.5	9	15	US-10-013-312-605	Sequence 605, App
19	28	31.5	9	15	US-10-013-312-1358	Sequence 1358, App
20	28	31.5	9	15	US-10-013-312-1522	Sequence 1522, App
21	28	31.5	9	15	US-10-013-312-1598	Sequence 1598, App
22	28	31.5	9	15	US-10-013-312-1693	Sequence 1693, App
23	28	31.5	9	15	US-10-013-312-1721	Sequence 1721, App
24	28	31.5	9	15	US-10-013-312-1810	Sequence 1810, App
25	28	31.5	9	15	US-10-013-312-1983	Sequence 1983, App
26	28	31.5	9	15	US-10-013-312-1983	Sequence 1983, App
27	28	31.5	9	15	US-10-013-312-2020	Sequence 2020, App
28	28	31.5	10	9	US-09-908-322-53	Sequence 53, Appl
29	28	31.5	10	10	US-09-783-931-53	Sequence 53, Appl
30	28	31.5	10	15	US-10-013-312-82	Sequence 82, Appl
31	28	31.5	10	15	US-10-013-312-196	Sequence 196, App
32	28	31.5	10	15	US-10-013-312-459	Sequence 459, App
33	28	31.5	10	15	US-10-013-312-560	Sequence 560, App
34	28	31.5	10	15	US-10-013-312-690	Sequence 690, App
35	28	31.5	10	15	US-10-013-312-2072	Sequence 2072, App
36	28	31.5	10	15	US-10-013-312-2241	Sequence 2241, App
37	28	31.5	10	15	US-10-013-312-2432	Sequence 2432, App
38	28	31.5	10	15	US-10-013-312-2450	Sequence 2450, App
39	28	31.5	13	14	US-10-234-816-33	Sequence 33, Appl
40	28	31.5	14	14	US-10-185-425-24	Sequence 24, Appl
41	28	31.5	14	16	US-10-871-776-24	Sequence 24, Appl
42	28	31.5	15	15	US-10-013-312-2620	Sequence 2620, App
43	28	31.5	15	15	US-10-013-312-2653	Sequence 2653, App
44	28	31.5	15	15	US-10-013-312-2691	Sequence 2691, App
45	28	31.5	15	15	US-10-013-312-2692	Sequence 2692, App
46	28	31.5	15	15	US-10-013-312-2781	Sequence 2781, App
47	28	31.5	15	15	US-10-013-312-2808	Sequence 2808, App
48	28	31.5	15	15	US-10-013-312-2824	Sequence 2824, App
49	28	31.5	15	16	US-10-769-831-7	Sequence 7, Appli
50	28	31.5	15	17	US-10-770-140-7	Sequence 7, Appli
51	28	31.5	15	17	US-10-770-304-6	Sequence 6, Appli
52	28	31.5	16	14	US-10-161-791-195	Sequence 195, Appl
53	28	31.5	16	15	US-10-319-315-49	Sequence 49, Appl
54	28	31.5	16	16	US-10-474-955-67	Sequence 67, Appl
55	27.5	30.9	14	10	US-09-991-225-68	Sequence 68, Appl
56	27.5	30.9	14	15	US-10-369-405-68	Sequence 68, Appl
57	27.5	30.9	18	9	US-09-984-056-95	Sequence 95, Appl
58	27.5	30.9	18	14	US-10-105-232-95	Sequence 95, Appl
59	27	30.3	10	14	US-10-185-815-89	Sequence 89, Appl
60	27	30.3	12	10	US-09-954-385-136	Sequence 136, App
61	27	30.3	12	17	US-10-912-512-136	Sequence 136, App
62	27	30.3	12	17	US-10-235-043-136	Sequence 136, App
63	27	30.3	15	10	US-09-749-873-125	Sequence 125, App
64	27	30.3	15	16	US-10-732-345-27	Sequence 27, Appl
65	27	30.3	16	14	US-10-267-251-7	Sequence 7, Appli
66	27	30.3	16	14	US-10-299-043-2	Sequence 2, Appli
67	26.5	29.8	18	9	US-09-829-855-240	Sequence 240, App
68	26.5	29.8	18	16	US-10-607-077A-240	Sequence 180, App
69	26	29.2	8	15	US-10-376-121A-182	Sequence 242, App
70	26	29.2	8	15	US-10-376-121A-185	Sequence 185, App
71	26	29.2	9	8	US-08-344-824-282	Sequence 282, App
72	26	29.2	9	16	US-10-777-053-88	Sequence 88, Appl
73	26	29.2	9	16	US-10-837-217-88	Sequence 88, Appl
74	26	29.2	10	8	US-08-344-824-393	Sequence 393, App
75	26	29.2	10	10	US-09-572-404B-1161	Sequence 1161, App
76	26	29.2	10	17	US-10-808-187-478	Sequence 478, App
77	26	29.2	10	17	US-10-801-590-200	Sequence 200, App
78	26	29.2	11	16	US-10-473-127-114	Sequence 114, App
79	26	29.2	12	17	US-10-935-642-18	Sequence 18, Appl
80	26	29.2	13	17	US-10-488-662-26	Sequence 26, Appl
81	26	29.2	13	17	US-10-488-662-27	Sequence 27, Appl
82	26	29.2	13	17	US-10-488-662-28	Sequence 28, Appl
83	26	29.2	14	10	US-09-992-665-52	Sequence 52, Appl
84	26	29.2	15	15	US-10-013-312-2882	Sequence 2882, App

85 26 29.2 15 15 US-10-682-420-121 Sequence 121, App
86 26 29.2 15 15 US-10-409-613-121 Sequence 121, App
87 26 29.2 15 15 US-10-442-180-121 Sequence 121, App
88 26 29.2 15 16 US-10-718-266-121 Sequence 121, App
89 26 29.2 15 17 US-10-775-337-121 Sequence 121, App
90 26 29.2 15 17 US-10-858-343-1 Sequence 1, Appli
91 26 29.2 15 17 US-10-637-011-121 Sequence 121, App
92 26 29.2 17 9 US-09-864-761-46994 Sequence 46994, A
93 26 29.2 17 14 US-10-138-089-18 Sequence 18, Appl
94 26 29.2 17 15 US-10-422-571-99 Sequence 99, Appl
95 26 29.2 18 8 US-08-945-038-12 Sequence 12, Appl
96 26 29.2 18 14 US-10-225-567A-1708 Sequence 1708, Ap
97 26 29.2 18 17 US-10-803-738-27 Sequence 27, Appl
98 25.5 28.7 12 15 US-10-649-873-122 Sequence 122, App
99 25 28.1 9 15 US-10-334-726-124 Sequence 124, App
100 25 28.1 9 17 US-10-487-259-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-281-652-2
; Sequence 2, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-2

Query Match 100.0%; Score 89; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQLLQVNMPEQGD 17
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Db 1 LQTPQLLQVNMPEQGD 17

RESULT 2
US-10-691-157-2
; Sequence 2, Application US/10691157
; Publication No. US20040266681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265.00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-157-2

Query Match 100.0%; Score 89; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQLLQVNMPEQGD 17
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Db 1 LQTPQLLQVNMPEQGD 17

RESULT 3
US-10-691-330-2
; Sequence 2, Application US/10691330
; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: Boldogh, Istvan
; APPLICANT: Stanton, G. John
; APPLICANT: Georgiades, Jerzy A.
; APPLICANT: Hughes, Thomas K., Jr.
; APPLICANT: Kruzel, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265.00390101
; CURRENT APPLICATION NUMBER: US/10/691,330
; CURRENT FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-330-2

Query Match 100.0%; Score 89; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQLLQVNMPEQGD 17
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Db 1 LQTPQLLQVNMPEQGD 17

RESULT 4
US-10-182-110-1
; Sequence 1, Application US/10182110
; Publication No. US20040171553A1
; GENERAL INFORMATION:
; APPLICANT: Regen Therapeutics plc
; APPLICANT: Georgiades, Jerzy A.
; TITLE OF INVENTION: Peptide Fragments of Colostrinin And Their Use
; FILE REFERENCE: AAT-14173
; CURRENT APPLICATION NUMBER: US/10/182,110

; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: GB0001825.9
; FILING DATE: 2000-01-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial

; FEATURE:
; OTHER INFORMATION: Truncated version of a peptide found in colostrin

US-10-182-110-1
Query Match 62.9%; Score 56; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQ 15
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Db 1 QPLLQVMMEPQ 11

RESULT 5

US-10-286-457-195
; Sequence 195, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 195
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based

; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-195

Query Match 37.1%; Score 33; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQP 6
| | | | |
Db 2 LQTPQP 7

RESULT 6

US-10-281-652-34
; Sequence 34, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND

; FILE REFERENCE: 265, 00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1

US-10-281-652-34
Query Match 37.1%; Score 33; DB 16; Length 15;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14
| | | | | : | |
Db 3 QPPQPLPPTVMFP 15

RESULT 8

US-10-691-330-34
; Sequence 34, Application US/10691330
; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: Boldogh, Istvan
; APPLICANT: Stanton, G. John
; APPLICANT: Georgiades, Jerzy A.
; APPLICANT: Hughes, Thomas K., Jr.
; APPLICANT: Kruzel, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265.00390101

; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-34

Query Match 37.1%; Score 33; DB 14; Length 15;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14
| | | | | : | |
Db 3 QPPQPLPPTVMFP 15

RESULT 7

US-10-691-157-34
; Sequence 34, Application US/10691157
; Publication No. US2004026681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADES, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUZEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265.00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-157-34

Query Match 37.1%; Score 33; DB 16; Length 15;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14
| | | | | : | |
Db 3 QPPQPLPPTVMFP 15

RESULT 8

US-10-691-330-34
; Sequence 34, Application US/10691330
; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: Boldogh, Istvan
; APPLICANT: Stanton, G. John
; APPLICANT: Georgiades, Jerzy A.
; APPLICANT: Hughes, Thomas K., Jr.
; APPLICANT: Kruzel, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265.00390101

; CURRENT APPLICATION NUMBER: US/10/691,330
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-330-34

Query Match 37.1%; Score 33; DB 17; Length 15;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQLQVMMEP 14
Db 3 QPPQLPPTVMFP 15

RESULT 9
US-10-346-162-130
; Sequence 130, Application US/10346162
; Publication No. US20030224390A1
; GENERAL INFORMATION:
; APPLICANT: KARO BIO USA, INC.
; APPLICANT: FOMKES, Dana M.
; APPLICANT: BARNETT, Thomas R.
; APPLICANT: BUHRER, Benjamin
; TITLE OF INVENTION: METHOD OF IDENTIFYING CONFORMATION-SENSITIVE BINDING PEPTIDES AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: PAIGE=1H
; CURRENT APPLICATION NUMBER: US/10/346,162
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US 09/614,865
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 09/860,688
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-346-162-130

Query Match 33.7%; Score 30; DB 15; Length 16;
Best Local Similarity 45.5%; Pred. No. 8.1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 PLLQVMMEPQG 16
Db 5 PLLMALLAPPG 15

RESULT 10
US-09-870-216C-3
; Sequence 3, Application US/09870216C
; Publication No. US20040138135A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
; FILE REFERENCE: 68126881210100
; CURRENT APPLICATION NUMBER: US/09/870,216C
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/209,391
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/226,256

; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/257,008
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-216C-3

Query Match 32.6%; Score 29; DB 11; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.5e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LQVMMEP 14
Db 2 LQLLMEP 8

RESULT 11
US-10-017-327-3
; Sequence 3, Application US/10017327
; Publication No. US20020155471A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS AND
; TITLE OF INVENTION: METHODS FOR USING SAME
; FILE REFERENCE: GZ 2101.20
; CURRENT APPLICATION NUMBER: US/10/017,327
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-327-3

Query Match 32.6%; Score 29; DB 13; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.5e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LQVMMEP 14
Db 2 LQLLMEP 8

RESULT 12
US-10-073-054-20
; Sequence 20, Application US/10073054
; Publication No. US20030167485A1
; GENERAL INFORMATION:
; APPLICANT: Garvan Institute of Medical Research
; APPLICANT: HERZOG, Herbert
; TITLE OF INVENTION: No. US20030167485A1el G-protein coupled receptor-encoding gene an
; TITLE OF INVENTION: therefor
; FILE REFERENCE: 1871-132 (93702-CIP/MRO)
; CURRENT APPLICATION NUMBER: US/10/073,054
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/308,696
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00805
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: AU P0386
; PRIOR FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: N-terminal peptide
US-10-073-054-20


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Query Match      32.6%; Score 29; DB 14; Length 10;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLQ 9
Db 2 TPQSLQ 8

RESULT 13
US-10-469-101-53
; Sequence 53, Application US/10469101
; Publication No. US20040071688A1
; GENERAL INFORMATION:
; APPLICANT: CARTER, Francis J.
; TITLE OF INVENTION: MODIFIED THROMBOPOIETIN WITH REDUCED
; FILE REFERENCE: MER-109
; CURRENT APPLICATION NUMBER: US/10/469,101
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: EP 01104702.4
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: PCT/EP02/01931
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-469-101-53

Query Match      32.6%; Score 29; DB 15; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 QPLQVMEPQG 16
Db 1 QSLGTQLPQG 12

RESULT 14
US-09-864-761-40147
; Sequence 40147, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40147
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005343.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
US-09-864-761-40147

Query Match      32.6%; Score 29; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLQV 10
Db 3 QPLQV 8

RESULT 15
US-10-013-312-33
; Sequence 33, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-33

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Query Match 31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||::|
Db 3 TPSPIIQ 9

RESULT 16

US-10-013-312-412
; Sequence 412, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 412
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-412

Query Match 31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||::|
Db 1 TPSPIIQ 7

RESULT 17

US-10-013-312-502
; Sequence 502, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 502
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-502

Query Match 31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||::|
Db 1 TPSPIIQ 7

RESULT 18

US-10-013-312-605
; Sequence 605, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 605
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-605

Query Match 31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||::|
Db 1 TPSPIIQ 7

RESULT 19

US-10-013-312-1358
; Sequence 1358, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1358
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1358

Query Match 31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||::|
Db 1 TPSPIIQ 7

RESULT 20

US-10-013-312-1522
; Sequence 1522, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1522
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1522

Query Match 31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||:|
Db 2 TPSPFIQ 8

RESULT 21
US-10-013-312-1598
; Sequence 1598, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1598
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1598

Query Match 31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||:|
Db 1 TPSPFIQ 7

RESULT 22
US-10-013-312-1693
; Sequence 1693, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED

; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1693
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1693

Query Match 31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||:|
Db 1 TPSPFIQ 7

RESULT 23
US-10-013-312-1721
; Sequence 1721, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1721
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1721

Query Match 31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||:|
Db 1 TPSPFIQ 7

RESULT 24
US-10-013-312-1810
; Sequence 1810, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1810

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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1810

Query Match      31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
Db 1 TPSPILQ 7

RESULT 25
US-10-013-312-1928
; Sequence 1928, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1928
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1928

Query Match      31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
Db 1 TPSPILQ 7

RESULT 26
US-10-013-312-1983
; Sequence 1983, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1983
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1983

Query Match      31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
Db 1 TPSPILQ 7

RESULT 27
US-10-013-312-2020
; Sequence 2020, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2020
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2020

Query Match      31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
Db 3 TPSPILQ 9

RESULT 28
US-09-908-322-53
; Sequence 53, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
```

```

; NAME: Mistrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
;
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
;
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-908-322-53
Query Match 31.5%; Score 28; DB 9; Length 10;
Best Local Similarity 50.0%; Pred.No.1e+03; 3; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches

QY 4 PQLPLQVMME 13
| | | | : |
Db 1 PQLPLVTEQE 10

RESULT 29
US-09-783-931-53
; Sequence 53, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
;
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
; AND FRAGMENTS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,931
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
;
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

```

Qy 3 TPQPLLQ 9
|||::|
Db 2 TPSPIIQ 8

RESULT 32

US-10-013-312-459
; Sequence 459, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 459
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-459

Query Match 31.5%; Score 28; DB 15; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||::|
Db 2 TPSPIIQ 8

RESULT 33

US-10-013-312-560
; Sequence 560, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 560
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-560

Query Match 31.5%; Score 28; DB 15; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||::|
Db 2 TPSPIIQ 8

RESULT 34

US-10-013-312-690

; Sequence 690, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 690
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-690

Query Match 31.5%; Score 28; DB 15; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||::|
Db 2 TPSPIIQ 8

RESULT 35

US-10-013-312-2072
; Sequence 2072, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2072
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2072

Query Match 31.5%; Score 28; DB 15; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||::|
Db 2 TPSPIIQ 8

RESULT 36

US-10-013-312-2241
; Sequence 2241, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2241
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2241

Query Match 31.5%; Score 28; DB 15; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||:|
Db 2 TPSP1IQ 8

RESULT 37

US-10-013-312-2432
; Sequence 2432, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AVA

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2432
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2432

Query Match 31.5%; Score 28; DB 15; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||:|
Db 1 TPSP1IQ 7

RESULT 38

US-10-013-312-2450
; Sequence 2450, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AVA

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30

; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2450
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2450

Query Match 31.5%; Score 28; DB 15; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
|||:|
Db 2 TPSP1IQ 8

RESULT 39

US-10-234-816-33
; Sequence 33, Application US/10234816
; Publication No. US20030157514A1
; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL PLECKSTRAIN HOMOLOG DOMAIN AND PR
; FILE REFERENCE: D0117 NP
; CURRENT APPLICATION NUMBER: US/10/234,816
; CURRENT FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-234-816-33

Query Match 31.5%; Score 28; DB 14; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTQP0LL 8
:|:|:|
Db 5 ETPRPLM 11

RESULT 40

US-10-185-425-24
; Sequence 24, Application US/10185425
; Publication No. US20030053984A1
; GENERAL INFORMATION:

; APPLICANT: Apotech Research and Development Ltd.
; APPLICANT: Tschoop, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Holler, Nils
; TITLE OF INVENTION: A Bimer or an Oligomer of a Dimer, Trimer, Quadromer, or Pentamer
; FILE REFERENCE: 1708.001US1
; CURRENT APPLICATION NUMBER: US/10/185,425
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: PCT/EP00/13032
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: DE 199 63 859.4
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Linker
US-10-185-425-24

Query Match 31.5%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 PQLLQVMEPQ 15
||| |
Db 3 PPKPKPKPE 14

Search completed: June 7, 2005, 23:31:32
Job time : 78.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:56:36 ; Search time 15.7636 Seconds
(without alignments)
103.763 Million cell updates/sec

Title: US-10-691-157-2

Perfect score: 89

Sequence: 1 LQTPQLQVMEFGD 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	28.1	14	2	C44823 synaptosomal-assoc
2	25	28.1	18	2	C435704 cytochrome P450 ol
3	25	28.1	18	2	F49215 urease (EC 3.5.1.5
4	24	27.0	10	2	A61218 alpha-gliadin 4Ha
5	24	27.0	15	2	A61391 alpha-1-antitrypsi
6	23	25.8	11	2	PC2330 cycloinulooligosac
7	23	25.8	12	2	S70344 amine oxidase (cop
8	23	25.8	15	2	E56819 PS I complex subun
9	23	25.8	16	2	A46236 transforming prote
10	23	25.8	16	2	P80210 28K protein 4209 -
11	23	25.8	18	2	I59649 human leukocyte an
12	21	23.6	10	2	B61218 alpha-gliadin 6Ha
13	21	23.6	12	2	PH1567 cerebrin 28 - huma
14	21	23.6	14	2	PH1566 cerebrin 30 - huma
15	21	23.6	14	2	PN0147 omega-gliadine 1 a
16	21	23.6	15	2	A42413 Ig heavy chain V r
17	21	23.6	15	2	A40634 orf19 3' of eryk -
18	21	23.6	17	2	PC1318 large granule L6 c
19	21	23.6	18	2	PN0149 beta-Gliadine 13 -
20	21	23.6	18	2	S78767 ribosomal protein
21	20	22.5	10	2	PX0030 triacylglycerol li
22	20	22.5	10	2	PQ0788 NADH2 dehydrogenas
23	20	22.5	13	2	D39690 neural cell adhesi
24	20	22.5	14	2	PC7075 guanylate cyclase
25	20	22.5	15	2	PA0021 protein QA300016 -
26	20	22.5	15	2	PN0148 omega-gliadine 3 -
27	20	22.5	15	2	PL0110 complement factor
28	20	22.5	15	2	A41436 alpha-macroglobuli
29	20	22.5	16	2	S00123 dihydrolipoamide S

30	20	22.5	16	2	D83794	hypothetical prote
31	20	22.5	17	2	S33609	extensin - maize (
32	20	22.5	17	2	B31769	T-cell receptor de
33	20	22.5	18	2	S10452	hypothetical prote
34	20	22.5	18	2	I78841	thrombopoietin rec
35	19	21.3	8	2	S21288	lectin - potato (f
36	19	21.3	9	2	S70345	amine oxidase (cop
37	19	21.3	10	2	D33098	214K exoantigen (v
38	19	21.3	10	2	A61007	hennetin (EC 3.4.-
39	19	21.3	11	2	S42587	cell protein - Bsc
40	19	21.3	11	2	S21127	precorrin methyltr
41	19	21.3	11	2	PN0044	protein kinase C i
42	19	21.3	12	2	A61309	glycoprotein hormo
43	19	21.3	13	2	S36668	hypothetical prote
44	19	21.3	14	2	I54945	gene C protein - E
45	19	21.3	14	2	A39239	actin 8 - slime mo
46	19	21.3	14	2	S12904	protein kinase (EC
47	19	21.3	15	2	A56891	gamma 1 gliadin -
48	19	21.3	15	2	F44823	synaptosomal-assoc
49	19	21.3	16	2	PH0763	T-cell receptor be
50	19	21.3	16	2	A45454	ankyrin-binding gl
51	19	21.3	16	2	A24099	crystal protein, 2
52	19	21.3	17	2	S41207	F420-non-reducing-
53	19	21.3	17	2	S15064	hypothetical prote
54	19	21.3	17	2	D48138	d(TTAGGG)n-binding
55	19	21.3	18	2	I52614	u-plasminogen acti
56	19	21.3	18	2	S52125	gamma2-gliadin P25
57	19	21.3	18	2	S56049	kidney stone prote
58	18.5	20.8	14	2	S00150	ovostatin - duck (
59	18.5	20.8	15	2	B41436	ovostatin - green
60	18.5	20.8	18	2	A61392	brain-associated s
61	18	20.2	9	2	A60108	exotoxin A - Strep
62	18	20.2	10	2	A61622	vitellogenin, 190K
63	18	20.2	11	2	A34662	Achatina cardio-ex
64	18	20.2	12	2	B44818	extracellular lipa
65	18	20.2	12	2	S67528	napin - rape (frag
66	18	20.2	12	2	S70337	napin small chain
67	18	20.2	12	2	PN0046	ATP synthase D cha
68	18	20.2	12	4	JX0315	aminotransferase c
69	18	20.2	13	2	A44818	extracellular lipa
70	18	20.2	13	2	S09716	2S albumin large c
71	18	20.2	13	2	PH1772	T cell receptor al
72	18	20.2	13	2	B47415	mannose-1-phosphat
73	18	20.2	13	2	B56864	dipeptidyl-peptida
74	18	20.2	14	2	S02078	ribulose-bisphosph
75	18	20.2	15	2	B39109	hypothetical 1.5K
76	18	20.2	15	2	PA0088	protein QP200051 -
77	18	20.2	15	2	A45103	7 alpha-hydroxy-4-
78	18	20.2	15	2	I78838	flc3 ligand isofor
79	18	20.2	15	2	A57003	hypothetical prote
80	18	20.2	16	2	PH0767	T-cell receptor be
81	18	20.2	16	2	PD0002	inulin fructotrans
82	18	20.2	17	2	A60570	Ig mu heavy chain
83	18	20.2	17	2	A35550	adrenocortical cel
84	18	20.2	17	2	B25348	glycogen(starch) s
85	18	20.2	18	2	S46418	NTF1 protein - cur
86	18	20.2	18	2	S28408	platelet-derived g
87	18	20.2	18	2	I46653	T-cell receptor de
88	18	20.2	18	2	A54195	Na+/K+-exchanging
89	17	19.1	8	2	S71299	IC12 protein - Par
90	17	19.1	8	2	S53008	citrate synthase -
91	17	19.1	9	2	A41978	calliPMRFamide 1 -
92	17	19.1	9	2	S26508	collagen alpha 2 (V
93	17	19.1	9	2	PC7074	translation elonga
94	17	19.1	10	2	S33844	alpha-2-macroglobu
95	17	19.1	10	2	S71948	matrix metalloprot
96	17	19.1	10	2	B59272	peptide-N4-(N-acet
97	17	19.1	10	2	E86128	hypothetical prote
98	17	19.1	11	2	S68637	acetylcholinestera
99	17	19.1	11	2	S23306	substance P - Atla
100	17	19.1	12	2	G49215	urease (EC 3.5.1.5

ALIGNMENTS

RESULT 1
C44823
synaptosomal-associated protein SNAP-25 peptide 8 - rabbit (fragment)
N:Alternate names: superprotein peptide 8
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C:Accession: C44823
R:Loewy, A.; Liu, W.S.; Baittinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A:Reference number: A44823; MUID:92044785; PMID:1941090
A:Accession: C44823
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <LOE>
A:Experimental source: visual tissue
A:Note: sequence extracted from NCBI backbone (NCBIP:64253)
C:Keywords: membrane trafficking

Query Match 28.1%; Score 25; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 5e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 VMMEPQGD 17
||: ||:
Db 3 VMLDQGE 10

RESULT 2
A35704
Cytochrome P450 olf2 - bovine (fragment)
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Bos primigenius taurus (cattle)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: A35704
R:Riazard, D.; Tal, N.; Rubinstein, M.; Khen, M.; Lancet, D.; Zupko, K.
Biochemistry 29, 7433-7440, 1990
A:Title: Identification and biochemical analysis of novel olfactory-specific cytochrome
A:Reference number: A35704; MUID:91027757; PMID:2121272
A:Accession: A35704
A:Molecule type: protein
A:Residues: 1-18 <LAZ>
A:CROSS-references: UNIPROT:P22779
C:Genetics:
A:Gene: CYP2A
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane protein

Query Match 28.1%; Score 25; DB 2; Length 18;
Best Local Similarity 46.2%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 PQLLLQVMMEPOG 16
||: ||:
Db 5 PGFQQQAFKELQG 17

RESULT 3
F49215
urease (EC 3.5.1.5) small chain UreA - Helicobacter mustelae (ATCC 43772) (fragment)
C:Species: Helicobacter mustelae
C>Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: F49215
R:Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.
Infect. Immun. 60, 5259-5266, 1992
A:Title: Purification and characterization of the urease enzymes of Helicobacter species
A:Reference number: A49215; MUID:93084378; PMID:1452359
A:Accession: F49215
A:Status: preliminary
A:Molecule type: protein

A:Residues: 1-18 <TUR>
A:CROSS-references: UNIPROT:Q9RSF6
A:Note: sequence extracted from NCBI backbone (NCBIP:119487)
C:Superfamily: urease, fused gamma/beta subunit; urease 11k chain homology; urease 12k c
C:Keywords: hydrolase

Query Match 28.1%; Score 25; DB 2; Length 18;
Best Local Similarity 33.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 TPQPLLQVMMEPOGD 17
||: ||:
Db 2 TPKELDKMHLVAGE 16

RESULT 4
A61218
alpha-gliadin 4Ha - grass (Haynaldia villosa) (fragment)
C:Species: Haynaldia villosa, Dasypyrum villosum
C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C:Accession: A61218
R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.
Biochem. Genet. 29, 207-211, 1991
A:Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynald
A:Reference number: A61218; MUID:91315394; PMID:1859356
A:Accession: A61218
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SHE>
A:CROSS-references: UNIPROT:Q7M1F7
C:Keywords: seed; storage protein

Query Match 27.0%; Score 24; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQTPQLLQ 9
||: ||:
Db 2 LRVFVPLQ 10

RESULT 5
A61391
alpha-1-antitrypsin homolog - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A61391
R:Tanaka, N.; Sekiya, S.; Takamizawa, H.; Kato, N.; Moriyama, Y.; Fujimura, S.
Jpn. J. Cancer Res. 82, 693-700, 1991
A:Title: Characterization of a 54 kDa, alpha-1-antitrypsin-like protein isolated from as
A:Reference number: A61391; MUID:91310496; PMID:1906855
A:Accession: A61391
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <VAN>
A:CROSS-references: UNIPROT:Q7M4R2

Query Match 27.0%; Score 24; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17
||| |||
Db 3 PQGD 6

RESULT 6
PC2330
cyclooligosaccharide fructanotransferase (EC 2.4.-.-) - Bacillus circulans (MCI-255)
C:Species: Bacillus circulans
C>Date: 21-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: PC2330
R:Kushibe, S.; Mitsui, K.; Yamagishi, M.; Yamada, K.; Morimoto, Y.

Biosci., Biotechnol. Biochem. 59, 31-34, 1995

A:Title: Purification and characterization of cycloolmulooligosaccharide fructanotransferase

A:Reference number: PC2330; MUID:95201377; PMID:7765973

A:Accession: PC2330

A:Molecule type: protein

A:Residues: 1-11 <XUS>

A:Cross-references: UNIPROT:Q7M0L3

C:Comment: This enzyme hydrolyzes beta-(2-1) glycosidic linkages and acts in intermolecular

C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 25.8%; Score 23; DB 2; Length 11;

Best Local Similarity 80.0%; Pred. No. 8.3e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 MEPOG 16

DB 7 NNPOG 11

RESULT 7

S70344

A:Title: amine oxidase (copper-containing) (EC 1.4.3.6) I - Aspergillus niger (fragments)

C:Species: Aspergillus niger

C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998

C:Accession: S70344

R:Frederick, I.; Pec, P.; Luhova, L.; Toyama, H.; Matsuhashita, K.; Hirota, S.; Kitagawa, T.

Biochim. Biophys. Acta 1295, 59-72, 1996

A:Title: Two amine oxidases from Aspergillus niger AKU 3302 contain topa quinone as the

A:Reference number: S70344; MUID:96283794; PMID:8679675

A:Accession: S70344

A>Status: Preliminary

A:Molecule type: protein

A:Residues: 1-7; 8-12 <FRE>

C:Keywords: oxidoreductase

Query Match 25.8%; Score 23; DB 2; Length 12;

Best Local Similarity 57.1%; Pred. No. 9.2e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 VMPEPQG 16

DB 1 VVIEPYG 7

RESULT 8

E56819

PS I complex subunit 8 - cucumber (fragment)

C:Species: Cucumis sativus (cucumber)

C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004

C:Accession: E56819

R:Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.

Biochim. Biophys. Acta 1059, 141-148, 1991

A:Title: Characterization of genes that encode subunits of cucumber PS I complex by N-te

A:Reference number: A56819; MUID:91355209; PMID:1883835

A:Accession: E56819

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <IWA>

A:Cross-references: UNIPROT:P42052

A:Note: sequence extracted from NCBI backbone (NCBI:P58606)

Query Match 25.8%; Score 23; DB 2; Length 15;

Best Local Similarity 30.8%; Pred. No. 1.2e+03;

Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 LQTPOLLOVME 13

DB 1 IQADXPTEQVIQD 13

RESULT 9

A46236

transforming protein myc, form 1 - mouse (fragment)

Query Match 25.8%; Score 23; DB 2; Length 18;

Best Local Similarity 55.6%; Pred. No. 1.4e+03;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C:Accession: A46236

R:Hann, S.R.; Sloan-Brown, K.; Spotts, G.D.

Genes Dev. 6, 1229-1240, 1992

A:Title: Translational activation of the non-AUG-initiated c-myc 1 protein at high cell

A:Reference number: A46236; MUID:92331929; PMID:1628829

A:Accession: A46236

A:Molecule type: mRNA

A:Residues: 1-16 <HAN>

A:Cross-references: GB:X01023

C:Genetics:

A:Start codon: CTG

C:Keywords: alternative initiators

Query Match 25.8%; Score 23; DB 2; Length 16;

Best Local Similarity 80.0%; Pred. No. 1.3e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQ 5

DB 7 LETPQ 11

RESULT 10

PS0210

28K protein 4209 - rice (strain Nihonbare) (fragment)

C:Species: Oryza sativa (rice)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C:Accession: PS0210

R:Tsugita, A.; Miyatake, N.

submitted to JIPID, April 1993

A:Reference number: PS0208

A:Accession: PS0210

A:Molecule type: protein

A:Residues: 1-16 <TSA>

A:Cross-references: UNIPROT:Q7M281

A:Experimental source: germ, bran, strain Nihonbare

C:Comment: molecular weight 28K, pI 7.3.

Query Match 25.8%; Score 23; DB 2; Length 16;

Best Local Similarity 37.5%; Pred. No. 1.3e+03;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 10 VMPEPQGD 17

DB 8 IVPNPEGD 15

RESULT 11

I59649

human leukocyte antigen alpha chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I59649

R:Fogdell, A.; Olerup, O.

Tissue Antigens 44, 19-24, 1994

A:Title: The DQA1*0104 allele is carried by DRB1*1001- and DRB1*1401-positive haplotypes

A:Reference number: I59649; MUID:95064785; PMID:7974465

A:Accession: I59649

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-18 <RES>

A:Cross-references: UNIPROT:Q30216; GB:S75685; NID:9913771; PIDN:AAB32621.1; PID:G913772

C:Genetics:

A:Gene: GDB:HLA-DQA1

A:Cross-references: GDB:120638; OMIM:146880

A:Map position: 6p21.3-6p21.3

Query Match 25.8%; Score 23; DB 2; Length 18;

Best Local Similarity 55.6%; Pred. No. 1.4e+03;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 LQVMMEPQ 16
| | | | |
Db 5 LTTWSPCG 13

RESULT 12

B61218
alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)
C:Species: Haynaldia villosa, Dasyphyrum villosum
C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C:Accession: B61218
R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.
Biochem. Genet. 29, 207-211, 1991
A>Title: alpha-type prolamin are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia
A:Reference number: A61218; MUID:91315394; PMID:1859356
A:Accession: B61218
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SHE>
A:Cross-references: UNIPROT:Q7M1F6
C:Keywords: seed; storage protein

Query Match 23.6%; Score 21; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQTPQPLQ 9
: : | | |
Db 1 VRVPVPLQ 9

RESULT 13

PH1567
cerebrin 28 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C:Accession: PH1567
R:Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.
J. Neurochem. 61, 533-540, 1993
A>Title: Micropurification of two human cerebrospinal fluid proteins by high performance
A:Reference number: PH1566; MUID:93329419; PMID:8336140
A:Accession: PH1567
A:Molecule type: protein
A:Residues: 1-12 <LEO>
A:Cross-references: UNIPROT:P41222

Query Match 23.6%; Score 21; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 PLLQVMMEP 14
| | | | |
Db 2 PPAQVSVQP 10

RESULT 14

PH1566
cerebrin 30 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: PH1566
R:Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.
J. Neurochem. 61, 533-540, 1993
A>Title: Micropurification of two human cerebrospinal fluid proteins by high performance
A:Reference number: PH1566; MUID:93329419; PMID:8336140
A:Accession: PH1566
A:Molecule type: protein
A:Residues: 1-14 <LEO>

Query Match 23.6%; Score 21; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 2.4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 PLLQVMMEP 14
| | | | |
Db 2 PPAQVSVQP 10

RESULT 15

PN0147
omega-gliadin 1 and 2 - Aegilops longissima (fragment)
C:Species: Aegilops longissima
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PN0147; PN0146
R:Odintsova, T.I.; Egorov, T.A.
Biokhimiia 55, 509-516, 1990
A>Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of
A:Reference number: PN0146; MUID:90283493; PMID:2354218
A:Accession: PN0147
A:Molecule type: protein
A:Residues: 1-14 <ODI>
A:Cross-references: UNIPROT:Q7M1V5
A:Experimental source: strain K-202
A>Note: omega-gliadin 2 (amino-terminal fragment)
A:Accession: PN0146
A:Molecule type: protein
A:Residues: 1-9 <OD2>
A:Experimental source: strain K-202
A>Note: omega-gliadin 1 (amino-terminal fragment)

Query Match 23.6%; Score 21; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
| | | |
Db 11 LQTP 14

RESULT 16

A42413
Ig heavy chain V region (LBL-copurifying) - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A42413
R:Bao, Z.; Muschler, J.; Horwitz, A.F.
J. Biol. Chem. 267, 4974-4980, 1992
A>Title: LBL, a novel, developmentally regulated, laminin-binding lectin.
A:Reference number: A42413; MUID:92165867; PMID:1531660
A:Accession: A42413
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <BAO>
C:Keywords: heterotetramer; immunoglobulin

Query Match 23.6%; Score 21; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
| | | |
Db 11 LQTP 14

RESULT 17

A40634
orf19 3' of eryK - Saccharopolyspora erythraea (fragment)
C:Species: Saccharopolyspora erythraea
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A40634
R:Stassi, D.; Donadio, S.; Staver, M.J.; Katz, L.
J. Bacteriol. 175, 182-189, 1993
A>Title: Identification of a Saccharopolyspora erythraea gene required for the final hy
A:Reference number: A40634; MUID:93106953; PMID:8416893
A:Accession: A40634

A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-15 <STA>
A;Cross-references: UNIPROT:Q04794
A;Note: sequence extracted from NCBI backbone (NCBIN:121243, NCBI:121244)

Query Match 23.6%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. NO. 2.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQP 6
: ||:
Db 7 VSTRPP 12

RESULT 18
PC1318
large granule L6 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)
C;Species: Tachyplesus tridentatus
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: PC1318
R;Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa
J. Biochem. 114, 307-316, 1993
A;Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridentatus)
A;Reference number: PC1309; MUID:94110249; PMID:8282718
A;Accession: PC1318
A;Molecule type: protein
A;Residues: 1-17 <SHI>
A;Cross-references: UNIPROT:P82151; UNIPROT:Q9USE9
C;Comment: This protein participates in immobilization of invading microbes.

Query Match 23.6%; Score 21; DB 2; Length 17;
Best Local Similarity 30.8%; Pred. NO. 2.9e+03;
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 2 QTPQPLQVMEP 14
: ||:
Db 5 QIPGKLMHITATP 17

RESULT 19
PN0149
beta-Gliadine 13 - Aegilops longissima (fragment)
C;Species: Aegilops longissima
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PN0149
R;Odintsova, T. I.; Egorov, T. A.
Biokhimiya 55, 509-516, 1990
A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of
A;Reference number: PN0146; MUID:90283493; PMID:2354218
A;Accession: PN0149
A;Molecule type: protein
A;Residues: 1-18 <ODI>
A;Cross-references: UNIPROT:Q7M1Z6
A;Experimental source: strain K-202
C;Superfamily: gliadin

Query Match 23.6%; Score 21; DB 2; Length 18;
Best Local Similarity 44.4%; Pred. NO. 3.1e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQLLQ 9
: ||:
Db 1 VRVPVPLQ 9

RESULT 20
S78767
ribosomal protein MRP-S29, mitochondrial - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78767
R;Graack, H. R.

A;Status: preliminary
A;Reference number: S78760
A;Accession: S78767
A;Molecule type: protein
A;Residues: 1-18 <GRA>
C;Keywords: mitochondrial
P;1-18/Product: ribosomal protein MRP-S29 (fragment) #status experimental <MAT>

Query Match 23.6%; Score 21; DB 2; Length 18;
Best Local Similarity 33.3%; Pred. NO. 3.1e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LLQVMEPQ 15
: ||:
Db 6 ILKAMQRP 14

RESULT 21
PX0030
triacylglycerol lipase (EC 3.1.1.3) II - Yeast (Geotrichum candidum) (fragments)
C;Species: Geotrichum candidum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: PX0030
R;Sugihara, A.; Shimada, Y.; Tominaga, Y.
J. Biochem. 107, 426-430, 1990
A;Title: Separation and characterization of two molecular forms of Geotrichum candidum I
A;Reference number: PX0030; MUID:90256718; PMID:2341377
A;Accession: PX0030
A;Molecule type: protein
A;Residues: 1-10 <SUG>
A;Cross-references: UNIPROT:P22394
C;Comment: Lipase catalyzes the hydrolysis of triacylglycerols. This fungus contains two
C;Keywords: carboxylic ester hydrolase

Query Match 22.5%; Score 20; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. NO. 2.4e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8
: ||:
Db 1 EAPRPXL 7

RESULT 22
PQ0788
NADH2 dehydrogenase (EC 1.6.99.3) 20K chain - fava bean mitochondrion (fragment)
N;Alternate names: complex I 20K chain; NADH-ubiquinone reductase 20K chain
C;Species: mitochondrion Vicia faba (fava bean)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: PQ0788
R;Leterme, S.; Boutry, M.
Plant Physiol. 102, 435-443, 1993
A;Title: Purification and preliminary characterization of mitochondrial complex I (NADH
A;Reference number: PQ0775; MUID:94151437; PMID:8108509
A;Accession: PQ0788
A;Molecule type: protein
A;Residues: 1-10 <LET>
A;Cross-references: UNIPROT:Q7M2G4
C;Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the th
ranging from 5K to 75K.
C;Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by
C;Genetics:
A;Genome: mitochondrion
C;Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 22.5%; Score 20; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. NO. 2.4e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QPLLQV 10
: ||||
Db 5 QVLLQV 10

RESULT 23
D39690
neural cell adhesion molecule, cardiac splice form +, -, + - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: D39690
Mol. Cell. Biol. 11, 1654-1661, 1991
R:Reyes, A.A.; Small, S.J.; Akeson, R.
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
A:Reference number: A39690; MUID:91141516; PMID:1996115
A:Accession: D39690
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-13 <REV>
A:CROSS-references: GB:M3970
A:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 22.5%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 14 PQGD 17
|
|
|
Db 8 PQGE 11

RESULT 24
PC7075
guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: PC7075
R:Tsuigita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsu, T.; Watanabe, Y.;
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of brain
A:Reference number: PC7072
A:Accession: PC7075
A:Molecule type: protein
A:Residues: 1-14 <TSU>
A:CROSS-references: UNIPROT:Q7M058
A:Experimental source: strain C57BL/6Cr Slc, male; brain, striatum
C:Keywords: brain; phosphorus-oxygen lyase

Query Match 22.5%; Score 20; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.5e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 14 PQGD 17
|
|
|
Db 9 PQGE 12

RESULT 25
PA0021
protein QA300016 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0021
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
A:Reference number: PA0001
A:Accession: PA0021
A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Experimental source: leaf

Query Match 22.5%; Score 20; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 3.7e+03; Mismatches 3; Conservative 1; Indels 0; Gaps 0;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 9 QVMEPQ 15
|
|
|
Db 5 EXVIEPQ 11

RESULT 26
PN0148
omega-gliadine 3 - Aegilops longissima (fragment)
C:Species: Aegilops longissima
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PN0148
R:Odintsova, T.I.; Egorov, T.A.
Biokhimiia 55, 509-516, 1990
A:Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of the
A:Reference number: PN0146; MUID:90283493; PMID:2354218
A:Accession: PN0148
A:Molecule type: protein
A:Residues: 1-15 <ODI>
A:Experimental source: strain K-202
A>Note: 11-Gln was also found

Query Match 22.5%; Score 20; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.7e+03; Mismatches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQ 5
|
|
|
Db 11 LXTPQ 15

RESULT 27
PL0110
complement factor B1-Bb and B2-Bb - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 15-Nov-1996
C:Accession: PL0110
R:Matsushita, M.; Okada, H.
Mol. Immunol. 26, 669-676, 1989
A:Title: Two forms of guinea pig factor B of the alternative complement pathway with dif
A:Reference number: A93136; MUID:89384686; PMID:2779589
A:Accession: PL0110
A:Molecule type: protein
A:Residues: 1-15 <MAT>
C:Keywords: complement alternate pathway; glycoprotein

Query Match 22.5%; Score 20; DB 2; Length 15;
Best Local Similarity 28.6%; Pred. No. 3.7e+03; Mismatches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 10 VVMEPQ 16
|
|
|
Db 2 ILDPAG 8

RESULT 28
A41436
alpha-macroglobulin - green sea turtle (fragment)
C:Species: Chelonia mydas (green sea turtle)
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 09-Jul-2004
C:Accession: A41436
R:Osada, T.; Sasaki, T.; Ikai, A.
J. Biochem. 103, 212-217, 1988
A:Title: Purification and characterization of alpha-macroglobulin and ovomacroglobulin
A:Reference number: A41436; MUID:88227890; PMID:2453503
A:Accession: A41436
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OSA>
A:CROSS-references: UNIPROT:Q7LZ35

Query Match 22.5%; Score 20; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 3.7e+03; Mismatches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 POPLLQVNM 12
|:|:|:
Db 2 PEPQYMLV 10

RESULT 29
S00123
dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) - bovine (fragment)
N;Alternate names: 2-oxoglutarate dehydrogenase complex chain E2; transsuccinylase
C;Species: Bos primigenius taurus (cattle)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00123
R;Bradford, A.P.; Aitken, A.; Beg, F.; Cook, K.G.; Yeaman, S.J.
FEBS Lett. 222, 211-214, 1987
A;Title: Amino acid sequence surrounding the lipoleic acid cofactor of bovine kidney 2-oxo-
A;Reference number: S00123; MUID:88005143; PMID:3115829
A;Accession: S00123
A;Molecule type: protein
A;Residues: 1-16 <BRA>
A;Cross-references: UNIPROT:P11179
C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology
C;Keywords: acyltransferase; coenzyme A; lipoamide; mitochondrion; oxidoreductase; tria
E;1-16/Domain: lipoyl/biotin-binding homology (fragment) <LPB>
F;5/Binding site: lipoamide (lys) (covalent) #status experimental

Query Match 22.5%; Score 20; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 4e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQTPQP 6
|:|:|:
Db 8 VQVPSP 13

RESULT 30
D83794
hypothetical protein BH1156 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D83794
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83794
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-16 <STO>
A;Cross-references: UNIPROT:Q9KQD5; GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BA048
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1156

Query Match 22.5%; Score 20; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 MMEPQG 16
|:|:|:
Db 10 MMELEG 15

RESULT 31
S33609
extensin - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: S33609
R;Murphy, J.M.; Hood, E.E.
Plant Mol. Biol. 21, 885-893, 1993
A;Title: Molecular basis for extensin size heterogeneity in two maize varieties.
A;Reference number: S33609; MUID:93222485; PMID:8467081

A;Accession: S33609
A;Molecule type: protein
A;Residues: 1-17 <MUR>
C;Keywords: glycoprotein; hydroxyproline

Query Match 22.5%; Score 20; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQP 6
|:|:|:
Db 13 TPKP 16

RESULT 32
B31769
T-cell receptor delta-2 chain J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 05-Nov-1999
C;Accession: B31769
R;Loh, E.Y.; Cwirla, S.; Serafini, A.T.; Phillips, J.H.; Lanier, L.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 9714-9718, 1988
A;Title: Human T-cell-receptor delta chain: genomic organization, diversity, and express
A;Reference number: A94221; MUID:89071766; PMID:2974163
A;Accession: B31769
A;Molecule type: DNA
A;Residues: 1-17 <LOH>
A;Cross-references: GB:L36386; NID:G540455; PIDN:AAA61108.1; PID:G540456
C;Keywords: T-cell receptor

Query Match 22.5%; Score 20; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 QVWMEP 14
|:|:|:
Db 12 QLIVEP 17

RESULT 33
S10452
hypothetical protein (bpha 5' region) - Aspergillus niger
C;Species: Aspergillus niger
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1997
C;Accession: S10452
R;van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.; van Balken
submitted to the EMBL Data Library, March 1990
A;Reference number: S10452
A;Accession: S10452
A;Molecule type: DNA
A;Residues: 1-18 <VAN>
A;Cross-references: EMBL:X52521; NID:G2336; PID:G2337

Query Match 22.5%; Score 20; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 4.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TPQPL 7
|:|:|:
Db 2 TDQPL 6

RESULT 34
I78841
thrombopoietin receptor - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I78841
R;Alexander, W.S.; Dunn, A.R.
Oncogene 10, 795-803, 1995
A;Title: Structure and transcription of the genomic locus encoding murine c-Mpl, a recep
A;Reference number: I58350; MUID:95166571; PMID:7862460
A;Accession: I78841

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-18 <RES>
A;Cross-references: GB:S76842; NID:g912990; PIDN:AAB33462.1; PID:g912991
C;Genetics:
A;Gene: c-mpl1

Query Match 22.5%; Score 20; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 4.6e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 PQLLQV 10
| | |
DB 5 PAFPLTV 11

RESULT 35

S21288
lectin - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: S21288
R;Miller, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
Biochem. J. 283, 813-821, 1992
A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization
A;Reference number: S21288; MUID:92272683; PMID:1590771
A;Accession: S21288
A;Molecule type: protein
A;Residues: 1-8 <MIL>
A;Cross-references: UNIPROT:Q7M1V6
A;Experimental source: var. Ulster Sceptre
C;Function:
A;Description: may be involved in defence mechanism of the plant
C;Keywords: hydroxyproline; lectin

Query Match 21.3%; Score 19; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TPQP 6
| | |
DB 4 TPSP 7

RESULT 36

S70345
amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragments)
C;Species: Aspergillus niger
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C;Accession: S70345
R;Preobort, I.; Pec, P.; Luhova, L.; Toyama, H.; Matsushita, K.; Hirota, S.; Kitagawa, T.
Biochim. Biophys. Acta 1295, 59-72, 1996
A;Title: Two amine oxidases from Aspergillus niger AXU 3302 contain topa quinone as the
A;Reference number: S70344; MUID:96283794; PMID:8679675
A;Accession: S70345
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5;6-9 <PRE>
C;Keywords: oxidoreductase

Query Match 21.3%; Score 19; DB 2; Length 9;
Best Local Similarity 37.5%; Pred. No. 2.8e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 10 VMPEQGD 17
| : | | |
DB 1 VVIEPNX 8

RESULT 37

D33098
214K exoantigen (version 1) - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum

C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: D33098
R;Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
A;Accession: D33098
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <NIC>

Query Match 21.3%; Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 MMPEP 14
| : | |
DB 4 MLEP 7

RESULT 38

A61007
hementin (EC 3.4.-.-) - Amazon leech (fragment)
C;Species: Haementeria ghilianii (Amazon leech)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A61007
R;Swadesh, J.K.; Huang, I.Y.; Budzynski, A.Z.
J. Chromatogr. 502, 359-369, 1990
A;Title: Purification and characterization of hementin, a fibrinogenolytic protease from
A;Reference number: A61007; MUID:90256973; PMID:2187898
A;Accession: A61007
A;Molecule type: protein
A;Residues: 1-10 <SWA>
A;Cross-references: UNIPROT:Q7M3P9
C;Keywords: anticoagulant; hydrolase; saliva

Query Match 21.3%; Score 19; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.5e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 MMPEQGD 17
| : | |
DB 3 LTPSPD 9

RESULT 39

S42587
celf protein - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: S42587
R;Guzzo, A.; DuBow, M.S.
Mol. Gen. Genet. 242, 455-460, 1994
A;Title: A luxAB transcriptional fusion to the cryptic celf gene of Escherichia coli dis
A;Reference number: S42587; MUID:94166755; PMID:8121401
A;Accession: S42587
A;Molecule type: DNA
A;Residues: 1-11 <GUZ>
C;Genetics:
A;Gene: celf

Query Match 21.3%; Score 19; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TPQP 6
| : | |
DB 6 TPHP 9

RESULT 40

S21127
precorrin methyltransferase - Salmonella typhimurium
C;Species: Salmonella typhimurium

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C:Accession: S21127
R:Roessner, C.A.; Warren, M.J.; Santander, P.J.; Atshaves, B.P.; Ozaki, S.; Stolowich, N.
FEBS Lett. 301, 73-78, 1992
A>Title: Expression of 9 Salmonella typhimurium enzymes for cobinamide synthesis. Ident
A:Reference number: S21127; MUID:93083628; PMID:1451790
A:Accession: S21127
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <ROE>

Query Match 21.3%; Score 19; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQTPQPL 7
: ||| :
Db 4 LQTPQTI 10

Search completed: June 7, 2005, 23:20:36
Job time : 17.7636 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 74.8 Seconds
(without alignments)
116.382 Million cell updates/sec

Title: US-10-691-157-2

Perfect score: 89
Sequence: 1 LQTPQLQVMEPQGD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	36.0	18	Q9TWM9	Q9twm9 tetrahymena
2	28	31.5	17	Q7Y013	Q7y013 zea mays (m
3	27	30.3	16	Q8LVE0	Q8lve0 trapa maxim
4	27	30.3	16	Q8LVE1	Q8lve1 punica gran
5	27	30.3	16	Q8LVE2	Q8lve2 lythrum sal
6	27	30.3	16	Q8MC15	Q8mc15 fuchsia hyb
7	27	30.3	16	Q8MC17	Q8mc17 ludwigia hy
8	27	30.3	16	Q8MC19	Q8mc19 quiscualis
9	27	30.3	16	Q8MC21	Q8mc21 combratum w
10	27	30.3	16	Q8MC23	Q8mc23 sonneratia
11	27	30.3	16	Q8MC25	Q8mc25 sonneratia
12	27	30.3	16	Q8MC27	Q8mc27 lagerstroem
13	27	30.3	16	Q8MC29	Q8mc29 duabanga gr
14	27	30.3	16	Q8MC31	Q8mc31 lagerstroem
15	27	30.3	16	Q8MC33	Q8mc33 rotala indi
16	27	30.3	16	Q8MC35	Q8mc35 heimia myrt
17	27	30.3	16	Q8MC37	Q8mc37 lawsonia in
18	27	30.3	16	Q8MC39	Q8mc39 amannia ba
19	27	30.3	16	Q8MC41	Q8mc41 nesaea lued
20	27	30.3	16	Q8MC43	Q8mc43 sonneratia
21	27	30.3	16	Q8MC45	Q8mc45 decodon ver
22	27	30.3	16	Q8MC47	Q8mc47 peplis port
23	27	30.3	16	Q8MC49	Q8mc49 pemphis aci
24	27	30.3	16	Q8MC51	Q8mc51 cuphea lanc
25	27	30.3	16	Q8MC53	Q8mc53 woodfordia
26	27	30.3	16	Q8MC58	Q8mc58 daphniphyll
27	27	30.3	16	Q8MET0	Q8met0 cercidiphyll
28	27	30.3	16	Q8MET2	Q8met2 saxifraga s
29	27	30.3	17	Q8LC19	Q8lc19 homo sapien
30	27	30.3	17	Q7LVQ4	Q7lvq4 homo sapien
31	27	30.3	17	Q9XQN9	Q9xqn9 sinapis alb

17	2	Q90XE2	Q90xe2 gallus gall
18	2	Q67216	Q67216 pennisetum
16	2	Q9UCH1	Q9uch1 homo sapien
16	2	Q9TRB4	Q9trb4 bos taurus
17	2	Q9APT4	Q9apt4 pseudomonas
18	1	CPAX_BOVIN	P22779 bos taurus
18	1	Q9R5F6	Q9r5f6 helicobacte
10	2	Q7M1F7	Q7m1f7 haynaldia v
15	2	Q6LCI3	Q6lc13 homo sapien
15	2	Q7M4R2	Q7m4r2 homo sapien
11	2	Q44237	Q44237 anabaena sp
11	2	Q7M0L3	Q7m0l3 bacillus ci
13	2	Q9UEE2	Q9uee2 homo sapien
15	1	PSAO_CUCSA	P42052 cucumis sat
16	2	Q96RT5	Q96rt5 homo sapien
16	2	Q7M281	Q7m281 oryza sativ
16	2	Q84RM4	Q84rm4 boea crassi
17	2	Q7X3X0	Q7x3x0 streptomyce
18	2	Q30216	Q30216 homo sapien
12	2	Q8CG32	Q8cg32 rattus sp.
13	2	Q88176	Q88176 mus musculu
13	2	Q8CIW3	Q8ciw3 mus musculu
14	1	TAT_HV1W2	P12509 human immun
14	1	TAT_HV128	P12511 human immun
16	1	CPAB_BOVIN	P81187 bos taurus
16	2	Q9NNZ2	Q9nnz2 homo sapien
16	2	Q64KC0	Q64kc0 sporophila
18	2	Q81CS8	Q81cs8 bacillus ce
8	2	Q9T2V3	Q9t2v3 begonia for
10	1	PAR6_PANRE	P82660 panagrellus
10	2	Q7M1F6	Q7m1f6 haynaldia v
10	2	Q7TSC5	Q7tsc5 mus musculu
14	2	Q7M1V5	Q7m1v5 aegilops lo
15	2	Q9X635	Q9x635 escherichia
15	2	Q9X637	Q9x637 klebsiella
16	1	FOR1_MYRGU	P81438 myrmecia gu
16	2	Q7SM54	Q7sm54 human t-lym
17	2	Q8V9K6	Q8v9k6 homo sapien
17	2	Q9EL24	Q9el24 human immun
18	1	LCTN_LAMGL	P83315 lama glama
18	2	Q7M1Z6	Q7m1z6 aegilops lo
18	2	Q9R5S8	Q9r5s8 treponema d
8	2	Q9AUJ4	Q9auj4 acinetobact
10	2	Q9UNF2	Q9unf2 homo sapien
10	2	Q7M2G4	Q7m2g4 vicia faba
11	1	RANC_RANPI	P08951 rana pipien
12	2	Q6X7V1	Q6x7v1 canis famil
13	2	Q6T675	Q6t675 papio anubi
13	2	Q81769	Q81769 hepatitis c
14	2	Q7RR89	Q7rr89 plasmodium
14	2	Q7M0S8	Q7m0s8 mus musculu
15	2	Q9TNQ1	Q9tnq1 mus sp. bet
15	2	Q9S8N8	Q9s8n8 hordeum vul
15	2	Q9QV72	Q9qv72 mus sp. i
15	2	Q7LZ35	Q7lzf35 chelonina gy
16	1	FOR2_MYRGU	P81437 myrmecia gu
16	1	ODOO_BOVIN	P11179 bos taurus
16	2	Q9TWK1	Q9twk1 mytilus edu
16	2	Q9TR99	Q9tr99 canis famil
16	2	Q9T2R0	Q9t2r0 solanum tub
16	2	Q9KD05	Q9kd05 bacillus ha
17	2	Q79E46	Q79e46 coxiella bu
17	2	Q9JLA7	Q9jla7 mus musculu
18	2	Q9UR73	Q9ur73 trichoderma
18	2	Q7LUR5	Q7lur5 homo sapien
18	2	Q9BRH2	Q9brh2 homo sapien
18	2	Q9UCF9	Q9ucf9 homo sapien
18	2	Q97773	Q97773 cercopithec
18	2	Q7YRH7	Q7yrh7 sus scrofa

ALIGNMENTS

```

RESULT 1
Q9TWM9 PRELIMINARY; PRT; 18 AA.
AC Q9TWM9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE NKTAG antigen (Fragment).
OS Tetrahymena pyriformis.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymenidae; Tetrahymenae; Tetrahymena.
OX NCBI_TaxID=5908;
RN [1]
RP SEQUENCE.
RX MEDLINE=94323706; PubMed=7519359;
RA Leary J.H.3rd, Evans D.L., Jaso-Friedmann L.;
RT "Partial amino acid sequence of a novel protozoan parasite antigen
RT that inhibits non-specific cytotoxic cell activity.";
RL Scand. J. Immunol. 40:158-164(1994).
SQ SEQUENCE 18 AA; 2082 MW; 13BCB737B1FF92A3 CRC64;

Query Match 36.0%; Score 32; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 LQVMEPQGD 17
Db 3 LQLPFPQGD 12

RESULT 2
Q7Y0I3 PRELIMINARY; PRT; 17 AA.
AC Q7Y0I3;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Isoamylase (Fragment).
GN Name=sul;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
RA Buckler E.S. IV.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY290391; AAP45416.1; -.
DT NON_TER 17
SQ SEQUENCE 17 AA; 1810 MW; E2913BED794C0670 CRC64;

Query Match 31.5%; Score 28; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQPLQV 10
Db 8 VSSPRPLAV 17

RESULT 3
Q8LVE0 PRELIMINARY; PRT; 16 AA.
AC Q8LVE0;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE PsaA (Fragment).
GN Name=psaA;
OS Trapa maximowiczii.

```

```

OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Trapa.
OX NCBI_TaxID=162053;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035729; AAL14139.1; -.
DR EMBL; AY035730; AAL14141.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 15.4%; Pred. No. 1.9e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLQVME 13
Db 3 IRSPEPEVKILVD 15

RESULT 4
Q8LVE1 PRELIMINARY; PRT; 16 AA.
AC Q8LVE1;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE PsaA (Fragment).
GN Name=psaA;
OS Punica granatum (Pomegranate).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Punica.
OX NCBI_TaxID=22663;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035724; AAL14129.1; -.
DR EMBL; AY035742; AAL14185.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 15.4%; Pred. No. 1.9e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLQVME 13
Db 3 IRSPEPEVKILVD 15

RESULT 5
Q8LVE2 PRELIMINARY; PRT; 16 AA.
AC Q8LVE2;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)

```

DE PsaA (Fragment).
 GN Name=psaA;
 OS Lythrum salicaria (Purple loosestrife).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Lythrum.
 OX NCBI_TaxID=13129;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035727; AAL414135.1; -.
 DR EMBL; AF421495; AAM45853.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;

Best Local Similarity 15.4%; Pred. No. 1.9e+03; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTQPPLQVWME 13
 ::||| :::::
 Db 3 IRSPEPEVKILVD 15

RESULT 6

Q8MC15
 ID Q8MC15 PRELIMINARY; PRT; 16 AA.
 AC Q8MC15;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE PsaA (Fragment).
 GN Name=psaA;
 OS Fuchsia hybrid cultivar.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Onagraceae; Fuchsia.
 OX NCBI_TaxID=133545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035746; AAL414173.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;

Best Local Similarity 15.4%; Pred. No. 1.9e+03; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTQPPLQVWME 13
 ::||| :::::
 Db 3 IRSPEPEVKILVD 15

RESULT 7

Q8MC17
 ID Q8MC17 PRELIMINARY; PRT; 16 AA.
 AC Q8MC17;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE PsaA (Fragment).
 GN Name=psaA;
 OS Ludwigia hyssopifolia.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Onagraceae; Ludwigia.
 OX NCBI_TaxID=155013;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035745; AAL414171.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;

Best Local Similarity 15.4%; Pred. No. 1.9e+03; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTQPPLQVWME 13
 ::||| :::::
 Db 3 IRSPEPEVKILVD 15

RESULT 8

Q8MC19
 ID Q8MC19 PRELIMINARY; PRT; 16 AA.
 AC Q8MC19;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE PsaA (Fragment).
 GN Name=psaA;
 OS Quisqualis indica (Rangoon creeper).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Combretaceae; Quisqualis.
 OX NCBI_TaxID=3956;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035744; AAL414169.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;

Best Local Similarity 15.4%; Pred. No. 1.9e+03; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTQPPLQVWME 13
 ::||| :::::
 Db 3 IRSPEPEVKILVD 15

RESULT 9

Q8MC21
 ID Q8MC21 PRELIMINARY; PRT; 16 AA.
 AC Q8MC21;

Q8MC29 PRELIMINARY; PRT; 16 AA.
 AC Q8MC29;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Psaa (Fragment).
 GN Name=psaa;
 OS Duabanga grandiflora.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Duabanga.
 OX NCBI_TaxID=122808;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035738; AAL14157.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVWME 13
 ::||| :::::
 Db 3 IRSPEPEVKILVD 15

RESULT 14

Q8MC31 PRELIMINARY; PRT; 16 AA.
 AC Q8MC31;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Psaa (Fragment).
 GN Name=psaa;
 OS Lagerstroemia speciosa (Queen crape myrtle).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Lagerstroemia.
 OX NCBI_TaxID=122810;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035737; AAL14155.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVWME 13
 ::||| :::::
 Db 3 IRSPEPEVKILVD 15

RESULT 15

Q8MC33 PRELIMINARY; PRT; 16 AA.
 AC Q8MC33;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Psaa (Fragment).
 GN Name=psaa;
 OS Rotala indica.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Rotala.
 OX NCBI_TaxID=162024;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035736; AAL14153.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVWME 13
 ::||| :::::
 Db 3 IRSPEPEVKILVD 15

RESULT 16

Q8MC35 PRELIMINARY; PRT; 16 AA.
 AC Q8MC35;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Psaa (Fragment).
 GN Name=psaa;
 OS Heimia myrtifolia.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Heimia.
 OX NCBI_TaxID=135798;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035735; AAL14151.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVWME 13
 ::||| :::::
 Db 3 IRSPEPEVKILVD 15

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RESULT 17
Q8MC37
ID Q8MC37 PRELIMINARY; PRT; 16 AA.
AC Q8MC37;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN Name=psaA;
OS Lawsonia inermis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Lawsonia.
OX NCBI_TaxID=141191;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences."
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035734; AAL14149.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 15.4%; Pred. No. 1.9e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQPLQVWME 13
Db ::||| :::::
3 IRSPEPVKILVD 15

RESULT 18
Q8MC39
ID Q8MC39 PRELIMINARY; PRT; 16 AA.
AC Q8MC39;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN Name=psaA;
OS Ammannia baccifera.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Ammannia.
OX NCBI_TaxID=162022;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences."
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035733; AAL14147.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 15.4%; Pred. No. 1.9e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQPLQVWME 13
Db ::||| :::::
3 IRSPEPVKILVD 15

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RESULT 19
Q8MC41
ID Q8MC41 PRELIMINARY; PRT; 16 AA.
AC Q8MC41;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN Name=psaA;
OS Nesaea luederitzi.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Nesaea.
OX NCBI_TaxID=162020;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences."
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035732; AAL14145.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 15.4%; Pred. No. 1.9e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQPLQVWME 13
Db ::||| :::::
3 IRSPEPVKILVD 15

RESULT 20
Q8MC43
ID Q8MC43 PRELIMINARY; PRT; 16 AA.
AC Q8MC43;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN Name=psaA;
OS Sonneratia caseolaris.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Sonneratia.
OX NCBI_TaxID=122814;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences."
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035731; AAL14143.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 15.4%; Pred. No. 1.9e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQPLQVWME 13
Db ::||| :::::
3 IRSPEPVKILVD 15

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RESULT	21
Q8MC45	
ID	PRELIMINARY; PRT; 16 AA.
AC	Q8MC45; 2002 (TrEMBLrel. 22, Created)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	PaaA (Fragment).
GN	Name=paaA;
OS	Decodon verticillatus (Swamp loosestrife).
OX	Chloroplast.
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC	Myrtales; Lythraceae; Decodon.
OX	NCBI_TaxID=162018;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Huang Y., Shi S.;
RT	"Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT	on Chloroplast rbcL Gene, paaA-ycf3 Spacer, and Nuclear rDNA Internal
RL	Transcribed Spacer (ITS) Sequences.";
RL	Int. J. Plant Sci. 163:215-225(2002).
DR	EMBL; AY035728; AAL14137.1; -
DR	GO; GO:0009507; C:chloroplast; IEA.
KW	Chloroplast.
FT	NON TER
ST	16
SEQ	SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
Query Match	30.3%; Score 27; DB 2; Length 16;
Best Local Similarity	15.4%; Pred. No. 1.9e+03;
Matches	2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
QY	1 LQTQPQLQVME 13
DB	3 IRSPEVKILVD 15
RESULT	22
Q8MC47	
ID	PRELIMINARY; PRT; 16 AA.
AC	Q8MC47; 2002 (TrEMBLrel. 22, Created)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	PaaA (Fragment).
GN	Name=paaA;
OS	Peplis portula.
OX	Chloroplast.
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC	Myrtales; Lythraceae; Peplis.
OX	NCBI_TaxID=162016;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Huang Y., Shi S.;
RT	"Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT	on Chloroplast rbcL Gene, paaA-ycf3 Spacer, and Nuclear rDNA Internal
RL	Transcribed Spacer (ITS) Sequences.";
RL	Int. J. Plant Sci. 163:215-225(2002).
DR	EMBL; AY035726; AAL14133.1; -
DR	GO; GO:0009507; C:chloroplast; IEA.
KW	Chloroplast.
FT	NON TER
ST	16
SEQ	SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
Query Match	30.3%; Score 27; DB 2; Length 16;
Best Local Similarity	15.4%; Pred. No. 1.9e+03;
Matches	2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
QY	1 LQTQPQLQVME 13
DB	3 IRSPEVKILVD 15

Db 3 IRSPEVKILVD 15
 ::|||:| :::::

RESULT 25
 Q8MC53
 ID Q8MC53 PRELIMINARY; PRT; 16 AA.
 AC Q8MC53;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE PsaA (Fragment).
 GN Name=psaA;
 OS Woodfordia fruticosa.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Woodfordia.
 OX NCBI_TaxID=141189;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL: AY035722; AAL14125.1; -.
 DR GO: GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVME 13
 ::|||:| :::::

Db 3 IRSPEVKILVD 15

RESULT 26
 Q8MES8
 ID Q8MES8 PRELIMINARY; PRT; 16 AA.
 AC Q8MES8;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE PSI P700 apoprotein A1 (Fragment).
 GN Name=PsaA;
 OS Daphniphyllum calycinum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Saxifragales; Daphniphyllaceae; Daphniphyllum.
 OX NCBI_TaxID=182071;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;
 RT "Phylogeny of the Altingiaceae based on cpDNA matK, PY-IGS and nrDNA
 RT ITS sequences.";
 RL Plant Syst. Evol. 230:13-24(2001).
 DR EMBL: AF377997; AAM45516.1; -.
 DR GO: GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVME 13

Db 3 IRSPEVKILVD 15
 ::|||:| :::::

RESULT 27
 Q8MET0
 ID Q8MET0 PRELIMINARY; PRT; 16 AA.
 AC Q8MET0;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE PSI P700 apoprotein A1 (Fragment).
 GN Name=PsaA;
 OS Cercidiphyllum japonicum (Katsura tree).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Saxifragales; Cercidiphyllaceae; Cercidiphyllum.
 OX NCBI_TaxID=13413;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;
 RT "Phylogeny of the Altingiaceae based on cpDNA matK, PY-IGS and nrDNA
 RT ITS sequences.";
 RL Plant Syst. Evol. 230:13-24(2001).
 DR EMBL: AF377996; AAM45514.1; -.
 DR GO: GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVME 13
 ::|||:| :::::

Db 3 IRSPEVKILVD 15

RESULT 28
 Q8MET2
 ID Q8MET2 PRELIMINARY; PRT; 16 AA.
 AC Q8MET2;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE PSI P700 apoprotein A1 (Fragment).
 GN Name=PsaA;
 OS Saxifraga stolonifera.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Saxifragales; Saxifragaceae; Saxifraga.
 OX NCBI_TaxID=182070;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;
 RT "Phylogeny of the Altingiaceae based on cpDNA matK, PY-IGS and nrDNA
 RT ITS sequences.";
 RL Plant Syst. Evol. 230:13-24(2001).
 DR EMBL: AF377995; AAM45512.1; -.
 DR GO: GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVME 13
 ::|||:| :::::

```

Db          3 IRSPEPEVKILVD 15

RESULT 29
Q6LC19
ID Q6LC19 PRELIMINARY; PRT; 17 AA.
AC Q6LC19;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Class II transactivator (Fragment).
GN Name=CIITA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98211702; PubMed=9551976;
RA Piskurich J.F., Wang Y., Linhoff M.W., White L.C., Ting J.P.;
RT "Identification of distinct regions of 5' flanking DNA that mediate
RT constitutive, IFN-gamma, STAT1, and TGF-beta-regulated expression of
RT the class II transactivator gene.";
RL J. Immunol. 160:233-240(1998).
DR EMBL; U94773; AAC39714.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1876 MW; 8ED60CDAF7606B70 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 2.1e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 POPLLQNMMEQ 15
|:|:|:|:|
Db 6 PRPAGSYLSEQ 17

RESULT 30
Q71VQ4
ID Q71VQ4 PRELIMINARY; PRT; 17 AA.
AC Q71VQ4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE MHC class II transactivator type III (Fragment).
GN Name=C2TA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97327562; PubMed=9184229; DOI=10.1093/emboj/16.10.2851;
RA Muhlethaler-Wettel A., Otten L.A., Steimle V., Mach B.;
RT "Expression of MHC class II molecules in different cellular and
RT functional compartments is controlled by differential usage of
RT multiple promoters of the transactivator CIITA.";
RL EMBO J. 16:2851-2860(1997).
DR EMBL; AF000003; AAB92363.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1876 MW; 8ED60CDAF7606B70 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 2.1e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 POPLLQNMMEQ 15
|:|:|:|:|
Db 6 PRPAGSYLSEQ 17

RESULT 31
Q9XQN9

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ID Q9XQN9 PRELIMINARY; PRT; 17 AA.
AC Q9XQN9;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Photosystem I P700 chlorophyll (Fragment).
GN Name=psaA;
OS Sinapis alba (White mustard) (Brassica hirta).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Sinapis.
OX NCBI_TaxID=3728;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Cotyledons;
RX MEDLINE=20136375; PubMed=10672444;
RA Sumner H., Pfannschmidt T., Link G.;
RT "Transcripts and sequence elements suggest differential promoter usage
RT within the ycf3-psaA gene cluster on mustard (Sinapis alba L.)
RT chloroplast DNA.";
RL Curr. Genet. 37:45-52(2000).
DR EMBL; AJ242660; CAB45538.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2008 MW; 99517FE691B89355 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 17;
Best Local Similarity 15.4%; Pred. No. 2.1e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVMME 13
|:|:|:|:|
Db 3 IRSPEPEVKILVD 15

RESULT 32
Q90XE2
ID Q90XE2 PRELIMINARY; PRT; 17 AA.
AC Q90XE2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Transforming growth factor beta 4 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22533207; PubMed=12646161; DOI=10.1016/S0006-291X(03)00300-0;
RA Pan H.J., Halper J.;
RT "Cloning, expression, and characterization of chicken transforming
RT growth factor beta 4.";
RL Biochem. Biophys. Res. Commun. 303:24-30(2003).
DR EMBL; AF395834; AAL05481.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1721 MW; 5080B3551E71BD63 CRC64;

Query Match 29.2%; Score 26; DB 2; Length 17;
Best Local Similarity 44.4%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 POPLLQNM 12
|:|:|:|:|
Db 3 PSPLLLALL 11

RESULT 33
Q67216
ID Q67216 PRELIMINARY; PRT; 18 AA.

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AC Q67216;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Photosystem I apoprotein A1 (Fragment).
GN Name=psaA;
OS Pennisetum americanum (Pearl millet).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Paniceae; Pennisetum.
OX NCBI_TaxID=4543;
RN [1]
RP SEQUENCE FROM N.A.
RA Nallar S.C., Nektalapudi S.C., Podile A.R.;
RT "Pennisetum glaucum clone PGB788 coding for IRF170.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY694132; AAU12166.1; -;
KW GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER.
SQ SEQUENCE 18 AA; 2111 MW; 008E617FE6945893 CRC64;

Query Match 29.2%; Score 26; DB 2; Length 18;
Best Local Similarity 15.4%; Pred. No. 3.2e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQLQVWME 13
: : : : :
Db 3 IRSPEVKIVVD 15

RESULT 34
Q9UCH1 PRELIMINARY; PRT; 16 AA.
AC Q9UCH1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE LIPOAMIDASE (EC 3.1.1.13) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=93228634; PubMed=8471055;
RT Hui D.Y., Hayakawa K., Oizumi J.;
RT "Lipoamidase activity in normal and mutagenized pancreatic cholesterol
RT esterase (bile salt-stimulated lipase).";
RL Biochem. J. 291:65-69(1993).
DR GO; GO:0004771; F:sterol esterase activity; IEA.
SQ SEQUENCE 16 AA; 1844 MW; 147321FA60374B3C CRC64;

Query Match 28.1%; Score 25; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 4.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQP 6
: : : :
Db 3 LENPQP 8

RESULT 35
Q9TRB4 PRELIMINARY; PRT; 16 AA.
AC Q9TRB4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE ATP-dependent 20 S proteasome activator (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=94342244; PubMed=8063704;
RA DeMartino G.N., Moomaw C.R., Zagnitko O.P., Proske R.J., Chu-Ping M.,
RA Afendis S.J., Swaffield J.C., Slaughter C.A.;
RT "PA700, an ATP-dependent activator of the 20 S proteasome, is an
RT ATPase containing multiple members of a nucleotide-binding protein
RT family.";
RL J. Biol. Chem. 269:20878-20884(1994).
SQ SEQUENCE 16 AA; 1878 MW; F70F74211EE26EDE CRC64;

Query Match 28.1%; Score 25; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. No. 4.2e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 PQLLQVWMEP 14
: : : : :
Db 4 PEPNFQLLDNP 14

RESULT 36
Q9APT4 PRELIMINARY; PRT; 17 AA.
AC Q9APT4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21142509; PubMed=11208781; DOI=10.1128/JB.183.3.843-853.2001;
RA Liang X., Phan X.Q.T., Olson M.V., Lory S.;
RT "Identification of a genomic island present in the majority of
RT pathogenic isolates of Pseudomonas aeruginosa.";
RL J. Bacteriol. 183:843-853(2001).
DR EMBL; AF241171; AAK01539.1; -;
KW Hypothetical protein.
SQ SEQUENCE 17 AA; 1954 MW; 68FDF0471E399969 CRC64;

Query Match 28.1%; Score 25; DB 2; Length 17;
Best Local Similarity 36.4%; Pred. No. 4.5e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 PQLLQVWMEP 14
: : : : :
Db 3 PWEVLDALEP 13

RESULT 37
CPAX_BOVIN STANDARD; PRT; 18 AA.
AC CPAX_BOVIN
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cytochrome P450 2A (OLP2) (Olfactive) (P52) (EC 1.14.14.1) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91027757; PubMed=2121272;
RA Lazard D., Tal N., Rubinstein M., Khen M., Lancet D., Zupko K.;
RT "Identification and biochemical analysis of novel olfactory-specific

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RT cytochrome P-450IIA and UDP-glucuronosyl transferase."
RL Biochemistry 29:7433-7440(1990).
CC -!- FUNCTION: Cytochromes P450 are a group of heme-thiolate
CC monooxygenases. In liver microsomes, this enzyme is involved in an
CC NADPH-dependent electron transport pathway. It oxidizes a variety
CC of structurally unrelated compounds, including steroids, fatty
CC acids, and xenobiotics.
CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR PIR: A35704; A35704.
DR InterPro: IPR001128; Cytochrome P450.
DR PROSITE: PS00086; CYTOCHROME P450; PARTIAL.
KW Direct protein sequencing; Electron transport; Endoplasmic reticulum;
KW Heme; Membrane; Microsome; Monooxygenase; Olfaction; Oxidoreductase.
FT NON_TER 1 1
FT VARIANT 6 6 G -> D.
FT VARIANT 11 11 A -> E.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2058 MW; F80746F76CCD77FF CRC64;
Query Match 28.1%; Score 25; DB 1; Length 18;
Best Local Similarity 46.2%; Pred. No. 4.8e+03;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 4 PQLLQVMEPQG 16
Db 5 PGQQQAPKELQG 17
RESULT 38
ID Q9RSF6 PRELIMINARY; PRT; 18 AA.
AC Q9RSF6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Urease small subunit (Fragment).
OS Helicobacter mustelae.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=217;
RN [1]
RP SEQUENCE.
RX MEDLINE=93084378; PubMed=1452359;
RA Turbett G.R., Hoj P.B., Horne R., Mee B.J.;
RA "Purification and characterization of the urease enzymes of
RT Helicobacter species from humans and animals.";
RL Infect. Immun. 60:5259-5266(1992).
DR PIR: F49215; F49215.
DR HSSP; P14916; 1E9Y.
DR GO; GO:0016151; P:nickel ion binding; IEA.
DR GO; GO:0009039; P:urease activity; IEA.
DR GO; GO:0006807; P:nitrogen metabolism; IEA.
DR InterPro: IPR002026; Urease gamma.
DR Pfam; PF00547; Urease gamma; 1.
SQ SEQUENCE 18 AA; 2060 MW; 29C8E0AB7E21805 CRC64;
Query Match 28.1%; Score 25; DB 2; Length 18;
Best Local Similarity 33.3%; Pred. No. 4.8e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Qy 3 TPQLQVMEPQGD 17
Db 2 TPKELDKMLHYAGE 16
RESULT 39
ID Q7M1F7 PRELIMINARY; PRT; 10 AA.
AC Q7M1F7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-gliadin 4Ha (Fragment).
OS Haynaldia villosa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Haynaldia.
OX NCBI_TaxID=40247;
RN [1]
RP SEQUENCE.
RX MEDLINE=91315394; PubMed=1859356;
RA Shawry P.R., Sabelli P.A., Parmar S., Lafandra D.;
RA "alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha
RT of Haynaldia villosa Schur (syn. Dasyphyrum villosum L.).";
RL Biochem. Genet. 29:207-211(1991).
DR PIR: A61218; A61218.
FT NON_TER 1 1
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1162 MW; 72F11BC772D72D4 CRC64;
Query Match 27.0%; Score 24; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 3.7e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LQTPQPLIQ 9
Db 2 LRVEVPQLQ 10
RESULT 40
ID Q6LCI3 PRELIMINARY; PRT; 15 AA.
AC Q6LCI3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Na+-phosphate cotransporter, type II (Fragment).
GN Name=NPT2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93317607; PubMed=8327470;
RA Magagnoli S., Werner A., Markovich D., Sorribas V., Stange G.,
RA Biber J., Murer H.;
RA "Expression cloning of human and rat renal cortex Na/Pi cotransport.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5979-5983(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96293539; PubMed=8693007; DOI=10.1073/pnas.93.14.7409;
RA Hartmann C.M., Hewson A.S., Kos C.H., Hilfiker H., Soumounou Y.,
RA Murer H., Tenenhouse H.S.;
RA "Structure of murine and human renal type II Na+-phosphate
RT cotransporter genes (Npt2 and NPT2).";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7409-7414(1996).
DR EMBL; U56684; AAD14856.1; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1770 MW; 23810E2056D88B8B CRC64;
Query Match 27.0%; Score 24; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 7 LLQVMEP 14
Db 1 LLKIIEP 8
Search completed: June 7, 2005, 23:18:51
Job time : 78.8 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 96.8727 Seconds
(without alignments)
71.864 Million cell updates/sec

Title: US-10-691-157-3

Perfect score: 98

Sequence: 1 DQPPDVKPLQPFQVQS 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003s.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	18	4	AAB72502 Colostrin
2	98	100.0	18	4	AAB59325 Ewe colos
3	98	100.0	18	4	AAB72248 Colostrin
4	98	100.0	18	4	AAB72534 Colostrin
5	98	100.0	18	5	AAB14579 Neural ce
6	98	100.0	18	5	AAM51038 Colostrin
7	98	100.0	18	5	AAD20230 Colostrin
8	98	100.0	18	8	ADN60297 Constitue
9	98	100.0	18	5	ADN74401 Ovine col
10	41	41.8	15	5	ABG67986 Human ADP
11	41	41.8	15	6	ADA24138 Alzheimer
12	39	39.8	16	2	AAK49858 Sequence
13	39	39.8	16	6	ABP83082 G protein
14	37	37.8	13	7	ADM75689 Potential
15	37	37.8	13	7	ADM74895 Potential
16	36	36.7	15	5	AAM47777 Short cha
17	35	35.7	12	5	ABG67771 Human ADP
18	35	35.7	12	6	ADA23910 Alzheimer
19	35	35.7	13	3	AAB26624 Partial s
20	34	34.7	13	5	ABB97740 Human pro
21	34	34.7	13	5	ABB97739 Human pro
22	34	34.7	13	7	ADM75160 Potential
23	33	33.7	15	3	AAB21134 Src homol
24	33	33.7	18	2	AAI41624 Mammalian
25	33	33.7	18	6	AAE34138 T-cell st

26	33	33.7	18	6	AAE34142 T-cell st
27	33	33.7	18	6	AAE34133 T-cell st
28	32	32.7	9	7	ADM48666 Human mat
29	32	32.7	11	3	AAB21124 Src homol
30	32	32.7	11	3	AAB21133 Src homol
31	32	32.7	17	4	AAU01841 Wheat pep
32	32	32.7	17	4	AAU01840 Wheat pep
33	32	32.7	17	8	ADH14690 Gliadin r
34	32	32.7	17	8	ADH14691 Gliadin r
35	32	32.7	18	2	AAW38909 Peptide r
36	31.5	32.1	17	8	ADH14808 Gliadin r
37	31.5	32.1	17	8	ADH14809 Gliadin r
38	31.5	32.1	18	8	ADH14821 Gliadin r
39	31	31.6	10	4	AAW37089 Human com
40	31	31.6	11	2	AAW17451 Consensus
41	31	31.6	11	5	ABP61522 Human KRP
42	31	31.6	15	2	AAW45819 Peptide r
43	31	31.6	15	2	AAW45614 Peptide r
44	31	31.6	15	2	AAW09376 Proline-r
45	31	31.6	16	2	AAW09377 Proline-r
46	31	31.6	17	2	AAW12220 Human ace
47	31	31.6	18	2	AAW09378 Proline-r
48	30.5	31.1	11	2	AAW44563 Encoded b
49	30.5	31.1	14	7	ADF14527 Epitope o
50	30.5	31.1	14	7	ADF14528 Epitope o
51	30	30.6	9	5	ABP55802 B15 clabs
52	30	30.6	9	5	ABG96846 Human leu
53	30	30.6	9	5	ABG96954 Human leu
54	30	30.6	9	5	ABG96698 Human leu
55	30	30.6	9	7	ADL98515 Human leu
56	30	30.6	9	7	ADL98788 Human leu
57	30	30.6	9	7	ADL98679 Human leu
58	30	30.6	9	7	ADL98396 Human leu
59	30	30.6	9	8	ADK03224 Hepatitis
60	30	30.6	10	8	ADK03219 Hepatitis
61	30	30.6	10	8	ADK03227 Hepatitis
62	30	30.6	11	7	ADC35017 Rho-like
63	30	30.6	13	5	ABB97741 Human pro
64	30	30.6	15	4	AAU01833 Wheat Gli
65	30	30.6	15	6	ABR30154 Human can
66	30	30.6	15	7	ADE70385 Human can
67	30	30.6	15	7	ADE70790 Human 161
68	30	30.6	15	7	ADE70192 Human 161
69	30	30.6	17	4	AAU01822 Wheat Gli
70	30	30.6	17	4	AAU01833 Wheat Gli
71	30	30.6	17	8	ADH16208 Gliadin r
72	30	30.6	17	8	ADH16203 Gliadin r
73	30	30.6	17	8	ADH14604 Gliadin r
74	30	30.6	17	8	ADH14670 Gliadin r
75	30	30.6	17	8	ADH14643 Gliadin r
76	30	30.6	17	8	ADH14661 Gliadin r
77	29.5	30.1	14	7	ADF14526 Epitope o
78	29.5	30.1	17	8	ADH14823 Gliadin r
79	29.5	30.1	18	3	AAW79501 Eimeria t
80	29	29.6	8	3	AAU82343 Human pap
81	29	29.6	9	5	ABG69555 Human CRP
82	29	29.6	10	2	AAW10268 Human ven
83	29	29.6	10	4	AAW96833 Human com
84	29	29.6	10	6	ABU90826 Peptide #
85	29	29.6	10	7	ADE70033 Human 161
86	29	29.6	11	3	AAE21127 Src homol
87	29	29.6	13	5	ABJ01202 Human Sox
88	29	29.6	13	5	ADG66864 Human ClF
89	29	29.6	13	5	ADG66869 Human ClF
90	29	29.6	13	8	ADR27634 Bythogae
91	29	29.6	15	1	AAW50841 Sequence
92	29	29.6	15	1	AAW82092 HRV2-deri
93	29	29.6	15	3	AAW93323 Antigenic
94	29	29.6	15	6	ABR30262 Human can
95	29	29.6	15	6	ABR30229 Human can
96	29	29.6	15	7	ADB67139 Human rhi
97	29	29.6	15	7	ADC35688 Peptide e
98	29	29.6	15	7	ADG14323 Human thi

99 29 29.6 15 8 AD015604 Ad015604 Human rhi
100 29 29.6 17 6 ABP82697 ABP82697 G protein

ALIGNMENTS

RESULT 1
AAB72502
ID AAB72502 standard; peptide; 18 AA.

XX AC AAB72502;
XX DT 09-MAY-2001 (first entry)
XX DE Colostrinin peptide #3.
XX KW Dermatological; oxidative stress regulator; colostrinin.
XX OS Unidentified.

XX FN WO200112650-A2.
XX PD 22-FEB-2001.
XX PF 17-AUG-2000; 2000WO-US022665.
XX PR 17-AUG-1999; 99US-0149310P.
XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;
XX DR WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the cell
PT with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations.

XX PS Claim 6; Page 25; 48pp; English.

XX The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPPDVEKPDLPQFQVQS 18
DB 1 DQPPDVEKPDLPQFQVQS 18

RESULT 2
AAB59325
ID AAB59325 standard; peptide; 18 AA.

XX AC AAB59325;

XX DT 21-MAR-2001 (first entry)

XX DE Ewe colostrinin peptide fragment B-10.

XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

OS Ovis sp.
XX WO2000075173-A2.
XX PN 14-DEC-2000.
XX PD 02-JUN-2000; 2000WO-GB002128.
XX PF 02-JUN-1999; 99GB-00012852.
XX PR (REGE-) REGEN THERAPEUTICS PLC.
XX PA Georgiades JA;
XX PI WPI; 2001-071058/08.
XX DR Peptides having an N-terminal amino acid sequence isolated from
XX colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.

XX PS Claim 7; Page 27; 63pp; English.

XX The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPPDVEKPDLPQFQVQS 18
DB 1 DQPPDVEKPDLPQFQVQS 18

RESULT 3
AAB72248
ID AAB72248 standard; peptide; 18 AA.

XX AC AAB72248;

XX DT 14-MAY-2001 (first entry)

XX DE Colostrinin derived cytokine inducing peptide SEQ ID 3.

XX Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.

XX OS Synthetic.

XX PN WO200111937-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US022818.

XX PR 17-AUG-1999; 99US-0149311P.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PA (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for

PT treating central nervous system diseases and bacterial and viral

PT infections, comprises administering colostrinin as an immunological

PT regulator.

XX

XX Claim 1; Page 34; 50pp; English.

PS

XX Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,

CC a proline rich polypeptide aggregate contained in colostrum. The peptides

CC have immune response modulatory activity, and are capable of inducing

CC cytokines. Colostrinin and its derived peptides are useful for inducing

CC cytokine production, for modulating an immunological response and for

CC inducing blood cell proliferation. The peptides are useful in the

CC treatment of disorders of the central nervous system, neurological

CC disorders, mental disorders, dementia, neurodegenerative diseases,

CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic

CC disorders of the immune system, bacterial and viral infections and

CC acquired immunological deficiencies

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQFQVQS 18

Db 1 DQPPDVEKPDLPQFQVQS 18

RESULT 4

AAB72534

ID AAB72534 standard; peptide; 18 AA.

AC AAB72534;

XX

XX 09-MAY-2001 (first entry)

XX

XX Colostrinin peptide #3.

XX

XX Neuroprotective; neural cell differentiation regulator; colostrinin;

KW colostrum.

XX

XX Unidentified.

OS

XX WO200112651-A2.

PN

XX

XX 22-FEB-2001.

PD

XX

XX 17-AUG-2000; 2000WO-US022774.

PF

XX

XX 17-AUG-1999; 99US-0149633P.

PR

XX (TEXA) UNIV TEXAS SYSTEM.

PA

XX

XX Boldogh I;

PI

XX

XX WPI; 2001-226545/23.

DR

XX

XX Use of colostrinin, its constituent peptide or analog as a neural cell

PT regulator, for promoting neural cell differentiation and treating damaged

PT neural cells in a patient.

PT

XX Claim 6; Page 21; 35pp; English.

PS

XX The present invention relates to a method for promoting neural cell

CC differentiation and treating damaged neural cells, using colostrinin and

CC colostrinin constituent peptides (e.g. the present peptide) as a neural

CC cell regulator. Colostrinin is a polypeptide complex found in colostrum

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQFQVQS 18

Db 1 DQPPDVEKPDLPQFQVQS 18

RESULT 5

AAO14579

ID AAO14579 standard; peptide; 18 AA.

XX

XX AAO14579;

AC

XX

XX 27-MAY-2002 (first entry)

DT

XX

XX Neural cell regulatory colostrinin peptide 3.

DE

XX

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX

XX Unidentified.

OS

XX

XX Key Location/Qualifiers

PH Modified-site 18 /note= "Optional C-terminal amide"

FT

XX

XX WO200213851-A1.

PN

XX

XX 21-FEB-2002.

PD

XX

XX 17-AUG-2000; 2000WO-US022777.

PF

XX

XX 17-AUG-2000; 2000WO-US022777.

PR

XX (TEXA) UNIV TEXAS SYSTEM.

PA

XX

XX Boldogh I, Stanton JG, Hughes TK;

PI

XX

XX WPI; 2002-269152/31.

DR

XX

XX Promoting cell differentiation in a patient involves use of blood cell

PT regulator selected from colostrinin, its constituent peptide and/or

PT analog.

PT

XX Claim 7; Page 21; 37pp; English.

PS

XX

XX The invention comprises a method for promoting cell differentiation (e.g.

CC neural cell differentiation). The method involves contacting cells with a

CC neural cell regulator (i.e. a colostrinin peptide) in order to change the

CC cells in morphology to form neural cells. Colostrinin is a proline-rich

CC polypeptide aggregate that is present in colostrum. The method of the

CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQFQVQS 18

Db 1 DQPPDVEKPDLPQFQVQS 18

RESULT 6

AAM51038


```
ADN60297
ID  ADN60297 standard; peptide; 18 AA.
XX
AC  ADN60297;
XX
DT  29-JUL-2004 (first entry)
XX
DE  Constituent peptide of colostrinin SEQ ID NO:3.
XX
KW  modulator; colostrinin; intracellular signaling molecule modulator;
KW  4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;
KW  DNA damage; beta-amyloid; retinoic acid; cytosstatic; 4HNE inhibitor;
KW  4HNE-protein adduct formation reduction;
KW  4HNE-mediated glutathione depletion inhibition; p53 inhibition;
KW  c-Jun NH2-terminal kinase inhibition.
XX
OS  Synthetic.
XX
PN  WO2004037851-A2.
XX
PD  06-MAY-2004.
XX
PF  22-OCT-2003; 2003WO-US033423.
XX
PR  22-OCT-2002; 2002US-0420369P.
XX
PA  (TEXA ) UNIV TEXAS SYSTEM.
PA  (BOLD// BOLDGCH I.
PA  (STAN//) STANTON J G.
PA  (GEOR//) GEORGIADIS J A.
PA  (HUGH//) HUGHES T K.
PA  (KRUZ//) KRUZEL M.
XX
PI  Boldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;
XX
WPI; 2004-365494/34.
XX
DR
XX
PT  Use of colostrinin for e.g. modulating an intracellular signaling
PT  molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a
PT  cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
PT  a cell.
XX
PS  Claim 6; SEQ ID NO 3; 46pp; English.
XX
CC  The present invention describes the use of a modulator selected from
CC  colostrinin, its constituent peptide, its active analogue, and a
CC  combination of these, for modulating an intracellular signaling molecule
CC  in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,
CC  inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
CC  and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
CC  The modulator has cytostatic activity, and can be used as a 4HNE
CC  inhibitor. The modulator is useful in the manufacture of a medicament for
CC  reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated
CC  glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,
CC  and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.
CC  Colostrinin, or its constituent peptide or active analogue is useful for
CC  inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
CC  or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
CC  The present sequence represents a synthetic constituent peptide of
CC  colostrinin, which can be used as a modulator in the present invention.
XX
SQ  Sequence 18 AA;
    Query Match      100.0%; Score 98; DB 8; Length 18;
    Best Local Similarity 100.0%; Pred. No. 3.7e-07;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 DQPPDVEKPDLPQFQVQS 18
    |||||
Db  1 DQPPDVEKPDLPQFQVQS 18

RESULT 9
ABG67986
ID  ABG67986 standard; peptide; 15 AA.
XX
AC  ABG67986;
XX
DT  07-OCT-2002 (first entry)
XX
DE  Human ADPI tryptic digest peptide #695.
```

```
ADS74401
ID  ADS74401 standard; peptide; 18 AA.
XX
AC  ADS74401;
XX
DT  16-DEC-2004 (first entry)
XX
DE  Ovine colostrinin peptide.
XX
KW  Colostrum; colostrinin; sheep; peptide purification.
XX
OS  Ovis aries.
XX
PN  WO2004081038-A1.
XX
PD  23-SEP-2004.
XX
PF  10-MAR-2004; 2004WO-GB001014.
XX
PR  11-MAR-2003; 2003GB-00005552.
XX
PR  08-MAR-2004; 2004GB-00005190.
XX
PA  (REGE-) REGEN THERAPEUTICS PLC.
XX
PI  Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;
XX
WPI; 2004-677519/66.
XX
DR
XX
PT  Recovering peptides such as colostrinin from mammalian colostrum, by
PT  mixing colostrum with alcohol to form alcohol phase containing peptides
PT  and precipitate, separating alcohol phase from precipitate, and
PT  recovering alcohol phase.
XX
PS  Disclosure; SEQ ID NO 18; 41pp; English.
XX
CC  The present sequence is that of a peptide that can be recovered from
CC  ovine colostrinin using the method of the invention. The invention
CC  provides a method for the recovery of peptides (especially colostrinin)
CC  from colostrum in substantially pure, biologically active form and in
CC  high yield. The method involves mixing the colostrum with an alcohol to
CC  form an alcohol phase containing the colostrinin and a precipitate
CC  containing higher molecular weight caseins and other proteins. Best
CC  results are obtained using methanol or ethanol of at least 80%, and
CC  preferably up to 100%, purity. The alcohol phase is then separated from
CC  the precipitate, and the colostrinin is separated from the alcohol,
CC  preferably by evaporation, to form a colostrinin-rich phase, which is
CC  recovered. A precipitation agent, such as ammonium sulfate, may be added
CC  either to the alcohol phase or, preferably, to the colostrinin-rich phase
CC  to induce precipitation of the colostrinin peptides. The method is
CC  generally applicable to the separation of peptides from fluids containing
CC  higher molecular weight proteins, lipids, carbohydrates and/or nucleic
CC  acids.
XX
SQ  Sequence 18 AA;
    Query Match      100.0%; Score 98; DB 8; Length 18;
    Best Local Similarity 100.0%; Pred. No. 3.7e-07;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 DQPPDVEKPDLPQFQVQS 18
    |||||
Db  1 DQPPDVEKPDLPQFQVQS 18

RESULT 10
ABG67986
ID  ABG67986 standard; peptide; 15 AA.
XX
AC  ABG67986;
XX
DT  07-OCT-2002 (first entry)
XX
DE  Human ADPI tryptic digest peptide #695.
```

XX Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
 KW Alzheimer's disease-associated feature; neuroprotective;
 KW Alzheimer's disease-associated protein isoform; nootropic;
 KW ADPI tryptic digest peptide.
 XX
 XX Homo sapiens.
 XX
 XX WO200246767-A2.
 XX
 XX 13-JUN-2002.
 XX
 XX 29-NOV-2001; 2001WO-GB005289.
 XX
 XX 08-DEC-2000; 2000US-0254431P.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 XX Herath HMAc, Parekh RB, Rohlf C;
 XX WPI; 2002-508575/54.
 XX
 XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT comprises detecting Alzheimer disease-associated features or Alzheimer
 PT disease-associated protein isoforms in brain tissue from the subject.
 XX
 XX Claim 7; Page 56; 427pp; English.
 XX
 XX The present invention relates to methods and compositions for the
 CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
 CC subject. The method comprises analysing a sample of brain tissue from a
 CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
 CC disease-associated features (ADPs), whose relative abundance correlates
 CC with the presence, absence, stage or severity of AD and comparing the
 CC abundance of each feature with the abundance of that chosen feature in
 CC brain tissue from persons free from AD. The invention also describes
 CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
 CC brain tissue. The methods and compositions of the invention are useful
 CC for the screening, diagnosis or prognosis of AD in a subject, for
 CC determining the stage or severity of AD in a subject, for identifying a
 CC subject at risk of developing AD, or for monitoring the effect of therapy
 CC administered to a subject having AD. Antibodies capable of binding to
 CC ADPIs are useful for treating or preventing AD, and for determining the
 CC efficacy of a given treatment regime. An agent that modulates the
 CC activity of ADPI is useful in the manufacture of a medicament for the
 CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
 CC human ADPI tryptic digest peptides
 XX
 XX Sequence 15 AA;
 XX
 XX Query Match 41.8%; Score 41; DB 5; Length 15;
 XX Best Local Similarity 47.1%; Pred. No. 44;
 XX Matches 8; Conservative 3; Mismatches 0; Indels 6; Gaps 1;
 XX
 XX QY 1 DQPPDVEKPDLPQFQVQ 17
 XX |||||:|
 XX 5 DQPPDIE-----FQIR 15
 XX
 XX
 XX RESULT 11
 XX ADA24138
 XX ID ADA24138 standard; peptide; 15 AA.
 XX
 XX AC ADA24138;
 XX
 XX 20-NOV-2003 (first entry)
 XX
 XX Alzheimer's disease-associated protein isoform tryptic peptide #747.
 XX
 XX human; Alzheimer's disease; vascular dementia; Lewy body dementia;
 KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
 KW Alzheimer's disease-associated protein isoform; ADPI.
 XX

OS Homo sapiens.
 XX
 XX US2003064411-A1.
 XX
 XX 03-APR-2003.
 XX
 XX 10-DEC-2001; 2001US-00014340.
 XX
 XX 08-DEC-2000; 2000US-0254431P.
 XX (HERA/) HERATH H M A C.
 XX (PARE/) PAREKH R B.
 XX (ROHL/) ROHLFF C.
 XX
 XX Herath HMAc, Parekh RB, Rohlf C;
 XX WPI; 2003-540784/51.
 XX
 XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT involves analyzing test sample of brain tissue from subject, and
 PT comparing feature in test sample with that of person(s) free from
 PT Alzheimer's disease.
 XX
 XX Disclosure; SEQ ID NO 747; 115pp; English.
 XX
 XX The invention relates to a method of screening or diagnosing Alzheimer's
 CC disease in a subject. The method is useful for screening, diagnosis or
 CC prognosis of Alzheimer's disease in a subject for determining the stage
 CC of severity of Alzheimer's disease in a subject, for identifying a
 CC subject at risk of developing Alzheimer's disease, or for monitoring the
 CC effect of therapy administered to a subject having Alzheimer's disease.
 CC The method is also useful in treating vascular dementia, Lewy body
 CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
 CC depression. The inventive method identifies sensitive and specific
 CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
 CC It provides therapeutic agents for Alzheimer's disease that works
 CC quickly, potentially, specifically with fewer side effects. The present
 CC sequence represents the amino acid sequence of a Alzheimer's disease-
 CC associated protein isoform tryptic peptide.
 XX
 XX Sequence 15 AA;
 XX
 XX Query Match 41.8%; Score 41; DB 6; Length 15;
 XX Best Local Similarity 47.1%; Pred. No. 44;
 XX Matches 8; Conservative 3; Mismatches 0; Indels 6; Gaps 1;
 XX
 XX QY 1 DQPPDVEKPDLPQFQVQ 17
 XX |||||:|
 XX 5 DQPPDIE-----FQIR 15
 XX
 XX
 XX RESULT 12
 XX AAR49858
 XX ID AAR49858 standard; peptide; 16 AA.
 XX
 XX AC AAR49858;
 XX
 XX 25-MAR-2003 (revised)
 XX DT 12-SEP-1994 (first entry)
 XX
 XX Sequence of tryptic digest peptide of bovine glial growth factor III (GGF
 XX III).
 XX
 XX Glial growth factor; GGF III; mitogen; Schwann cell.
 XX
 XX Bos taurus.
 XX
 XX WO9404560-A1.
 XX
 XX 03-MAR-1994.
 XX
 XX 13-AUG-1993; 93WO-GB001721.
 XX

PR 14-AUG-1992; 92GB-00017316.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA Goodearl ADJ, Stroobant P, Waterfield MD;
 PI WPI; 1994-083104/10.
 XX
 DR New polypeptide factor and peptide(s) from bovine pituitary - having
 XX mitogenic activity in stimulating division of Schwann cells, used for
 PT therapy, prophylaxis, diagnosis of neuro-degenerative disease, glial cell
 PT tumours, etc.
 XX
 XX Claim 32; Page 31; 44pp; English.
 XX
 CC A novel polypeptide was purified from bovine pituitaries. It has
 CC mitogenic activity stimulating the division of Schwann cells, and
 CC exhibits a mol. wt. of 43-35kD when carrying native glycosylation. It was
 CC digested with trypsin and lysylendopeptidase to obtain novel peptides
 CC AAR49858-R49866 and AAR49867-R49871 respectively. When peptides AAR49862-
 CC R49866 were sequenced to completion it was found that none of these
 CC sequences is apparently related to GGF-I or GGF-II peptide sequences. A
 CC polypeptide config. any of the sequences in AAR49858- AAR49871 is claimed,
 CC as is DNA encoding each of the peptides. The final lys in the sequence is
 CC bracketed. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 16 AA;
 Query Match 39.8%; Score 39; DB 2; Length 16;
 Best Local Similarity 66.7%; Pred. No. 91;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 6 VERPDLPQF 14
 Db : |||||
 2 ISKPDLPKF 10

RESULT 13
 ABP83082
 ID ABP83082 standard; peptide; 16 AA.
 XX
 AC ABP83082;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1755.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX
 OS Homo sapiens.
 XX
 XX WO200261087-A2.
 XX
 XX 08-AUG-2002.
 XX
 XX 19-DEC-2001; 2001WO-US050107.
 XX
 XX 19-DEC-2000; 2000US-0257144P.
 XX
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 PA
 XX Burmer GC, Roush CL, Brown JP;
 FI
 XX

DR WPI; 2003-046718/04.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX
 XX Claim 1; Fig 2; 523pp; English.
 XX
 CC The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABP242523 to ABP242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX
 XX Sequence 16 AA;
 Query Match 39.8%; Score 39; DB 6; Length 16;
 Best Local Similarity 50.0%; Pred. No. 91;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 QPDPVEKPDLP 13
 Db : |||||
 5 RPPDIRKSDSSP 16

RESULT 14
 ADM75689
 ID ADM75689 standard; peptide; 13 AA.
 XX
 AC ADM75689;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Potential human MHC class II binding human Factor VIII peptide #909.
 XX
 DE human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
 KW MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
 XX
 XX Homo sapiens.
 OS
 XX WO2003087161-A1.
 XX
 XX 23-OCT-2003.
 XX
 XX 17-APR-2003; 2003WO-EP004063.
 XX
 XX 18-APR-2002; 2002EP-00008712.
 XX
 XX 24-MAR-2003; 2003EP-00006554.
 XX
 XX (MERE) MERCK PATENT GMBH.
 XX
 XX Jones T, Baker M, Carr FJ;
 FI

XX WPI; 2003-845307/78.
 XX New modified human Factor VIII molecule being substantially non-
 PT immunogenic or less immunogenic than non-modified human Factor VIII,
 PT useful in preparing a composition for treating e.g., Gaucher's disease.
 XX
 XX Disclosure; Fig 1; 68pp; English.
 XX
 CC The invention relates to a novel modified human Factor VIII molecule. The
 CC modified human Factor VIII molecule being substantially non-immunogenic
 CC or less immunogenic than a non-modified human Factor VIII and having
 CC essentially the same biological specificity and activity when used in
 CC vivo. The modified human Factor VIII molecule comprises specifically
 CC altered amino acid residues compared with the non-modified parental
 CC molecule, where the altered amino acid residues cause a reduction or an
 CC elimination of one or more of the T-cell epitopes, which act in the
 CC parental non-modified molecule as MHC class II binding ligands and
 CC stimulate T-cells. The potential MHC class II binding activity peptide is
 CC useful for the manufacture of the modified Factor VIII molecule or a
 CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.
 CC The modified Factor VIII molecule is useful in preparing a composition
 CC for treating e.g., Gaucher's disease. This sequence represents a human
 CC Factor VIII peptide with potential human MHC class II binding activity of
 CC the invention.
 XX
 XX Sequence 13 AA;
 SQ

Query Match 37.8%; Score 37; DB 7; Length 13;
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPVVEKPD 11
 ||| : ||:
 Db 5 PPDAQNPD 13

RESULT 15
 ADM74895
 ID ADM74895 standard; peptide; 13 AA.
 AC
 XX ADM74895;
 XX
 XX 03-JUN-2004 (first entry)
 DT
 XX
 DE Potential human MHC class II binding human Factor VIII peptide #115.
 XX
 KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
 KW MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
 XX
 XX Homo sapiens.
 OS
 XX WO2003087161-A1.
 FN
 XX
 PD 23-OCT-2003.
 XX
 XX 17-APR-2003; 2003WO-EP004063.
 PF
 XX 18-APR-2002; 2002EP-00008712.
 PR
 XX 24-MAR-2003; 2003EP-00006554.
 XX
 XX (MERE) MERCK PATENT GMBH.
 PA
 XX Jones T, Baker M, Carr FJ;
 PI
 XX WPI; 2003-845307/78.
 DR
 XX
 PT New modified human Factor VIII molecule being substantially non-
 PT immunogenic or less immunogenic than non-modified human Factor VIII,
 PT useful in preparing a composition for treating e.g., Gaucher's disease.
 XX
 XX Disclosure; Fig 1; 68pp; English.
 XX

CC The invention relates to a novel modified human Factor VIII molecule. The
 CC modified human Factor VIII molecule being substantially non-immunogenic
 CC or less immunogenic than a non-modified human Factor VIII and having
 CC essentially the same biological specificity and activity when used in
 CC vivo. The modified human Factor VIII molecule comprises specifically
 CC altered amino acid residues compared with the non-modified parental
 CC molecule, where the altered amino acid residues cause a reduction or an
 CC elimination of one or more of the T-cell epitopes, which act in the
 CC parental non-modified molecule as MHC class II binding ligands and
 CC stimulate T-cells. The potential MHC class II binding activity peptide is
 CC useful for the manufacture of the modified Factor VIII molecule or a
 CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.
 CC The modified Factor VIII molecule is useful in preparing a composition
 CC for treating e.g., Gaucher's disease. This sequence represents a human
 CC Factor VIII peptide with potential human MHC class II binding activity of
 CC the invention.
 XX
 XX Sequence 13 AA;
 SQ

Query Match 37.8%; Score 37; DB 7; Length 13;
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPVVEKPD 11
 ||| : ||:
 Db 4 PPDAQNPD 12

RESULT 16
 AAM47777
 ID AAM47777 standard; peptide; 15 AA.
 XX
 AC AAM47777;
 XX
 DT 26-FEB-2002 (first entry)
 DE
 XX Short chain dehydrogenase 32 peptide fragment.
 XX
 KW Short chain dehydrogenase 32; tumour; haemopathy; HIV infection;
 KW immunological disease; inflammation; gene therapy; cytostatic;
 KW haemostatic; virucide; immunomodulatory; antiinflammatory.
 XX
 OS Unidentified.
 OS
 PN CN1307114-A.
 XX
 PD 08-AUG-2001.
 XX
 PF 28-JAN-2000; 2000CN-00111584.
 XX
 PR 28-JAN-2000; 2000CN-00111584.
 XX
 PA (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
 XX
 XX Mao Y, Xie Y;
 PI
 XX WPI; 2002-026893/04.
 DR
 XX New polypeptide for treating malignant tumors and HIV infection,
 PT comprises the polypeptide-short chain dehydrogenase 32 and polynucleotide
 PT for coding said polypeptide.
 XX
 XX Example 6; Page 27 (Disclosure); 33pp; Chinese.
 PS
 XX The present invention relates to short chain dehydrogenase 32 (AAM47776).
 CC The protein and its coding sequence are useful for treating various
 CC diseases, such as malignant tumours, haemopathy, HIV infection,
 CC immunological diseases and inflammations. The present sequence is an N-
 CC terminal peptide fragment of the protein, which was used in an example
 CC from the present invention
 XX
 XX Sequence 15 AA;
 SQ

```
Query Match      36.7%; Score 36; DB 5; Length 15;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPDVEKPDLPQ 13
   |||||
DB 5 PPDVEGDDCLP 15

RESULT 17
ABG67771
ID ABG67771 standard; peptide; 12 AA.
XX
AC ABG67771;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human ADPI tryptic digest peptide #480.
XX
KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
KW Alzheimer's disease-associated feature; neuroprotective;
KW Alzheimer's disease-associated protein isoform; nootropic;
KW ADPI tryptic digest peptide.
XX
OS Homo sapiens.
XX
PN WO200246767-A2.
XX
PD 13-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-CB005289.
XX
PR 08-DEC-2000; 2000US-0254431P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlf C;
XX
DR WPI; 2002-508575/54.
XX
PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT comprises detecting Alzheimer disease-associated features or Alzheimer
PT disease-associated protein isoforms in brain tissue from the subject.
XX
PS Claim 7; Page 55; 427pp; English.
XX
CC The present invention relates to methods and compositions for the
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
CC subject. The method comprises analysing a sample of brain tissue from a
CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
CC disease-associated features (ADFs), whose relative abundance correlates
CC with the presence, absence, stage or severity of AD and comparing the
CC abundance of each feature with the abundance of that chosen feature in
CC brain tissue from persons free from AD. The invention also describes
CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
CC brain tissue. The methods and compositions of the invention are useful
CC for the screening, diagnosis or prognosis of AD in a subject, for
CC determining the stage or severity of AD in a subject, for
CC subject at risk of developing AD, or for monitoring the effect of therapy
CC administered to a subject having AD. Antibodies capable of binding to
CC ADPIs are useful for treating or preventing AD, and for determining the
CC efficacy of a given treatment regime. An agent that modulates the
CC activity of ADPI is useful in the manufacture of a medicament for the
CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
CC human ADPI tryptic digest peptides
XX
SQ Sequence 12 AA;

Query Match      35.7%; Score 35; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPDVEKPDLPQ 12
   |||||
DB 3 PPSAEYDPLR 12

RESULT 19
AAB26624
ID AAB26624 standard; peptide; 13 AA.
XX
```

```
Db 3 PPSAEYDPLR 12
   |||||
ID ADA23910 standard; peptide; 12 AA.
XX
AC ADA23910;
XX
DT 20-NOV-2003 (first entry)
XX
DE Alzheimer's disease-associated protein isoform tryptic peptide #519.
XX
KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;
KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
KW Alzheimer's disease-associated protein isoform; ADPI.
XX
OS Homo sapiens.
XX
PN US2003064411-A1.
XX
PD 03-APR-2003.
XX
PF 10-DEC-2001; 2001US-00014340.
XX
PR 08-DEC-2000; 2000US-0254431P.
XX
PA (HERA/) HERATH H M A C.
PA (PARE/) PAREKH R B.
PA (ROHL/) ROHLFF C.
XX
PI Herath HMAC, Parekh RB, Rohlf C;
XX
DR WPI; 2003-540784/51.
XX
PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT involves analyzing test sample of brain tissue from subject, and
PT comparing feature in test sample with that of person(s) free from
PT Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 519; 115pp; English.
XX
CC The invention relates to a method of screening or diagnosing Alzheimer's
CC disease in a subject. The method is useful for screening, diagnosis or
CC prognosis of Alzheimer's disease in a subject for determining the stage
CC of severity of Alzheimer's disease in a subject, for identifying a
CC subject at risk of developing Alzheimer's disease, or for monitoring the
CC effect of therapy administered to a subject having Alzheimer's disease.
CC The method is also useful in treating vascular dementia, Lewy body
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
CC depression. The inventive method identifies sensitive and specific
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
CC It provides therapeutic agents for Alzheimer's disease that works
CC quickly, potentially, specifically with fewer side effects. The present
CC sequence represents the amino acid sequence of a Alzheimer's disease-
CC associated protein isoform tryptic peptide.
XX
SQ Sequence 12 AA;

Query Match      35.7%; Score 35; DB 6; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPDVEKPDLPQ 12
   |||||
DB 3 PPSAEYDPLR 12

RESULT 19
AAB26624
ID AAB26624 standard; peptide; 13 AA.
XX
```

AC AAB26624;
 XX 22-JAN-2001 (first entry)
 DT
 XX Partial sequence #24 of Breast Cancer-Associated Protein Isoform.
 DE
 KW BPI; breast cancer-associated protein isoform; gene therapy;
 KW breast cancer.
 XX
 OS Homo sapiens.
 XX
 XX WO200055628-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 13-MAR-2000; 2000WO-GB000908.
 XX
 XX 12-MAR-1999; 99GB-00005817.
 XX
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 XX Amess B, Townsend RR, Parekh RB, Waterfield MD, O'hare MJ;
 XX
 XX WPI; 2000-602142/57.
 DR
 XX Screening, diagnosis of breast cancer and monitoring the effectiveness of
 PT breast cancer therapy, involves detecting breast cancer-associated
 PT features and breast cancer-associated protein isoforms.
 XX
 XX Disclosure; Page 14; 86pp; English.
 PS
 XX The present invention relates to the screening, diagnosis and prognosis
 CC of breast cancer, for monitoring the effectiveness of breast cancer
 CC treatment in a human, comprising identifying the presence or absence of
 CC breast cancer-associated features (BF) or breast cancer-associated
 CC protein isoforms (BPIs). Antibodies derived from BF and BPIs may be
 CC useful for the treatment and screening of breast cancer, in particular
 CC metastatic breast cancer. The present sequence is the partial sequence of
 CC a BPI
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 35.7%; Score 35; DB 3; Length 13;
 Best Local Similarity 60.0%; Pred. No. 2.7e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 3 PPDVEKPDQLQ 12
 DB ||| |||:
 4 PPSAEVPLLR 13
 RESULT 20
 ABB97740
 ID ABB97740 standard; peptide; 13 AA.
 AC
 XX ABB97740;
 XX
 XX 11-JUL-2002 (first entry)
 DT
 XX Human procathepsin W epitope peptide #120.
 DE
 XX Human; procathepsin W; cathepsin W; monoclonal antibody; epitope.
 KW
 XX Homo sapiens.
 OS
 XX WO200226831-A1.
 XX
 XX 04-APR-2002.
 PD
 XX 09-JUL-2001; 2001WO-EP007877.
 PF
 XX 29-SEP-2000; 2000DE-01048727.
 PR
 XX
 XX

PA (LABS-) LABSOFT DIAGNOSTICS AG.
 XX
 XX Weber E;
 PI
 XX WPI; 2002-330095/36.
 DR
 XX New hybridoma cell lines that produces antibodies specific for human
 PT cathepsin W, useful e.g. for diagnosis, therapy and drug targeting.
 PT
 XX Disclosure; Fig 1; 23pp; German.
 PS
 XX The present invention relates to hybridoma cell lines that produce
 CC monoclonal antibodies directed against a defined epitope of human
 CC (pro)cathepsin W, which are produced by fusing myeloma cells with spleen
 CC cells from an animal that has been immunised with recombinant
 CC procathepsin W. The antibodies produced are useful for analysis,
 CC diagnosis (detection of human (pro)cathepsin W), purification of
 CC (pro)cathepsin W (also for clarifying processing of the precursor and
 CC functional significance of the mature protein), for drug targeting and
 CC for therapeutic use. The present sequence is an epitope of human
 CC procathepsin W
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 34.7%; Score 34; DB 5; Length 13;
 Best Local Similarity 62.5%; Pred. No. 3.8e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 6 VEKPDLPQ 13
 DB ||| |||:
 3 VQKPDMPK 10
 RESULT 21
 ABB97739
 ID ABB97739 standard; peptide; 13 AA.
 XX
 XX ABB97739;
 AC
 XX 11-JUL-2002 (first entry)
 DT
 XX Human procathepsin W epitope peptide #119.
 DE
 XX Human; procathepsin W; cathepsin W; monoclonal antibody; epitope.
 KW
 XX Homo sapiens.
 OS
 XX WO200226831-A1.
 PN
 XX 04-APR-2002.
 PD
 XX 09-JUL-2001; 2001WO-EP007877.
 PF
 XX 29-SEP-2000; 2000DE-01048727.
 PR
 XX (LABS-) LABSOFT DIAGNOSTICS AG.
 PA
 XX Weber E;
 PI
 XX WPI; 2002-330095/36.
 DR
 XX New hybridoma cell lines that produces antibodies specific for human
 PT cathepsin W, useful e.g. for diagnosis, therapy and drug targeting.
 PT
 XX Disclosure; Fig 1; 23pp; German.
 PS
 XX The present invention relates to hybridoma cell lines that produce
 CC monoclonal antibodies directed against a defined epitope of human
 CC (pro)cathepsin W, which are produced by fusing myeloma cells with spleen
 CC cells from an animal that has been immunised with recombinant
 CC procathepsin W. The antibodies produced are useful for analysis,
 CC diagnosis (detection of human (pro)cathepsin W), purification of
 CC (pro)cathepsin W (also for clarifying processing of the precursor and
 CC

CC functional significance of the mature protein), for drug targeting and
 CC for therapeutic use. The present sequence is an epitope of human
 CC procathepsin W

XX
 SQ Sequence 13 AA;

Query Match 34.7%; Score 34; DB 5; Length 13;
 Best Local Similarity 62.5%; Pred. No. 3.8e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13
 ||: ||: ||:
 Db 6 VQKEDMKP 13

RESULT 22

ADM75160
 ID ADM75160 standard; peptide; 13 AA.

XX
 AC ADM75160;

XX
 DT 03-JUN-2004 (first entry)

XX
 DE Potential human MHC class II binding human Factor VIII peptide #380.

XX
 KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
 MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.

XX
 OS Homo sapiens.

XX
 PN WO2003087161-A1.

XX
 PD 23-OCT-2003.

XX
 PF 17-APR-2003; 2003WO-EP004063.

XX
 PR 18-APR-2002; 2002EP-00008712.

PR 24-MAR-2003; 2003EP-00006554.

XX
 PA (MERE) MERCK PATENT GMBH.

XX
 PI Jones T, Baker M, Carr FU;

XX
 DR WPI; 2003-845307/78.

XX
 PT New modified human Factor VIII molecule being substantially non-
 immunogenic or less immunogenic than non-modified human Factor VIII,
 useful in preparing a composition for treating e.g., Gaucher's disease.

XX
 PS Disclosure; Fig 1; 68pp; English.

XX
 CC The invention relates to a novel modified human Factor VIII molecule. The
 modified human Factor VIII molecule being substantially non-immunogenic
 or less immunogenic than a non-modified human Factor VIII and having
 essentially the same biological specificity and activity when used in
 vivo. The modified human Factor VIII molecule comprises specifically
 altered amino acid residues compared with the non-modified parental
 molecule, where the altered amino acid residues cause a reduction or an
 elimination of one or more of the T-cell epitopes, which act in the
 parental non-modified molecule as MHC class II binding ligands and
 stimulate T-cells. The potential MHC class II binding activity peptide is
 useful for the manufacture of the modified Factor VIII molecule or a
 vaccine in order to reduce immunogenicity to Factor VIII in a patient.
 The modified Factor VIII molecule is useful in preparing a composition
 for treating e.g., Gaucher's disease. This sequence represents a human
 Factor VIII peptide with potential human MHC class II binding activity of
 the invention.

XX
 SQ Sequence 13 AA;

Query Match 34.7%; Score 34; DB 7; Length 13;
 Best Local Similarity 38.5%; Pred. No. 3.8e+02;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 4 PDVEKPDLPQPV 16
 ||: ||: ||:
 Db 1 PDAQNPDMSEFFKM 13

RESULT 23

AAB21134
 ID AAB21134 standard; peptide; 15 AA.

XX
 AC AAB21134;

XX
 DT 19-JAN-2001 (first entry)

XX
 DE Src homology 3 domain binding peptide #11.

XX
 KW Src homology domain 3; SH3; protein-protein interaction; cancer;
 signal transduction inhibition; immune suppression-associated disease.

XX
 OS Synthetic.

XX
 PN WO200047607-A1.

XX
 PD 17-AUG-2000.

XX
 PF 12-FEB-2000; 2000WO-KR000107.

XX
 PR 12-FEB-1999; 99AU-00008643.

PR 02-JUN-1999; 99KR-00020282.

XX
 PA (YOON/) YOON J H.

PA (HANY/) HAN Y T.

XX
 PI Yoon JH, Han YT, Lee KY;

XX
 DR WPI; 2000-533010/48.

XX
 PT Synthetic peptides useful for treating cancers and immunosuppressive
 disorders by disrupting interactions of the SH (Src homology) 2 and SH3
 motifs of Src family kinase proteins.

XX
 PS Claim 3; Page 35; 40pp; English.

XX
 CC The present sequence is a synthetic peptide which has a high affinity for
 the src homology 3 (SH3) domain of protein kinases. Protein kinases are
 involved in signal transduction pathways, and this peptide can be used to
 inhibit these, by disrupting protein-protein interactions, in the
 treatment of cancer, particularly hepatocellular carcinoma, cervical
 cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-
 associated diseases

XX
 SQ Sequence 15 AA;

Query Match 33.7%; Score 33; DB 3; Length 15;
 Best Local Similarity 41.7%; Pred. No. 6.1e+02;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQ 12
 ||: ||: ||:
 Db 2 ERPPVPNPDPYE 13

RESULT 24

AAY41624

ID AAY41624 standard; peptide; 18 AA.

XX
 AC AAY41624;

XX
 DT 02-DEC-1999 (first entry)

XX
 DE Mammalian ion channel proline rich motif containing peptide #18.

XX
 KW SH3 domain; binding motif; potassium channel; protein tyrosine kinase;

KW proline rich.
XX
OS Rattus sp.
XX
PN US955259-A.
XX
PD 21-SEP-1999.
XX
PF 19-DEC-1996; 96US-00769745.
XX
PR 19-DEC-1996; 96US-00769745.
XX
PA (UYBR-) UNIV BRANDEIS.
XX
PI Holmes TC, Levitan IB;
XX
DR WPI; 1999-560490/47.
XX
XX Identification of compounds that modulate potassium ion channel binding
with protein tyrosine kinase SH3 domains.
XX
PS Disclosure; Col 8; 18pp; English.
XX
CC A method has been developed for determining if a compound modulates the
binding of a potassium ion channel to the SH3 domain of a protein
tyrosine kinase by contacting the channel with a polypeptide comprising
the SH3 domain and the compound to be assessed and measuring channel-SH3
binding. The method is useful for assessing the ability of a compound to
modulate the formation of channel-SH3 domain complexes to improve the
understanding of mechanisms of potassium channel blockage and assess the
ability of potential therapeutics to inhibit blockage. AAY41607 to
CC AAY41644 represent mammalian ion channel peptides with proline-rich
CC motifs
XX
SQ Sequence 18 AA;
Query Match 33.7%; Score 33; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 7.4e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 2 QPVDVEKPDLPQ 13
|||: |||
DB 6 QPPESSPPPLP 17
RESULT 25
AAE34138
ID AAE34138 standard; peptide; 18 AA.
AC AAE34138;
XX
DT 02-MAY-2003 (first entry)
XX
DE T-cell stimulatory gluten peptide #17.
XX
KW Human leukocyte antigen; HLA; T-cell receptor; giardiasis; celiac sprue;
KW food-related immune enteropathy; tropical sprue; gluten sensitivity;
KW food allergy; protozoacide; antiinflammatory; immunosuppressive; gluten.
XX
OS Unidentified.
XX
PN WO200283722-A2.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-NL000235.
XX
PR 12-APR-2001; 2001EP-00201377.
PR 16-NOV-2001; 2001EP-00204383.
XX
PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
XX
PI Drijfhout JW, Koning F, Mcadam SN, Sollid LM;
XX
XX proline rich.
XX
OS Rattus sp.
XX
PN US955259-A.
XX
PD 21-SEP-1999.
XX
PF 19-DEC-1996; 96US-00769745.
XX
PR 19-DEC-1996; 96US-00769745.
XX
PA (UYBR-) UNIV BRANDEIS.
XX
PI Holmes TC, Levitan IB;
XX
DR WPI; 1999-560490/47.
XX
XX Identification of compounds that modulate potassium ion channel binding
with protein tyrosine kinase SH3 domains.
XX
PS Disclosure; Col 8; 18pp; English.
XX
CC A method has been developed for determining if a compound modulates the
binding of a potassium ion channel to the SH3 domain of a protein
tyrosine kinase by contacting the channel with a polypeptide comprising
the SH3 domain and the compound to be assessed and measuring channel-SH3
binding. The method is useful for assessing the ability of a compound to
modulate the formation of channel-SH3 domain complexes to improve the
understanding of mechanisms of potassium channel blockage and assess the
ability of potential therapeutics to inhibit blockage. AAY41607 to
CC AAY41644 represent mammalian ion channel peptides with proline-rich
CC motifs
XX
SQ Sequence 18 AA;
Query Match 33.7%; Score 33; DB 6; Length 18;
Best Local Similarity 46.7%; Pred. No. 7.4e+02;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3 PPDVEKPDLPQFQVQ 17
|||: |||
DB 2 PPQQPYPPQPPFQSQ 16
RESULT 26
AAE34142
ID AAE34142 standard; peptide; 18 AA.
AC AAE34142;
XX
DT 02-MAY-2003 (first entry)
XX
DE T-cell stimulatory gluten peptide #21.
XX
KW Human leukocyte antigen; HLA; T-cell receptor; giardiasis; celiac sprue;
KW food-related immune enteropathy; tropical sprue; gluten sensitivity;
KW food allergy; protozoacide; antiinflammatory; immunosuppressive; gluten.
XX
OS Unidentified.
XX
PN WO200283722-A2.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-NL000235.
XX
PR 12-APR-2001; 2001EP-00201377.
PR 16-NOV-2001; 2001EP-00204383.
XX
PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
XX
PI Drijfhout JW, Koning F, Mcadam SN, Sollid LM;
XX
XX Novel isolated or recombinant human leukocyte antigen-DQ restricted T-
cell receptor for treating food-related immune enteropathy such as celiac
sprue, tropical sprue, giardiasis and food allergies of childhood.
XX
PS Disclosure; Fig 2; 64pp; English.
XX
CC The present invention relates to novel isolated or recombinant human
leukocyte antigen (HLA)-DQ restricted T-cell receptor or its functional
equivalent and/or fragment, capable of recognising a prolamine-derived
peptide. The invention relates to recombinant or synthetic prolamine
derived peptides involved in food-related immune enteropathy. The
pharmaceutical composition is useful to treat food-related immune
enteropathies such as celiac sprue, tropical sprue, giardiasis or food
allergies of childhood. It is useful to induce tolerance, treat gluten-
sensitivity and to eliminate gluten-sensitive T-cells. Sequences of the
invention are useful to decrease the amount of toxic prolamine-derived
peptides in food or food components and to select and/or breed a cereal.
CC The cereal is useful for inclusion in a diet for a gluten sensitive
individual. Blocking substances are useful to decrease the binding of HLA
-DQ restricted T-cell receptor to a prolamine-derived peptide involved in
food-related immune enteropathy for depletion of T-cells bearing the HLA-
DQ restricted T-cell receptor. The present sequence is T-cell stimulatory
gluten peptide. This sequence is used in the invention
XX
SQ Sequence 18 AA;
Query Match 33.7%; Score 33; DB 6; Length 18;
Best Local Similarity 46.7%; Pred. No. 7.4e+02;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3 PPDVEKPDLPQFQVQ 17
|||: |||
DB 2 PPQQPYPPQPPFQSQ 16
RESULT 26
AAE34142
ID AAE34142 standard; peptide; 18 AA.
AC AAE34142;
XX
DT 02-MAY-2003 (first entry)
XX
DE T-cell stimulatory gluten peptide #21.
XX
KW Human leukocyte antigen; HLA; T-cell receptor; giardiasis; celiac sprue;
KW food-related immune enteropathy; tropical sprue; gluten sensitivity;
KW food allergy; protozoacide; antiinflammatory; immunosuppressive; gluten.
XX
OS Unidentified.
XX
PN WO200283722-A2.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-NL000235.
XX
PR 12-APR-2001; 2001EP-00201377.
PR 16-NOV-2001; 2001EP-00204383.
XX
PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
XX
PI Drijfhout JW, Koning F, Mcadam SN, Sollid LM;
XX
XX Novel isolated or recombinant human leukocyte antigen-DQ restricted T-
cell receptor for treating food-related immune enteropathy such as celiac
sprue, tropical sprue, giardiasis and food allergies of childhood.
XX

XX PA (ISIS-) ISIS INNOVATION LTD.
 XX PI Anderson RP, Hill AVS, Jewell DP;
 XX DR WPI; 2001-300179/31.
 XX DR
 XX PT Diagnosing coeliac disease or susceptibility to the disease in an
 PT individual, by detecting in vitro or in vivo T cells which bind
 PT immunodominant T cell epitope obtained from naturally occurring homolog
 PT of gliadin.
 XX PS
 XX PS Example 11; Page 58; 107pp; English.
 XX CC The sequence represents a gliadin peptide corresponding to A-gliadin 57-
 CC 73 which is naturally polymorphic in that region and is antagonistic to A
 CC -gliadin 57-73 Q865 interferon gamma ELISpot (not defined) response. The
 CC peptides of the invention are used to test mammalian (preferably human)
 CC susceptibility to coeliac disease (gluten intolerance). The peptides are
 CC contacted with a blood sample and T cell recognition measured, a positive
 CC T-cell recognition indicating a susceptibility to coeliac disease. The
 CC peptides are useful for inducing tolerance in an individual and
 CC antagonists to the peptides are useful for treating or preventing coeliac
 CC disease in an individual and for producing an antibody specific to them
 CC or a wild-type sequence. A mutant gliadin protein (or its fragment of 15
 CC amino acids in length) whose wild-type sequence can be modified by
 CC transglutaminase to a sequence that comprises the epitope, but which has
 CC been modified in such a way that it does not contain sequence which can
 CC be modified by transglutaminase to a sequence that comprise the epitope
 CC is useful for decreasing the ability of gliadin protein to cause Coeliac
 CC disease. Nucleic acids encoding proteins antagonistic to the T-cell
 CC binding of the epitopes are useful for obtaining a transgenic plant cell
 CC or seed and for the production of a protein. The resultant crop plant is
 CC useful for obtaining a product of a wheat plant, especially grain, which
 CC is optionally processed into flour or another grain product. Food
 CC comprising the antagonistic protein is useful instead of a wild-type
 CC gliadin
 XX SQ Sequence 17 AA;
 XX
 XX Query Match 32.7%; Score 32; DB 4; Length 17;
 XX Best Local Similarity 45.5%; Pred. No. 9.7e+02;
 XX Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 3 PPDVEKPDLPQ 13
 Db ||::|
 7 PPPLPYQTQP 17
 RESULT 32
 AAU01840
 ID AAU01840 standard; peptide; 17 AA.
 XX AC AAU01840;
 XX DT 07-SEP-2001 (first entry)
 XX DE Wheat peptide antagonist for A-gliadin 57-73 Q865 #2.
 XX KW Wheat; A-gliadin; 57-75 Q865; coeliac disease; gluten intolerance;
 KW T-cell binding; antagonist; transglutaminase; transgenic plant.
 XX OS Triticum aestivum.
 XX PN WO200125793-A2.
 XX PD 12-APR-2001.
 XX PF 02-OCT-2000; 2000WO-GB003760.
 XX PR 01-OCT-1999; 99GB-00023306.
 XX PA (ISIS-) ISIS INNOVATION LTD.
 XX PI Anderson RP, Hill AVS, Jewell DP;

XX PI Anderson RP, Hill AVS, Jewell DP;
 XX DR WPI; 2001-300179/31.
 XX DR
 XX PT Diagnosing coeliac disease or susceptibility to the disease in an
 PT individual, by detecting in vitro or in vivo T cells which bind
 PT immunodominant T cell epitope obtained from naturally occurring homolog
 PT of gliadin.
 XX PS
 XX PS Example 11; Page 58; 107pp; English.
 XX CC The sequence represents a gliadin peptide corresponding to A-gliadin 57-
 CC 73 which is naturally polymorphic in that region and is antagonistic to A
 CC -gliadin 57-73 Q865 interferon gamma ELISpot (not defined) response. The
 CC peptides of the invention are used to test mammalian (preferably human)
 CC susceptibility to coeliac disease (gluten intolerance). The peptides are
 CC contacted with a blood sample and T cell recognition measured, a positive
 CC T-cell recognition indicating a susceptibility to coeliac disease. The
 CC peptides are useful for inducing tolerance in an individual and
 CC antagonists to the peptides are useful for treating or preventing coeliac
 CC disease in an individual and for producing an antibody specific to them
 CC or a wild-type sequence. A mutant gliadin protein (or its fragment of 15
 CC amino acids in length) whose wild-type sequence can be modified by
 CC transglutaminase to a sequence that comprises the epitope, but which has
 CC been modified in such a way that it does not contain sequence which can
 CC be modified by transglutaminase to a sequence that comprise the epitope
 CC is useful for decreasing the ability of gliadin protein to cause Coeliac
 CC disease. Nucleic acids encoding proteins antagonistic to the T-cell
 CC binding of the epitopes are useful for obtaining a transgenic plant cell
 CC or seed and for the production of a protein. The resultant crop plant is
 CC useful for obtaining a product of a wheat plant, especially grain, which
 CC is optionally processed into flour or another grain product. Food
 CC comprising the antagonistic protein is useful instead of a wild-type
 CC gliadin
 XX SQ Sequence 17 AA;
 XX
 XX Query Match 32.7%; Score 32; DB 4; Length 17;
 XX Best Local Similarity 45.5%; Pred. No. 9.7e+02;
 XX Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 3 PPDVEKPDLPQ 13
 Db ||::|
 7 PPPLPYQTQP 17
 RESULT 33
 ADH14690
 ID ADH14690 standard; peptide; 17 AA.
 XX AC ADH14690;
 XX DT 11-MAR-2004 (first entry)
 XX DE Gliadin related epitope peptide.
 XX KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 KW vaccine.
 XX OS Synthetic.
 XX PN WO2003104273-A2.
 XX PD 18-DEC-2003.
 XX PF 05-JUN-2003; 2003WO-GB002450.
 XX PR 05-JUN-2002; 2002GB-00012885.
 XX PA (ISIS-) ISIS INNOVATION LTD.
 XX PI Anderson RP, Hill AVS, Jewell DP;

XX WPI; 2004-043640/04.
 XX Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.
 XX
 XX Example 11; Page 84; 177pp; English.
 XX
 CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 17 AA;
 CC
 CC Query Match 32.7%; Score 32; DB 8; Length 17;
 CC Best Local Similarity 45.5%; Pred. No. 9.7e+02;
 CC Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 3 PPDVEKPDLPQ 13
 Db ||:: ||
 7 PPELPYPQTQP 17
 RESULT 34
 ADH14691
 ID ADH14691 standard; peptide; 17 AA.
 XX
 AC ADH14691;
 XX
 XX 11-MAR-2004 (first entry)
 XX
 DE Gliadin related epitope peptide.
 XX
 DE coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 KW vaccine.
 KW Synthetic.
 OS
 XX WO2003104273-A2.
 PN
 XX 18-DEC-2003.
 PD
 XX
 XX 05-JUN-2003; 2003WO-GE002450.
 PF
 XX
 XX 05-JUN-2002; 2002GB-00012885.
 PR
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 PA
 XX
 XX Anderson RP, Hill AVS, Jewell DP;
 PI
 XX WPI; 2004-043640/04.
 DR
 XX Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.
 XX
 XX Example 11; Page 84; 177pp; English.
 PS
 XX
 CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has

CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 17 AA;
 CC
 CC Query Match 32.7%; Score 32; DB 8; Length 17;
 CC Best Local Similarity 45.5%; Pred. No. 9.7e+02;
 CC Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 3 PPDVEKPDLPQ 13
 Db ||:: ||
 7 PPELPYPQTQP 17
 RESULT 35
 AAW38909
 ID AAW38909 standard; peptide; 18 AA.
 XX
 AC AAW38909;
 XX
 XX 27-MAR-1998 (first entry)
 DT
 XX
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:305.
 DE
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;
 KW PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 OS Synthetic.
 XX
 XX WO9730074-A1.
 PN
 XX 21-AUG-1997.
 PD
 XX 14-FEB-1997; 97WO-US002298.
 PF
 XX 16-FEB-1996; 96US-00602999.
 PR
 XX (CYTO-) CYTOGEN CORP.
 XX (UYNC-) UNIV NORTH CAROLINA.
 PA
 XX Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ, Fowlkes DM;
 PI Rider JE;
 PI
 XX WPI; 1997-424972/39.
 DR
 XX Src homology region 3 binding peptide - used to activate Src tyrosine
 PT kinase(s) and to stimulate immune response by increasing production of
 PT certain lymphokine(s), e.g. interleukin-1.
 XX
 XX Claim 22; Page 90; 131pp; English.
 PS
 XX
 CC The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain
 CC of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which
 CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain
 CC of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding peptides
 CC can be used in the method to identify inhibitors of their binding to
 CC their respective SH3 domains, which could be used to modulate the
 CC pharmacological activity of proteins or polypeptide containing the SH3
 CC domain. The peptides can also be used to activate Src or Src-related
 CC protein tyrosine kinases, to stimulate the immune response by increasing

CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha
 CC and interleukin-1, or to deliver a conjugated molecule to certain
 CC cellular compartments containing Src or Src related proteins

XX Sequence 18 AA;

Query Match 32.7%; Score 32; DB 2; Length 18;
 Best Local Similarity 43.8%; Pred. NO. 1e+03;
 Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLPQFQVQ 17
 ||| |||
 Db 3 QPPVFPFPQPIVQ 18

RESULT 36
 ADH14808
 ID ADH14808 standard; peptide; 17 AA.

XX AC ADH14808;

XX DT 11-MAR-2004 (first entry)

XX DE Gliadin related epitope peptide.

XX KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 KW vaccine.

XX OS Synthetic.

XX PN WO2003104273-A2.

XX PD 18-DEC-2003.

XX PF 05-JUN-2003; 2003WO-GB002450.

XX PR 05-JUN-2002; 2002GB-00012885.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PI Anderson RP, Hill AVS, Jewell DP;

XX WPI; 2004-043640/04.

XX Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.

XX Example 13; Page 95; 177pp; English.

XX The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

XX Sequence 17 AA;

Query Match 32.1%; Score 31.5; DB 8; Length 17;
 Best Local Similarity 50.0%; Pred. NO. 1.1e+03;
 Matches 8; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 2 QPPDVEKPDLPQFQVQ 17
 ||| : |||||
 Db 2 QQPPFPQIQ-QPPFPQ 16

RESULT 37

ADH14809
 ID ADH14809 standard; peptide; 17 AA.

XX AC ADH14809;

XX DT 11-MAR-2004 (first entry)

XX DE Gliadin related epitope peptide.

XX KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 KW vaccine.

XX OS Synthetic.

XX PN WO2003104273-A2.

XX PD 18-DEC-2003.

XX PF 05-JUN-2003; 2003WO-GB002450.

XX PR 05-JUN-2002; 2002GB-00012885.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PI Anderson RP, Hill AVS, Jewell DP;

XX WPI; 2004-043640/04.

XX Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.

XX Example 13; Page 95; 177pp; English.

XX The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

XX Sequence 17 AA;

Query Match 32.1%; Score 31.5; DB 8; Length 17;
 Best Local Similarity 50.0%; Pred. NO. 1.1e+03;
 Matches 8; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 2 QPPDVEKPDLPQFQVQ 17
 ||| : |||||
 Db 2 QQPPFPQIQ-QPPFPQ 16

RESULT 38

ADH14821
 ID ADH14821 standard; peptide; 18 AA.

XX AC ADH14821;

XX DT 11-MAR-2004 (first entry)

XX DE Gliadin related epitope peptide.

XX KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KW vaccine.
 XX
 OS Synthetic.
 XX
 PN WO2003104273-A2.
 XX
 PT
 PD 18-DEC-2003.
 XX
 XX
 PF 05-JUN-2003; 2003WO-GB002450.
 XX
 PR 05-JUN-2002; 2002GB-00012885.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 XX
 PI Anderson RP, Hill AVS, Jewell DP;
 XX
 XX WPI; 2004-043640/04.
 DR
 XX Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.
 XX
 PS Example 13; Page 95; 17pp; English.
 XX
 CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 18 AA;
 SQ
 Query Match 32.1%; Score 31.5; DB 8; Length 18;
 Best Local Similarity 53.8%; Pred. No. 1.2e+03;
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
 QY 2 QPDPVEKPLQPF 14
 DB ||| :|| |||
 ||| :|| |||
 2 QPFPQPFQ-QPF 13
 RESULT 39
 AAG97089
 ID AAG97089 standard; peptide; 10 AA.
 XX
 AC AAG97089;
 XX
 DT 18-SEP-2001 (first entry)
 XX
 DE Human complementary peptide, SEQ ID NO: 3283.
 XX
 KW Human; complementary peptide; ligand; drug discovery; drug design.
 XX
 OS Homo sapiens.
 XX
 PN WO200142277-A2.
 XX
 PD 14-JUN-2001.
 XX
 PF 13-DEC-2000; 2000WO-GB004776.
 XX
 PR 13-DEC-1999; 99GB-00029464.
 XX
 PA (PROT-) PROTEOM LTD.
 XX

PI Roberts GW, Heal JR;
 XX
 DR WPI; 2001-408419/43.
 XX
 PT A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.
 XX
 PS Example 4; Page 515; 646pp; English.
 XX
 CC The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided
 CC in the specification
 XX
 SQ Sequence 10 AA;
 Query Match 31.6%; Score 31; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 7.7e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 PPDVEKP 9
 DB ||| :||
 ||| :||
 3 PPTVQKP 9
 RESULT 40
 AAW17451
 ID AAW17451 standard; peptide; 11 AA.
 XX
 AC AAW17451;
 XX
 DT 17-JUN-1997 (first entry)
 XX
 DE Consensus antibacterial peptide from Podisus maculiventris.
 XX
 KW Podisus maculiventris; proline-rich; pathogenic; bacteria; bug;
 KW Gram negative; plant treatment.
 XX
 OS Podisus maculiventris.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 11
 FT /note= "X= a peptide residue comprising at least one
 FT tripeptide Pro-Arg-Pro motif"
 XX
 PN FR2732345-A1.
 XX
 PD 04-OCT-1996.
 XX
 PF 03-APR-1995; 95FR-00004130.
 XX
 PR 03-APR-1995; 95FR-00004130.
 XX
 PA (RHON) RHONE POULENC AGROCHIMIE.
 XX
 PI Bulet P, Hoffman J, Hetru C, Tchernych S;
 XX
 DR WPI; 1996-457711/46.
 XX
 PT proline-rich antibacterial peptide(s) from Podisus maculiventris - esp.
 PT useful to protect plants against pathogenic bacteria, also for
 PT antibacterial therapy of animals.
 XX
 PS Claim 1; Page 14; 16pp; English.
 XX
 CC AAW17451 is a generic sequence of an antibacterial peptide from the bug
 CC Podisus maculiventris. The proline-rich peptide has antibacterial
 CC activity against gram negative bacteria. It is useful for protecting
 CC plants against pathogenic bacteria, but could also be used for

CC antibacterial therapy of animals, including humans. For specific examples

CC see AAW09375-W09378

XX

SQ Sequence 11 AA;

Query Match 31.6%; Score 31; DB 2; Length 11;

Best Local Similarity 62.5%; Pred. No. 8.6e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VEKPDLPQ 13

|:|:|:|

Db 1 VDKPDYRP 8

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Job time : 99.8727 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:57:32 ; Search time 24.5455 Seconds
(without alignments)
54.743 Million cell updates/sec

Title: US-10-691-157-3

Perfect score: 98

Sequence: 1 DQPPDVKPLQPFQVQS 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 183464

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:**

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- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:**
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- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:**
- 5: /cgn2_6/ptodata/1/iaa/pCTUS_COMB.pep:**
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	18	4	US-09-641-803-3
2	33	33.7	14	2	US-07-963-538B-10
3	33	33.7	18	2	US-08-763-745-20
4	32	32.7	18	3	US-08-602-999A-305
5	32	32.7	18	4	US-09-500-124-305
6	31	31.6	17	1	US-08-318-200-21
7	31	31.6	18	1	US-08-336-618-11
8	30.5	31.1	11	2	US-08-343-443B-74
9	30.5	31.1	11	2	US-08-343-443B-94
10	29	29.6	8	4	US-10-365-908-98
11	29	29.6	15	4	US-09-914-259-70
12	29	29.6	17	1	US-08-144-121-12
13	29	29.6	17	2	US-08-735-893-12
14	29	29.6	18	3	US-09-461-697-200
15	28	28.6	11	4	US-09-906-393A-9
16	28	28.6	12	1	US-08-190-788A-43
17	28	28.6	12	1	US-08-190-788A-52
18	28	28.6	12	1	US-08-190-788A-284
19	28	28.6	12	1	US-08-383-474B-48
20	28	28.6	12	1	US-08-383-474B-57
21	28	28.6	12	1	US-08-383-474B-285
22	28	28.6	12	1	US-08-465-391A-43
23	28	28.6	12	1	US-08-465-391A-52
24	28	28.6	12	1	US-08-465-391A-284
25	28	28.6	12	2	US-08-464-538B-43
26	28	28.6	12	2	US-08-464-538B-52
27	28	28.6	12	2	US-08-464-538B-283

28	28	28.6	12	2	US-08-463-076E-87	Sequence 87, Appl
29	28	28.6	12	2	US-08-463-076E-96	Sequence 96, Appl
30	28	28.6	12	2	US-08-463-076E-357	Sequence 357, Appl
31	28	28.6	12	4	US-09-428-082B-673	Sequence 673, App
32	28	28.6	12	4	US-09-428-082B-683	Sequence 683, App
33	28	28.6	12	4	US-09-428-082B-958	Sequence 958, App
34	28	28.6	13	2	US-08-347-335A-13	Sequence 13, Appl
35	28	28.6	15	1	US-08-467-083-53	Sequence 53, Appl
36	28	28.6	15	1	US-08-414-417B-53	Sequence 53, Appl
37	28	28.6	15	2	US-08-486-348A-53	Sequence 53, Appl
38	28	28.6	15	3	US-08-468-545B-53	Sequence 53, Appl
39	28	28.6	15	3	US-08-466-680B-53	Sequence 53, Appl
40	28	28.6	15	4	US-09-354-533-53	Sequence 53, Appl
41	28	28.6	16	1	US-08-150-788A-170	Sequence 170, App
42	28	28.6	16	1	US-08-383-474B-173	Sequence 173, App
43	28	28.6	16	1	US-08-465-391A-170	Sequence 170, App
44	28	28.6	16	2	US-08-464-538B-170	Sequence 170, App
45	28	28.6	16	2	US-08-463-076E-223	Sequence 223, App
46	28	28.6	16	4	US-09-428-082B-786	Sequence 786, App
47	28	28.6	17	1	US-08-150-788A-169	Sequence 169, App
48	28	28.6	17	1	US-08-190-788A-230	Sequence 230, App
49	28	28.6	17	1	US-08-190-788A-233	Sequence 233, App
50	28	28.6	17	1	US-08-190-788A-234	Sequence 234, App
51	28	28.6	17	1	US-08-383-474B-172	Sequence 172, App
52	28	28.6	17	1	US-08-383-474B-233	Sequence 233, App
53	28	28.6	17	1	US-08-383-474B-236	Sequence 236, App
54	28	28.6	17	1	US-08-383-474B-237	Sequence 237, App
55	28	28.6	17	1	US-08-465-391A-169	Sequence 169, App
56	28	28.6	17	1	US-08-465-391A-230	Sequence 230, App
57	28	28.6	17	1	US-08-465-391A-233	Sequence 233, App
58	28	28.6	17	1	US-08-465-391A-234	Sequence 234, App
59	28	28.6	17	2	US-08-464-538B-169	Sequence 169, App
60	28	28.6	17	2	US-08-464-538B-230	Sequence 230, App
61	28	28.6	17	2	US-08-464-538B-233	Sequence 233, App
62	28	28.6	17	2	US-08-464-538B-234	Sequence 234, App
63	28	28.6	17	2	US-08-463-076E-222	Sequence 222, App
64	28	28.6	17	2	US-08-463-076E-284	Sequence 284, App
65	28	28.6	17	2	US-08-463-076E-287	Sequence 287, App
66	28	28.6	17	2	US-08-463-076E-288	Sequence 288, App
67	28	28.6	17	3	US-08-602-999A-338	Sequence 338, App
68	28	28.6	17	4	US-09-500-124-338	Sequence 338, App
69	28	28.6	17	4	US-09-428-082B-785	Sequence 785, App
70	28	28.6	17	4	US-09-428-082B-844	Sequence 844, App
71	28	28.6	17	4	US-09-428-082B-847	Sequence 847, App
72	28	28.6	17	4	US-09-428-082B-848	Sequence 848, App
73	27	27.6	8	1	US-07-923-724-48	Sequence 48, Appl
74	27	27.6	8	2	US-08-609-426A-38	Sequence 48, Appl
75	27	27.6	8	2	US-08-374-652C-38	Sequence 38, Appl
76	27	27.6	9	2	US-08-146-028-431	Sequence 431, App
77	27	27.6	9	2	US-08-146-028-432	Sequence 432, App
78	27	27.6	9	2	US-08-146-028-433	Sequence 433, App
79	27	27.6	9	3	US-08-723-425A-431	Sequence 431, App
80	27	27.6	9	3	US-08-723-425A-432	Sequence 432, App
81	27	27.6	9	3	US-08-723-425A-433	Sequence 433, App
82	27	27.6	9	3	US-08-112-206-431	Sequence 431, App
83	27	27.6	9	3	US-08-112-206-432	Sequence 432, App
84	27	27.6	9	3	US-08-112-206-433	Sequence 433, App
85	27	27.6	9	3	US-09-518-046-148	Sequence 148, App
86	27	27.6	9	4	US-09-790-497A-379	Sequence 379, App
87	27	27.6	9	4	US-09-790-497A-380	Sequence 380, App
88	27	27.6	9	4	US-09-790-497A-381	Sequence 381, App
89	27	27.6	9	4	US-09-790-497A-564	Sequence 564, App
90	27	27.6	9	4	US-09-790-497A-565	Sequence 565, App
91	27	27.6	9	4	US-09-790-497A-566	Sequence 566, App
92	27	27.6	9	4	US-09-576-824A-379	Sequence 379, App
93	27	27.6	9	4	US-09-576-824A-380	Sequence 380, App
94	27	27.6	9	4	US-09-576-824A-381	Sequence 381, App
95	27	27.6	9	4	US-09-680-497-431	Sequence 431, App
96	27	27.6	9	4	US-09-680-497-432	Sequence 432, App
97	27	27.6	9	4	US-09-680-497-433	Sequence 433, App
98	27	27.6	9	4	US-10-365-908-122	Sequence 122, App
99	27	27.6	10	3	US-08-762-428A-1	Sequence 1, Appl
100	27	27.6	10	4	US-10-365-908-114	Sequence 114, App

ALIGNMENTS

RESULT 1
US-09-641-803-3
; Sequence 3, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-3

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQFQVQS 18
Db 1 DQPPDVEKPDLPQFQVQS 18

RESULT 2
US-07-963-538B-10
; Sequence 10, Application US/07963538B
; Patent No. 5851983
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, TAKASHI
; APPLICANT: KAMIMURA, TAKASHI
; APPLICANT: MASUDA, KENICHI
; APPLICANT: OKADA, MASAHIRO
; APPLICANT: OHTSUKA, EIKO
; APPLICANT: IMAIZUMI, ATSUSHI
; APPLICANT: WATANABE, KUNIHITO
; APPLICANT: SUGA, TETSUYA
; APPLICANT: MATSUMOTO, YOHICHI
; APPLICANT: TAKEUCHI, AKIKO
; TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
; TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
; TITLE OF INVENTION: TECHNOLOGY
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD LLP
; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/963,538B

; FILING DATE: 20-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/843,359
; FILING DATE: 25-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/408,483
; FILING DATE: 22-AUG-1989
; APPLICATION NUMBER: JP 4-212399
; FILING DATE: 17-JUL-1992
; APPLICATION NUMBER: JP 4-212398
; FILING DATE: 17-JUL-1992
; APPLICATION NUMBER: JP 3-355553
; FILING DATE: 24-DEC-1991
; APPLICATION NUMBER: JP 62-330219
; FILING DATE: 28-DEC-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: TEJN-005/020US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5070
; TELEFAX: 415-857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-963-538B-10

Query Match 33.7%; Score 33; DB 2; Length 14;
Best Local Similarity 53.8%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLP 13
Db 1 DDPPTVELQGLVP 13

RESULT 3
US-08-769-745-20
; Sequence 20, Application US/08769745
; Patent No. 5955259
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; TITLE OF INVENTION: Channel Activity
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Rat
US-08-769-745-20

Query Match 33.7%; Score 33; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 97;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLP 13
Db 6 QPPSSPPPLLP 17

RESULT 4
US-08-602-999A-305
; Sequence 305, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirostock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-305
Query Match 32.7%; Score 32; DB 3; Length 18;
Best Local Similarity 43.8%; Pred. NO. 1.4e+02;
Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 2 QPPDVEKPDLPQFQVQ 17
DB 3 QPPYPPPPYQPIYPQ 18
RESULT 5
US-08-602-999A-305
; Sequence 305, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/502,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirostock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-305
Query Match 32.7%; Score 32; DB 4; Length 18;
Best Local Similarity 43.8%; Pred. NO. 1.4e+02;
Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 2 QPPDVEKPDLPQFQVQ 17
DB 3 QPPYPPPPYQPIYPQ 18
RESULT 6
US-08-318-200-21
; Sequence 21, Application US/08318200
; Patent No. 5578496
; GENERAL INFORMATION:
; APPLICANT: Atassi, M. Z.
; APPLICANT: Ashizawa, T.
; TITLE OF INVENTION: N-TERMINAL PVA- OR PEG-CONJUGATED
; TITLE OF INVENTION: PEPTIDES FOR EPIOTOPE-SPECIFIC IMMUNOSUPPRESSION
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,200
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/965,670
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-318-200-21

Query Match 31.6%; Score 31.; DB 1; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 PDVEXPDLPQF 14
| : : : : :
DB 3 PESDQPDLSNF 13

RESULT 7
US-08-336-618-11
; Sequence 11, Application US/08336618
; Patent No. 5763590
; GENERAL INFORMATION:
; APPLICANT: Peattie, Debra A.
; APPLICANT: Harding, Matthew W.
; APPLICANT: Livingston, David J.
; TITLE OF INVENTION: ISOLATION OF AN MR 52,000 FK506 BINDING
; TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
; TITLE OF INVENTION: CDNA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hamilton, Brook, Smith and Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/336,618
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/963,325
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/777,752
; FILING DATE: 11-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: VP191-06A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-336-618-11

Query Match 31.6%; Score 31.; DB 1; Length 18;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DQPPDVEXPD 10
| : : : : :
DB 7 DQPADAEWRD 16

RESULT 8
US-08-343-443B-74
; Sequence 74, Application US/08343443B
; Patent No. 5968734
; GENERAL INFORMATION:
; APPLICANT: Aurias, Alain
; APPLICANT: Delattre, Olivier
; APPLICANT: Desmaze, Chantal
; APPLICANT: Melot, Thomas
; APPLICANT: Peter, Martine
; APPLICANT: Ploougastel, Beatrice
; APPLICANT: Thomas, Gilles
; APPLICANT: Zucman, Jessica
; TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
; TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
; TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
; TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
; TITLE OF INVENTION: TRANSLOCATIONS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 South Fifteenth Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AEDIT 1.0 DOS text editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,443B
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00494
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/06123
; FILING DATE: 20-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6121P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-343-443B-74

Query Match 31.1%; Score 30.5; DB 2; Length 11;
Best Local Similarity 46.2%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 4 PDVEXPDLPQFV 16
| : : : : :
DB 1 PDL---DLDPYQI 10

RESULT 9
US-08-343-443B-94
; Sequence 94, Application US/08343443B
; Patent No. 5968734
; GENERAL INFORMATION:
; APPLICANT: Aurias, Alain
; APPLICANT: Delattre, Olivier
; APPLICANT: Desmaze, Chantal
; APPLICANT: Melot, Thomas
; APPLICANT: Peter, Martine
; APPLICANT: Ploougastel, Beatrice
; APPLICANT: Thomas, Gilles
; APPLICANT: Zucman, Jessica
; TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
; TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
; TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
; TITLE OF INVENTION: TUMORS AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 South Fifteenth Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AEDIT 1.0 DOS text editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343.443B
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00494
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/06123
; FILING DATE: 20-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6121P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-343-443B-94

Query Match 31.1%; Score 30.5; DB 2; Length 11;
Best Local Similarity 46.2%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

Qy 4 PDVEKPDLPQFQV 16
||| |||
Db 1 PDL---DLDPYQI 10

RESULT 10
US-10-365-908-98
; Sequence 98, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.

; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-98

Query Match 29.6%; Score 29; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPDV 6
|||||
Db 2 QPPDV 6

RESULT 11
US-09-914-259-70
; Sequence 70, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human rhinovirus 2
US-09-914-259-70

Query Match 29.6%; Score 29; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLOP 13
|||||
Db 9 PDLOP 13

RESULT 12
US-08-144-121-12
; Sequence 12, Application US/08144121
; Patent No. 5610031
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 27-OCT-1993
; APPLICATION NUMBER: US/08/144,121
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: (MGP-0780.0) MGP-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-144-121-12

Query Match 29.6%; Score 29; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DQPPDVEKPD 10
   : ||| :
Db 1 DENPDIECAD 10

RESULT 13
US-08-735-893-12
; Sequence 12, Application US/08735893
; Patent No. 5914317
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,893
; FILING DATE: 18-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/144,121
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: (MGP-0780.1) MGP-021DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
```

```
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-735-893-12

Query Match 29.6%; Score 29; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DQPPDVEKPD 10
   : ||| :
Db 1 DENPDIECAD 10

RESULT 14
US-09-461-697-200
; Sequence 200, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-697-200

Query Match 29.6%; Score 29; DB 3; Length 18;
Best Local Similarity 54.5%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 VEKPDLPQFQV 16
   : ||| :
Db 1 MEKPKLQRHQL 11

RESULT 15
US-09-906-393A-9
; Sequence 9, Application US/09906393A
; Patent No. 6780984
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-9

Query Match 28.6%; Score 28; DB 4; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.2e+02;
```


Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PDVEKPD 10
||:|:
Db 1 PDAKPE 7

RESULT 16

US-08-190-788A-43
; Sequence 43, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David W.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-43

Query Match 28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||:|:
Db 6 QPYSVQS 12

RESULT 17

US-08-190-788A-52
; Sequence 52, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David W.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the

; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-52

Query Match 28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||:|:
Db 6 QPYSVQS 12

RESULT 18

US-08-190-788A-284
; Sequence 284, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David W.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,567
FILING DATE: 05-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.1
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 284:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 5
OTHER INFORMATION: /note= "naphthylalanine."
US-08-190-788A-284

Query Match 28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0;

QY 12 QPQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 19
US-08-383-474B-48
Sequence 48, Application US/08383474B
Patent No. 5767234
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: the IL-1 Receptor
NUMBER OF SEQUENCES: 314
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend & Townsend & Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,474B
FILING DATE: 01-FEB-1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER:
FILING DATE: 02-FEB-1994
REGISTRATION NUMBER: 36,691
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.3
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-383-474B-48

Query Match 28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0;

QY 12 QPQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 20
US-08-383-474B-57
Sequence 57, Application US/08383474B
Patent No. 5767234
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: the IL-1 Receptor
NUMBER OF SEQUENCES: 314
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend & Townsend & Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,474B
FILING DATE: 01-FEB-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.3
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-383-474B-57

Query Match 28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0;

QY 12 QPQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 21
US-08-383-474B-285
; Sequence 285, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David W.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383.474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 285:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 5
; OTHER INFORMATION: /note= "naphthylalanine."
US-08-383-474B-285

Query Match 28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 22
US-08-465-391A-43
; Sequence 43, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillippe R.
; APPLICANT: Leahy, Ellen M.

; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465.391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331viel, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-391A-43

Query Match 28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 23
US-08-465-391A-52
; Sequence 52, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California

;
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331viel, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-465-391A-52

Query Match 28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 QPQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 24
US-08-465-391A-284
; Sequence 284, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A

;
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331viel, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 284:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 5
; OTHER INFORMATION: /note="naphthylalanine."
; US-08-465-391A-284

Query Match 28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 QPQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 25
US-08-464-538B-43
; Sequence 43, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,538B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-43

Query Match 28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 12 QPFOVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 26
US-08-464-538B-52
Sequence 52, Application US/08464538B
Patent No. 5861476
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Philippe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 402
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-52

Query Match 28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 12 QPFOVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 27
US-08-464-538B-283
Sequence 283, Application US/08464538B
Patent No. 5861476
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Philippe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 402
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 283:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 5
; OTHER INFORMATION: /note= "naphthylalanine."
US-08-464-538B-283

Query Match      28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      12 QPFOVQS 18
      ||: |||
Db      6 QPYSVQS 12

RESULT 28
US-08-463-076E-87
; Sequence 87, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; - APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
; REGISTRATION NUMBER: 39,381
; REFERENCE/DOCKET NUMBER: 16528A-001850US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-076E-87

Query Match      28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      12 QPFOVQS 18
      ||: |||
Db      6 QPYSVQS 12

RESULT 29
US-08-463-076E-96
; Sequence 96, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; - APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
; REGISTRATION NUMBER: 39,381
; REFERENCE/DOCKET NUMBER: 16528A-001850US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-076E-87

Query Match      28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      12 QPFOVQS 18
      ||: |||
Db      6 QPYSVQS 12

RESULT 30
US-08-463-076E-357
; Sequence 357, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; - APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
; REGISTRATION NUMBER: 39,381
; REFERENCE/DOCKET NUMBER: 16528A-001850US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-076E-96

Query Match      28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      12 QPFOVQS 18
      ||: |||
Db      6 QPYSVQS 12
```

; REGISTRATION NUMBER: 39,381
 ; REFERENCE/DOCKET NUMBER: 16528A-001850US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 357:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 5
 ; OTHER INFORMATION: /product= "OTHER"
 ; OTHER INFORMATION: /note= "Xaa = naphthylalanine"
 US-08-463-076E-357

Query Match 28.6%; Score 28; DB 2; Length 12;
 Best Local Similarity 71.4%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFOVQS 18
 ||: |||
 Db 6 QPYSVQS 12

RESULT 31

US-09-428-082B-673
 ; Sequence 673, Application US/09428082B
 ; Patent No. 6660843
 ; GENERAL INFORMATION:
 ; APPLICANT: FEIGE, ULRICH
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: CHEETHAM, JANET C.
 ; APPLICANT: BOONE, THOMAS CHARLES
 ; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 ; FILE REFERENCE: A-527
 ; CURRENT APPLICATION NUMBER: US/09/428,082B
 ; CURRENT FILING DATE: 1999-10-22
 ; PRIOR APPLICATION NUMBER: 60/105,371
 ; PRIOR FILING DATE: 1998-10-23
 ; NUMBER OF SEQ ID NOS: 1133
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 673
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
 US-09-428-082B-673

Query Match 28.6%; Score 28; DB 4; Length 12;
 Best Local Similarity 71.4%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFOVQS 18
 ||: |||
 Db 6 QPYSVQS 12

RESULT 32

US-09-428-082B-683
 ; Sequence 683, Application US/09428082B
 ; Patent No. 6660843
 ; GENERAL INFORMATION:
 ; APPLICANT: FEIGE, ULRICH
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: CHEETHAM, JANET C.
 ; APPLICANT: BOONE, THOMAS CHARLES
 ; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 ; FILE REFERENCE: A-527

; CURRENT APPLICATION NUMBER: US/09/428,082B
 ; CURRENT FILING DATE: 1999-10-22
 ; PRIOR APPLICATION NUMBER: 60/105,371
 ; PRIOR FILING DATE: 1998-10-23
 ; NUMBER OF SEQ ID NOS: 1133
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 683
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
 US-09-428-082B-683

Query Match 28.6%; Score 28; DB 4; Length 12;
 Best Local Similarity 71.4%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFOVQS 18
 ||: |||
 Db 6 QPYSVQS 12

RESULT 33

US-09-428-082B-958
 ; Sequence 958, Application US/09428082B
 ; Patent No. 6660843
 ; GENERAL INFORMATION:
 ; APPLICANT: FEIGE, ULRICH
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: CHEETHAM, JANET C.
 ; APPLICANT: BOONE, THOMAS CHARLES
 ; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 ; FILE REFERENCE: A-527
 ; CURRENT APPLICATION NUMBER: US/09/428,082B
 ; CURRENT FILING DATE: 1999-10-22
 ; PRIOR APPLICATION NUMBER: 60/105,371
 ; PRIOR FILING DATE: 1998-10-23
 ; NUMBER OF SEQ ID NOS: 1133
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 958
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
 ; NAME/KEY: misc feature
 ; LOCATION: (5)..(5)
 ; OTHER INFORMATION: Position 5, Xaa = naphthylalanine
 US-09-428-082B-958

Query Match 28.6%; Score 28; DB 4; Length 12;
 Best Local Similarity 71.4%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFOVQS 18
 ||: |||
 Db 6 QPYSVQS 12

RESULT 34

US-08-347-335A-13
 ; Sequence 13, Application US/08347335A
 ; Patent No. 5856163
 ; GENERAL INFORMATION:
 ; APPLICANT: Hashida, Miyoko
 ; APPLICANT: Abo, Masanobu
 ; APPLICANT: Takamura, Yukiko
 ; APPLICANT: Kirk, Ole
 ; APPLICANT: Halkier, Torben
 ; APPLICANT: Pedersen, Sven
 ; APPLICANT: Patkar, Shamkant A.

;; APPLICANT: Hansen, Mogens T.
;; TITLE OF INVENTION: NOVEL ENZYMES
;; NUMBER OF SEQUENCES: 32
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 58561630 No. 5856163disk of No. 5856163th America, Inc.
;; STREET: 405 Lexington Avenue, 64th Floor
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States of America
;; ZIP: 10174-6401
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/347.335A
;; FILING DATE: 22-DEC-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lambiris, Elias J.
;; REGISTRATION NUMBER: 33,728
;; REFERENCE/DOCKET NUMBER: 3706.204-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-867-0123
;; TELEFAX: 212-878-9655
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-347-335A-13

Query Match 28.6%; Score 28; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 KPDLOPF 14
DB 3 EPDLMPY 9

RESULT 35
US-08-467-083-53
; Sequence 53, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sharkey, Richard G.
;; REGISTRATION NUMBER: 32,629
;; REFERENCE/DOCKET NUMBER: 920010.448C2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; TELEX: 3723836 SEEDANBERRY
;; INFORMATION FOR SEQ ID NO: 53:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
US-08-467-083-53

Query Match 28.6%; Score 28; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QPPDVEKPDLO 12
DB 5 QPEYVNPQDVR 15

RESULT 36
US-08-414-417B-53
; Sequence 53, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-414-417B-53

Query Match 28.6%; Score 28; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QPPDVEKPDLO 12
DB 5 QPEYVNPQDVR 15


```
RESULT 37
US-08-486-348A-53
; Sequence 53, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-486-348A-53
;
; Query Match 28.6%; Score 28; DB 2; Length 15;
; Best Local Similarity 45.5%; Pred. No. 4.6e+02;
; Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
;
Qy 2 QPPDVEKPDQ 12
|||:|:|:
Db 5 QPEYVNPQDVR 15

RESULT 38
US-08-486-348A-53
; Sequence 53, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-486-348A-53
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; Query Match 28.6%; Score 28; DB 2; Length 15;
; Best Local Similarity 45.5%; Pred. No. 4.6e+02;
; Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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Db 5 QPEYVNPQDVR 15

RESULT 39
US-08-466-680B-53
; Sequence 53, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466.680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-466-680B-53
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; Query Match 28.6%; Score 28; DB 3; Length 15;
; Best Local Similarity 45.5%; Pred. No. 4.6e+02;
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Db 5 QPEYVNPQDVR 15

RESULT 40
US-08-466-680B-53
; Sequence 53, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466.680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-466-680B-53
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; Query Match 28.6%; Score 28; DB 3; Length 15;
; Best Local Similarity 45.5%; Pred. No. 4.6e+02;
; Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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Db 5 QPEYVNPQDVR 15
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Db 5 QPEYVNPQDVR 15

RESULT 40
US-09-354-533-53
; Sequence 53, Application US/09354533
; Patent No. 6664370
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,533
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-354-533-53

Query Match 28.6%; Score 28; DB 4; Length 15;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Db 5 QPEYVNPQDVR 15

Search completed: June 7, 2005, 23:23:12
Job time : 25.5455 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 23:00:52 ; Search time 81 Seconds
(without alignments)
85.185 Million cell updates/sec

Title: US-10-691-157-3

Perfect score: 98

Sequence: 1 DQPDVKEPDLQPFQVQS 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	98	100.0	18	16	US-10-691-157-3
3	98	100.0	18	17	US-10-691-330-3
4	41	41.8	15	14	US-10-014-340-759
5	39	39.8	16	14	US-10-225-567A-1755
6	35	35.7	12	14	US-10-014-340-526
7	33	33.7	18	16	US-10-474-955-56
8	33	33.7	18	15	US-10-474-955-61
9	33	33.7	18	16	US-10-474-955-65
10	32	32.7	9	14	US-10-350-258-6
11	32	32.7	16	17	US-10-901-601-6
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Sequence 3, Appli					
Sequence 759, App					
Sequence 1755, Ap					
Sequence 526, App					
Sequence 56, Appl					
Sequence 61, Appl					
Sequence 65, Appl					
Sequence 6, Appli					

12	32.7	18	14	US-10-161-791-305	Sequence 305, App
13	31.6	10	10	US-09-572-404B-3283	Sequence 3283, Ap
14	31.6	11	15	US-10-601-837-34	Sequence 34, Appl
15	30.6	11	14	US-10-022-066-144	Sequence 144, App
16	30.6	11	14	US-10-022-066-374	Sequence 374, App
17	30.6	15	15	US-10-149-138-3845	Sequence 3845, Ap
18	30.6	15	16	US-10-149-138-3845	Sequence 3845, Ap
19	29.6	8	9	US-09-891-823-98	Sequence 98, Appl
20	29.6	8	14	US-10-365-908-98	Sequence 98, Appl
21	29.6	8	16	US-10-871-138-98	Sequence 98, Appl
22	29.6	9	14	US-10-033-662-36	Sequence 36, Appl
23	29.6	10	10	US-09-572-404B-3027	Sequence 3027, Ap
24	29.6	13	10	US-09-992-665-47	Sequence 47, Appl
25	29.6	13	16	US-10-468-496-1356	Sequence 1356, Ap
26	29.6	13	16	US-10-468-496-1361	Sequence 1361, Ap
27	29.6	15	14	US-10-080-608A-70	Sequence 70, Appl
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29	29.6	15	15	US-10-371-067-1	Sequence 1, Appli
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33	29.6	18	9	US-09-922-261-200	Sequence 200, App
34	28.6	9	15	US-10-107-532-25	Sequence 25, Appl
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38	28.6	9	15	US-10-107-532-3286	Sequence 3286, Ap
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40	28.6	10	15	US-10-107-532-284	Sequence 284, App
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42	28.6	10	15	US-10-107-532-1418	Sequence 1418, Ap
43	28.6	10	15	US-10-107-532-1923	Sequence 1923, Ap
44	28.6	10	15	US-10-107-532-2499	Sequence 2499, Ap
45	28.6	10	15	US-10-107-532-3566	Sequence 3566, Ap
46	28.6	10	15	US-10-107-532-4968	Sequence 4968, Ap
47	28.6	10	15	US-10-107-532-5105	Sequence 5105, Ap
48	28.6	10	17	US-10-734-049A-64	Sequence 64, Appl
49	28.6	11	10	US-09-906-393A-9	Sequence 9, Appli
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58	28.6	12	15	US-10-651-723-958	Sequence 958, App
59	28.6	12	15	US-10-645-761-673	Sequence 673, App
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71	28.6	15	9	US-09-354-533-53	Sequence 53, Appl
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73	28.6	15	15	US-10-647-005-53	Sequence 53, Appl
74	28.6	16	15	US-10-609-217-786	Sequence 786, App
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80	28.6	17	14	US-10-161-791-338	Sequence 338, App
81	28.6	17	15	US-10-609-217-785	Sequence 785, App
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83	28.6	17	15	US-10-609-217-847	Sequence 847, App
84	28.6	17	15	US-10-609-217-848	Sequence 848, App

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ALIGNMENTS

RESULT 1
US-10-281-652-3
; Sequence 3, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-3

Query Match 100.0%; Score 98; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DQPPDVEKPDLPQFQVQS 18

RESULT 2
US-10-691-157-3
; Sequence 3, Application US/10691157
; Publication No. US20040266681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265.00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; CURRENT FILING DATE: 2003-10-22

Query Match 100.0%; Score 98; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
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; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-157-3

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Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 3, Application US/10691330
; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: Boldogh, Istvan
; APPLICANT: Stanton, G. John
; APPLICANT: Georgiades, Jerzy A.
; APPLICANT: Hughes, Thomas K., Jr.
; APPLICANT: Kruzel, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265.00390101
; CURRENT APPLICATION NUMBER: US/10/691,330
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 60/420,369
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US-10-691-330-3

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Best Local Similarity 100.0%; Pred. No. 4.1e-07;
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US-10-014-340-759
; Sequence 759, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340

; CURRENT FILING DATE: 2001-12-10
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; SEQ ID NO 759
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; ORGANISM: Homo sapiens
US-10-014-340-759

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RESULT 5
US-10-225-567A-1755
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; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
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; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1755

Query Match 39.8%; Score 39; DB 14; Length 16;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QPDVEKPDLPQ 13
:|:|:|
Db 5 RPDIRKDSRP 16

RESULT 6
US-10-014-340-526
; Sequence 526, Application US/10014340
; Publication No. US2003006441A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 526
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-526

Query Match 35.7%; Score 35; DB 14; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLPQ 12
|||:|
Db 3 PPSAEYDLP 12

RESULT 7
US-10-474-955-56
; Sequence 56, Application US/10474955
; Publication No. US20040241161A1
; GENERAL INFORMATION:
; APPLICANT: Drifhout, Jan W.
; APPLICANT: Koning, Frits
; APPLICANT: McAdam, Stephan N.
; APPLICANT: Ludwig, Solliid Magne
; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
; FILE REFERENCE: 2799/71244-PCT-US
; CURRENT APPLICATION NUMBER: US/10/474,955
; CURRENT FILING DATE: 2003-10-13
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide sequence in pool 51
; NAME/KEY: MISC FEATURE
; LOCATION: (7)..(8)
; OTHER INFORMATION: "Y" on position 7 is P/S
US-10-474-955-56

Query Match 33.7%; Score 33; DB 16; Length 18;
Best Local Similarity 46.7%; Pred. No. 6.4e+02;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLPQFFVQ 17
:|:|:|
Db 2 PPQPYFPQPPPSQ 16

RESULT 8
US-10-474-955-61
; Sequence 61, Application US/10474955
; Publication No. US20040241161A1
; GENERAL INFORMATION:
; APPLICANT: Drifhout, Jan W.
; APPLICANT: Koning, Frits
; APPLICANT: McAdam, Stephan N.
; APPLICANT: Ludwig, Solliid Magne
; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
; FILE REFERENCE: 2799/71244-PCT-US
; CURRENT APPLICATION NUMBER: US/10/474,955
; CURRENT FILING DATE: 2003-10-13
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide sequence in pool 54
; NAME/KEY: MISC FEATURE
; LOCATION: (7)..(8)
; OTHER INFORMATION: "Y" on position 7 is P/S
US-10-474-955-61

Query Match 33.7%; Score 33; DB 16; Length 18;
Best Local Similarity 46.7%; Pred. No. 6.4e+02;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 PPQVEKPDLPQFQV 17
|||
DB 2 PPQPYQPQPPPSQ 16

RESULT 9

US-10-474-955-65
; Sequence 65, Application US/10474955
; Publication No. US20040241161A1
; GENERAL INFORMATION:
; APPLICANT: Drifhout, Jan W.
; APPLICANT: Koning, Frits
; APPLICANT: McAdam, Stephan N.
; APPLICANT: Ludwig, Solid Magne
; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS A
; FILE REFERENCE: DQ BINDING PROLAMINE-DERIVED PEPTIDES
; CURRENT APPLICATION NUMBER: US/10/474,955
; CURRENT FILING DATE: 2003-10-13
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 65
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide sequence in pool 57
; NAME/KEY: MISC FEATURE
; LOCATION: (7)-(8)
; OTHER INFORMATION: "Y" on position 7 is P/S
US-10-474-955-65

Query Match 33.7%; Score 33; DB 16; Length 18;
Best Local Similarity 46.7%; Pred. No. 6.4e+02;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 PPQVEKPDLPQFQV 17
|||
DB 2 PPQPYQPQPPPSQ 16

RESULT 10

US-10-350-258-6
; Sequence 6, Application US/10350258
; Publication No. US20030139345A1
; GENERAL INFORMATION:
; APPLICANT: MATTHIAS RATH
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND METHODS FOR TREATING CANCER INVASION AND M
; FILE REFERENCE: 119577/23
; CURRENT APPLICATION NUMBER: US/10/350,258
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/351,317
; PRIOR FILING DATE: January 23, 2002
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-350-258-6

Query Match 32.7%; Score 32; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPQVEKPD 10
|||
DB 2 PPQVQVVD 9

RESULT 11

US-10-901-601-6
; Sequence 6, Application US/10901601
; Publication No. US20050095253A1
; GENERAL INFORMATION:
; APPLICANT: Cancer Research Campaign Technology Limited
; APPLICANT: Durrant, Linda G
; APPLICANT: Spendlove, Ian
; TITLE OF INVENTION: Tumour Associated Antigen 791Tgp72
; FILE REFERENCE: SJK/B95758875
; CURRENT APPLICATION NUMBER: US/10/901,601
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: PCT/GB99/00582
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: GB 9804065.2
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-901-601-6

Query Match 32.7%; Score 32; DB 17; Length 16;
Best Local Similarity 63.6%; Pred. No. 7.8e+02;
Matches .7; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 3 PPQVEKPDLPQ 13
|||
DB 5 PPQV--PNAQP 13

RESULT 12

US-10-161-791-305
; Sequence 305, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-305

Query Match 32.7%; Score 32; DB 14; Length 18;
Best Local Similarity 43.8%; Pred. No. 8.9e+02;
Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLPFFQVQ 17
Db 3 QPPYPPPPYQPIYQ 18

RESULT 13
US-09-572-404B-3283
; Sequence 3283, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3283
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 291-300 and may interact with
; OTHER INFORMATION: Sequence 3284 in this patent.
US-09-572-404B-3283

Query Match 31.6%; Score 31; DB 10; Length 10;
Best Local Similarity 71.4%; Pred. No. 6.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPDVEKP 9
Db 3 PPTVQKP 9

RESULT 14
US-10-601-837-34
; Sequence 34, Application US/10601837
; Publication No. US20040053309A1
; GENERAL INFORMATION:
; APPLICANT: Holt, Gordon D
; APPLICANT: Kelly, Michael D
; APPLICANT: Kennedy, Sandra J
; APPLICANT: Moyeses, Christopher
; TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment of Kidney
; FILE REFERENCE: Response
; CURRENT APPLICATION NUMBER: US/10/601,837
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: PCT/GB01/05777
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: US 60/260392
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 34
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Ratus No. US20040053309A1vegicus
US-10-601-837-34

Query Match 31.6%; Score 31; DB 15; Length 11;
Best Local Similarity 55.6%; Pred. No. 7.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 EKPDLOPQ 15
Db 2 DNPMLPPQ 10

RESULT 15
US-10-022-066-144
; Sequence 144, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLJMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 144
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: MOD RES
; LOCATION: (1)_
; OTHER INFORMATION: Unknown amino acid
; NAME/KEY: MOD RES
; LOCATION: (3)_
; OTHER INFORMATION: Unknown amino acid
US-10-022-066-144

Query Match 30.6%; Score 30; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQPPDVE 7
Db 4 DPPEDMZ 10

RESULT 16
US-10-022-066-374
; Sequence 374, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLJMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
US-10-022-066-374

;; PRIOR FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: 09/465,321
;; PRIOR FILING DATE: 1999-12-17
;; PRIOR APPLICATION NUMBER: 09/974,366
;; PRIOR FILING DATE: 2001-10-10
;; NUMBER OF SEQ ID NOS: 638
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 374
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: peptide
;; FEATURE:
;; NAME/KEY: MOD_RES
;; LOCATION: (1)
;; OTHER INFORMATION: Unknown amino acid
;; FEATURE:
;; NAME/KEY: MOD_RES
;; LOCATION: (3)
;; OTHER INFORMATION: Unknown amino acid
US-10-022-066-374

Query Match 30.6%; Score 30; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DPPDVE 7
| | | | |
Db 4 DPPDMZ 10

RESULT 17
US-10-149-138-3845
;; Sequence 3845, Application US/10149138
;; Publication No. US20040018971A1
;; GENERAL INFORMATION:
;; APPLICANT: Fikes, John
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Celis, Esteban
;; APPLICANT: Keogh, Elissa
;; TITLE OF INVENTION: Inducing Cellular Immune Responses to
;; FILE REFERENCE: 2060.0140001
;; CURRENT APPLICATION NUMBER: US/10/149,138
;; PRIOR FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: PCT/US00/33591
;; PRIOR FILING DATE: 2000-12-11
;; PRIOR APPLICATION NUMBER: US 09/458,299
;; PRIOR FILING DATE: 1999-12-11
;; NUMBER OF SEQ ID NOS: 4641
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3845
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3845

Query Match 30.6%; Score 30; DB 15; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDEVKPDLPQ 13
| | | | |
Db 1 PEYVNPQDVRP 11

RESULT 18
US-10-149-138-3845
;; Sequence 3845, Application US/10149138
;; Publication No. US20040121946A9
;; GENERAL INFORMATION:
;; APPLICANT: Fikes, John
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Celis, Esteban
;; APPLICANT: Keogh, Elissa
;; TITLE OF INVENTION: Inducing Cellular Immune Responses to
;; FILE REFERENCE: 2060.0140001
;; CURRENT APPLICATION NUMBER: US/10/149,138
;; CURRENT FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: PCT/US00/33591
;; PRIOR FILING DATE: 2000-12-11
;; PRIOR APPLICATION NUMBER: US 09/458,299
;; PRIOR FILING DATE: 1999-12-11
;; NUMBER OF SEQ ID NOS: 4641
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3845
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3845

Query Match 30.6%; Score 30; DB 16; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDEVKPDLPQ 13
| | | | |
Db 1 PEYVNPQDVRP 11

RESULT 19
US-09-891-823-98
;; Sequence 98, Application US/09891823
;; Publication No. US20020110566A1
;; GENERAL INFORMATION:
;; APPLICANT: Neefe, John R.
;; APPLICANT: Boux, Leslie J.
;; APPLICANT: Winnett, Mark T.
;; APPLICANT: Goldstone, Stephen E.
;; APPLICANT: Siegel, Marvin
;; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
;; FILE REFERENCE: 12071-003001
;; CURRENT APPLICATION NUMBER: US/09/891,823
;; CURRENT FILING DATE: 2001-10-19
;; PRIOR APPLICATION NUMBER: US 60/214,202
;; PRIOR FILING DATE: 2000-06-26
;; NUMBER OF SEQ ID NOS: 140
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 98
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Human papilloma virus
US-09-891-823-98

Query Match 29.6%; Score 29; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPDV 6
| | | | |
Db 2 QPPDV 6

RESULT 20
US-10-365-908-98
; Sequence 98, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-98

Query Match 29.6%; Score 29; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPDV 6
| | | | |
Db 2 QPPDV 6

RESULT 21
US-10-871-138-98
; Sequence 98, Application US/10871138
; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-98

Query Match 29.6%; Score 29; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPDV 6
| | | | |
Db 2 QPPDV 6

RESULT 22
US-10-033-662-36
; Sequence 36, Application US/10033662

; Publication No. US20030092197A1
; GENERAL INFORMATION:
; APPLICANT: Herman, et al.
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Cancer
; FILE REFERENCE: 9195-081
; CURRENT APPLICATION NUMBER: US/10/033,662
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-662-36

Query Match 29.6%; Score 29; DB 14; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KPDLQP 13
| | | | |
Db 1 KPDLSP 6

RESULT 23
US-09-572-404B-3027
; Sequence 3027, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3027
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in GUCY2D OR GUC2D OR RETGC1 OR RETGC OR GUC1A4
; OTHER INFORMATION: CORD6 at 1069-1078 and may interact with Sequence 3028 in this pa
US-09-572-404B-3027

Query Match 29.6%; Score 29; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13
| | | | |
Db 2 PDLQP 6

RESULT 24
US-09-992-665-47
; Sequence 47, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 13
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-47

Query Match 29.6%; Score 29; DB 10; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLPQ 13
| | | | |
Db 1 QPPGMSPPPPP 12

RESULT 25

US-10-468-496-1356
; Sequence 1356, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita

; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; FILE REFERENCE: MER-117

; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1356
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope

US-10-468-496-1356

Query Match 29.6%; Score 29; DB 16; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQPPDV 6
| | | | |
Db 7 DPPPDP 12

RESULT 26

US-10-468-496-1361
; Sequence 1361, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita

; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED

; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1361
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope

US-10-468-496-1361

Query Match 29.6%; Score 29; DB 16; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQPPDV 6
| | | | |
Db 6 DPPPDP 11

RESULT 27

US-10-080-608A-70
; Sequence 70, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:

; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human rhinovirus 2

US-10-080-608A-70

Query Match 29.6%; Score 29; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13
| | | | |
Db 9 PDLQP 13

RESULT 28

US-10-370-685-159
; Sequence 159, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:

; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF.P-004

; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 159
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human rhinovirus 2
US-10-370-685-159

Query Match 29.6%; Score 29; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLPQ 13
| | | | |
Db 9 PDLPQ 13

RESULT 29
US-10-371-067-1
; Sequence 1, Application US/10371067
; Publication No. US20040018587A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Williams, Mark K
; APPLICANT: Goldberg, Edward B
; TITLE OF INVENTION: Nanostructures containing antibody assembly subunits
; FILE REFERENCE: NANF-P-003
; CURRENT APPLICATION NUMBER: US/10/371,067
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/136,225
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 09/236,949
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/542,003
; PRIOR FILING DATE: 1995-10-12
; PRIOR APPLICATION NUMBER: 08/322,760
; PRIOR FILING DATE: 1994-10-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: (Antibody 8F5) Complexed With Peptide From Human Rhinovirus
; OTHER INFORMATION: (Serotype 2) Viral Capsid Protein Vp2 (Residues 156 -170)
US-10-371-067-1

Query Match 29.6%; Score 29; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLPQ 13
| | | | |
Db 9 PDLPQ 13

RESULT 30
US-10-225-567A-1370
; Sequence 1370, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1370
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1370

Query Match 29.6%; Score 29; DB 14; Length 17;
Best Local Similarity 41.7%; Pred. No. 2.2e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 7 EKPDLPQFQVOS 18
: | | | | : |
Db 6 KNPDLPQAIRAS 17

RESULT 31
US-10-443-349-12
; Sequence 12, Application US/10443349
; Publication No. US20040023856A1
; GENERAL INFORMATION:
; APPLICANT: Burgesson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; FILE REFERENCE: 10287/021003
; CURRENT APPLICATION NUMBER: US/10/443,349
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/161,872
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 08/735,893
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-443-349-12

Query Match 29.6%; Score 29; DB 15; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DQPPDVKEPD 10
: | | | : |
Db 1 DENPDIECAD 10

RESULT 32
US-10-841-139-12
; Sequence 12, Application US/10841139
; Publication No. US20040208881A1
; GENERAL INFORMATION:
; APPLICANT: Burgesson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; FILE REFERENCE: 10287/021003
; CURRENT APPLICATION NUMBER: US/10/841,139
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US/10/443,349
; PRIOR FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/161,872
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 08/735,893
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-841-139-12

Query Match 29.6%; Score 29; DB 16; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DOPDVEKPD 10
| : ||| : |
DB 1 DENPDIECAD 10

RESULT 33
US-09-922-261-200
; Sequence 200, Application US/09922261
; Patent No. US20020111471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR FILING DATE: 1999-12-14
; PRIOR FILING DATE: US/09/461,697
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-261-200

Query Match 29.6%; Score 29; DB 9; Length 18;
Best Local Similarity 54.5%; Pred. No. 2.4e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 VEKPDLPQPFQV 16
: ||| : ||| :
DB 1 MEKPKLQRHQL 11

RESULT 34
US-10-107-532-25
; Sequence 25, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Paris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112

; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-25

Query Match 28.6%; Score 28; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QPPDVEKP 9
|| : |||
DB 1 QPEPLEKP 8

RESULT 35
US-10-107-532-652
; Sequence 652, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Paris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 652
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-652

Query Match 28.6%; Score 28; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QPPDVEKP 9
|| : |||
DB 2 QPEPLEKP 9

RESULT 36
US-10-107-532-2214
; Sequence 2214, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Paris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.

; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE REFERENCE: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2214
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-2214

Query Match 28.6%; Score 28; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 QPDPVEKP 9
||| :|||
Db 1 QPEPLEKP 8

RESULT 37
US-10-107-532-2776
; Sequence 2776, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Paris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE REFERENCE: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2776
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-2776

Query Match 28.6%; Score 28; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 QPDPVEKP 9
||| :|||
Db 1 QPEPLEKP 8

RESULT 38
US-10-107-532-3286
; Sequence 3286, Application US/10107532

; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Paris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE REFERENCE: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3286
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-3286

Query Match 28.6%; Score 28; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 QPDPVEKP 9
||| :|||
Db 1 QPEPLEKP 8

RESULT 39
US-10-107-532-3991
; Sequence 3991, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Paris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE REFERENCE: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3991
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-3991

Query Match 28.6%; Score 28; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
|| :|||
Db 1 QPEPLEKP 8

```

RESULT 40
US-10-107-532-284
; Sequence 284, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Paris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE REFERENCE: Entitled 158P3D2 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-284

```

Query Match 28.6%; Score 28; DB 15; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.8e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
|| :|||
Db 1 QPEPLEKP 8

Search completed: June 7, 2005, 23:31:34
 Job time : 83 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:56:36 ; Search time 16.6909 Seconds
(without alignments)
103.763 Million cell updates/sec

Title: US-10-691-157-3

Perfect score: 98

Sequence: 1 DQPPDVKPDLPQFQVQS 18

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	30.6	10	2	urease (EC 3.5.1.5)
2	29	29.6	15	2	protein kinase (EC 2.7.1.1)
3	29	29.6	15	2	plastoquinol-plast
4	28.5	29.1	17	2	fatty acid ethyl e
5	27	27.6	9	2	tetrameric protein
6	25.5	26.0	17	4	hypothetical EWSR1
7	25	25.5	15	2	apolipoprotein A-I
8	24	24.5	10	2	alpha-gliadin 6Ha
9	24	24.5	14	2	bradykinin-like pe
10	24	24.5	18	2	beta-Gliadin 13 -
11	24	24.5	18	2	Na+/K+-exchanging
12	23	23.5	9	2	cytochrome-c oxida
13	23	23.5	11	2	phyllotoxin - Rohd
14	23	23.5	12	2	vepakinin M - hor
15	23	23.5	12	2	vepakinin X - hor
16	23	23.5	13	2	Ig lambda chain V-
17	23	23.5	15	2	protein QF200051 -
18	23	23.5	18	2	enkephalin-degradi
19	22	22.4	12	2	tachykinin - Afric
20	22	22.4	16	2	insulin-like growt
21	21	21.4	11	2	ribosomal protein
22	21	21.4	12	2	tachykinin - Afric
23	21	21.4	15	2	dystrophin-associa
24	21	21.4	16	2	leukocyte elastase
25	21	21.4	17	2	caldesmon - rabbit
26	21	21.4	18	2	microtubule-associ
27	20	20.4	8	2	gene thiolase prote
28	20	20.4	9	2	bradykinin - horn
29	20	20.4	9	2	ATPase R1 subunit

30	20	20.4	9	2	A43065	hydroxyproline-3-b
31	20	20.4	9	2	A61363	bradykinin - commo
32	20	20.4	10	2	A60476	S-layer protein -
33	20	20.4	11	2	S13279	Ile-Ser-bradykinin
34	20	20.4	11	2	YHHU	morphogenetic neur
35	20	20.4	11	2	YHBO	morphogenetic neur
36	20	20.4	11	2	YHJFYH	morphogenetic neur
37	20	20.4	11	2	YHXAE	morphogenetic neur
38	20	20.4	11	2	YHRT	morphogenetic neur
39	20	20.4	12	2	C64030	hypothetical prote
40	20	20.4	13	2	S15755	actin 7 - soybean
41	20	20.4	13	2	A61361	bradykinin-like pe
42	20	20.4	15	2	A49155	vasotocin-associa
43	20	20.4	15	2	I49407	placental calcium-
44	20	20.4	15	2	B39109	hypothetical 1.5K
45	20	20.4	15	2	F57789	galbladder stone
46	20	20.4	17	1	A61339	vesiculakinin 1 - e
47	20	20.4	17	2	B61334	trypsin (EC 3.4.21
48	20	20.4	17	2	S15754	actin 6 - soybean
49	20	20.4	17	2	S05033	photosystem II pro
50	20	20.4	17	2	S59481	hydroxyproline-ric
51	20	20.4	18	2	S29166	guinaldine oxidore
52	20	20.4	18	2	A56798	dermatan sulfate p
53	19.5	19.9	11	2	C37196	bradykinin-potenti
54	19.5	19.9	11	2	D37196	bradykinin-potenti
55	19.5	19.9	15	4	I38032	hypothetical MNI/T
56	19	19.4	7	2	S71299	ICL2 protein - Par
57	19	19.4	7	2	PT0283	Ig heavy chain CRD
58	19	19.4	8	2	I48935	apolipoprotein A-I
59	19	19.4	9	2	C58502	kidney and bladder
60	19	19.4	9	2	A26744	bradykinin-like pe
61	19	19.4	9	2	A61057	Thr-6 bradykinin -
62	19	19.4	9	2	A60579	bradykinin-like pe
63	19	19.4	9	2	A61358	bradykinin-like pe
64	19	19.4	10	2	A32543	cardioexcitatory n
65	19	19.4	11	2	D45900	complement C3b rec
66	19	19.4	11	2	B26744	megascollakinin -
67	19	19.4	12	2	A46794	hypothetical prote
68	19	19.4	12	2	S27024	Na+/K+-exchanging
69	19	19.4	12	2	S27023	Na+/K+-exchanging
70	19	19.4	12	2	S07206	kaesin - Senegal
71	19	19.4	13	2	T08533	hypothetical prote
72	19	19.4	13	2	S22995	hypothetical prote
73	19	19.4	13	2	A33660	osteoclast functio
74	19	19.4	13	2	S21152	tryptophyllin-rela
75	19	19.4	15	2	PS0185	27K protein A 3.4/
76	19	19.4	15	2	PS0221	gastrin-releasing
77	19	19.4	15	2	PC1313	small granule S6 c
78	19	19.4	16	2	D49655	T-cell-receptor be
79	19	19.4	16	2	PH0759	T-cell receptor be
80	19	19.4	17	2	S50901	chlorophyll a/b-bi
81	19	19.4	17	2	S78421	ribosomal protein
82	19	19.4	17	2	S10786	enamelin, 26K - bo
83	18.5	18.9	11	1	XASNSA	bradykinin-potenti
84	18.5	18.9	15	2	S29207	avenin gamma-4 - o
85	18.5	18.9	15	2	PM0004	chlorophyll a/b-bi
86	18	18.4	6	2	S78764	ribosomal protein
87	18	18.4	7	2	I48086	DNA topoisomerase
88	18	18.4	8	2	PT0030	inulinase (EC 3.2.
89	18	18.4	9	2	B46250	alpha-adaptin - bo
90	18	18.4	9	2	A61620	locustamytotropin I
91	18	18.4	10	2	A61007	hementin (EC 3.4.-
92	18	18.4	11	2	S21127	precocorrin methyltr
93	18	18.4	11	2	PS0257	31K protein 3208 -
94	18	18.4	11	2	D56979	collagen alpha 1(I)
95	18	18.4	11	2	FQ0231	beta-glucosidase (
96	18	18.4	12	2	S36899	ribosomal protein
97	18	18.4	12	2	S51737	T-cell receptor be
98	18	18.4	12	2	B44787	calliMIRamide 1 -
99	18	18.4	12	2	S71380	lebetin 1 isoform
100	18	18.4	13	2	PT0331	Ig heavy chain CRD

ALIGNMENTS

RESULT 1
C35389 urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)
C:Species: Morganella morganii
C:Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004
C:Accession: C35389
R:Hu, L.F.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A:Title: Morganella morganii urease: purification, characterization, and isolation of gene
A:Reference number: A35389; MUID:90264298; PMID:2345135
A:Accession: C35389
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <HUA>
A:Cross-references: UNIPROT:P17339
C:Keywords: hydrolase

Query Match 30.6%; Score 30; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDVEK 8
|||
Db 5 PPEVK 10

RESULT 2
S20410 protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)
N:Alternate names: LHCI protein kinase
C:Species: chloroplast Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: S20410
R:Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.
FEBS Lett. 298, 33-35, 1992
A:Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cytochrome b6
A:Reference number: S20410; MUID:92183823; PMID:1544419
A:Accession: S20410
A:Molecule type: protein
A:Residues: 1-15 <GAL>
A:Cross-references: UNIPROT:Q9T2K8
C:Genetics:
C:Genome: chloroplast
C:Function:
A:Description: is responsible for the regulation of energy distribution between photosynthesis and
A:Note: does not exhibit redox-controlled activation
C:Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphotransferase

Query Match 29.6%; Score 29; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PDVEKDL 11
|||||
Db 5 PDVEKSTL 12

RESULT 3
PA0041 plastocyanin reductase (EC 1.10.99.1) - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: PA0041
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Taugita, A.
submitted to JPIB, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
A:Reference number: PA0001
A:Accession: PA0041
A:Molecule type: protein
A:Residues: 1-15 <KAM>

A:Cross-references: UNIPROT:Q9ZR03; UNIPROT:Q94BI4; UNIPROT:Q9FYB6
A:Experimental source: leaf
C:Keywords: oxidoreductase

Query Match 29.6%; Score 29; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DQPPDVEK 8
|:|:|
Db 7 DRVPMEX 14

RESULT 4

A42920 fatty acid ethyl ester synthase-II - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42920
R:Bora, P.S.; Wu, X.; Spilburg, C.A.; Lange, L.G.
J. Biol. Chem. 267, 13217-13221, 1992
A:Title: Purification and characterization of fatty acid ethyl ester synthase-II from human liver
A:Reference number: A42920; MUID:92317032; PMID:1618826
A:Accession: A42920
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-17 <BOR>
A:Cross-references: UNIPROT:Q9UDD6
A:Experimental source: myocardium
A:Note: sequence extracted from NCBI backbone (NCBI:P107742)

Query Match 29.1%; Score 28.5; DB 2; Length 17;
Best Local Similarity 46.2%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 1 DQPPDVEKPDLP 13
:|:|:|
Db 1 EDPPD---PDTP 10

RESULT 5

S66419 tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C:Accession: S66419
R:Kuwabara, T.
FEBS Lett. 371, 195-198, 1995
A:Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of spinach
A:Reference number: S66419; MUID:95402209; PMID:7672127
A:Accession: S66419
A:Molecule type: protein
A:Residues: 1-9 <KUW>
A:Cross-references: UNIPROT:Q9T2K8; UNIPROT:Q41388

Query Match 27.6%; Score 27; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDVEK 8
|:|:|
Db 5 PDVEK 9

RESULT 6

I51887 hypothetical EWSR1/FLI1 mutant fusion protein, type 1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C:Accession: I51887
R:Downing, J.R.; Head, D.R.; Parham, D.M.; Douglass, E.C.; Hulshof, M.G.; Link, M.P.; McAninch, J.
Am. J. Pathol. 143, 1294-1300, 1993
A:Title: Detection of the (11;22)(q24;q12) translocation of Ewing's sarcoma and peripheral neuroepithelioma

A:Reference number: I51887; MUID:94056652; PMID:8238248

A:Accession: I51887

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-17 <DOM>

A:Cross-references: GB:S66911; NID:g440935; PIDN:AAB28655.1; PID:g440936

C:Comment: This sequence is the chimeric product of a translocation mutation.

C:Genetics:

A:Gene: EWSR1/FLI1; EWS/FLI-1

A:Map position: 22q12/11q24

C:Keywords: fusion protein

Query Match 26.0%; Score 25.5; DB 4; Length 17;

Best Local Similarity 46.2%; Pred. No. 7.9e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 1 DQPPDVEKPDLPQ 13

| | | |

Db 7 DEGPDL---DLDP 16

RESULT 7

A60221

apolipoprotein A-I - common carp (fragment)

C:Species: Cyprinus carpio (common carp)

C>Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004

C:Accession: A60221

R:Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.

J. Neurochem. 55, 1237-1243, 1990

A:Title: Fish apolipoprotein-A-I has heparin binding activity: implication for nerve reg

A:Reference number: A60221; MUID:90376100; PMID:2118944

A:Accession: A60221

A:Molecule type: protein

A:Residues: 1-15 <HAR>

A:Cross-references: UNIPROT:Q7LZ45

A:Note: protein from plasma and from optic nerve yielded the same sequence

C:Keywords: lipid binding; lipoprotein

Query Match 25.5%; Score 25; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPP 4

| | | |

Db 1 DQPP 4

RESULT 8

B61218

alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)

C:Species: Haynaldia villosa, Dasypyrum villosum

C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004

C:Accession: B61218

R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.

Biochem. Genet. 29, 207-211, 1991

A:Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynald

A:Reference number: A61218; MUID:91315394; PMID:1859356

A:Accession: B61218

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <SHE>

A:Cross-references: UNIPROT:Q7M1F6

C:Keywords: seed; storage protein

Query Match 24.5%; Score 24; DB 2; Length 10;

Best Local Similarity 62.5%; Pred. No. 7.4e+02;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13

| | | | |

Db 3 VPVPQLQP 10

Query Match

24.5%; Score 24; DB 2; Length 18;

RESULT 9

A61362

bradykinin-like peptide III - Japanese pond frog

C:Species: Rana nigromaculata (Japanese pond frog)

C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C:Accession: A61362

R:Nakajima, T.

Chem. Pharm. Bull. 16, 2088-2089, 1968

A:Title: On the third active peptide on smooth muscle in the skin of Rana nigromaculata

A:Reference number: A61362; MUID:69117202; PMID:5751736

A:Accession: A61362

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <NAK>

A:Cross-references: UNIPROT:Q7LZ53

C:Superfamily: unassigned animal peptides

C:Keywords: skin

Query Match 24.5%; Score 24; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16

| | | | |

Db 3 PGFSPPRV 10

RESULT 10

PN0149

beta-Gliadine 13 - Aegilops longissima (fragment)

C:Species: Aegilops longissima

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: PN0149

R:Odintsova, T.I.; Egorov, T.A.

Biokhimiia 55, 509-516, 1990

A:Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of

A:Reference number: PN0146; MUID:90283493; PMID:2354218

A:Accession: PN0149

A:Molecule type: protein

A:Residues: 1-18 <ODI>

A:Cross-references: UNIPROT:Q7M1Z6

A:Experimental source: strain K-202

C:Superfamily: gliadin

Query Match 24.5%; Score 24; DB 2; Length 18;

Best Local Similarity 62.5%; Pred. No. 1.4e+03;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13

| | | | |

Db 3 VPVPQLQP 10

RESULT 11

A54195

Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)

C:Species: Squalus acanthias (spiny dogfish)

C>Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A54195

R:Esman, M.; Karlisch, S.J.; Sottrup-Jensen, L.; Marsh, D.

Biochemistry 33, 8044-8050, 1994

A:Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-AT

A:Reference number: A54195; MUID:94297020; PMID:8025109

A:Accession: A54195

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <ESM>

A:Cross-references: UNIPROT:Q9PSP6

A:Experimental source: rectal gland

A:Note: sequence extracted from NCBI backbone (NCBIP:149363)

C:Keywords: hydrolase

Chem. Pharm. Bull. 24, 2896-2897, 1976

A;Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the ves
A;Reference number: A61360; MUID:77114342; PMID:1017116

A;Accession: A61360

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <KIS>

A;Cross-references: UNIPROT:Q7M3T3

C;Superfamily: unassigned animal peptides

C;Keywords: hydroxyproline; venom

F;4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 23.5%; Score 23; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16
| | | | |
Db 4 PGFSPFRI 11

RESULT 15

A61359

vespakinin x - hornet (Vespa xanthoptera)

C;Species: Vespa xanthoptera

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C;Accession: A61359

R;Yasuhara, T.; Yoshida, H.; Nakajima, T.

Chem. Pharm. Bull. 25, 936-941, 1977

A;Title: Chemical investigation of the hornet (Vespa xanthoptera Cameron) venom. The str
A;Reference number: A61359; MUID:87187853; PMID:264186

A;Accession: A61359

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <YAS>

A;Cross-references: UNIPROT:Q7M3T2

C;Superfamily: unassigned animal peptides

C;Keywords: venom

Query Match 23.5%; Score 23; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16
| | | | |
Db 4 PGFSPFRI 11

RESULT 16

G61458

Ig lambda chain V-II region (AZI) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996

C;Accession: G61458; PLO159

R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989

A;Title: Expression of a public idotype by human monoclonal IGM directed to myelin-ass
A;Reference number: A61458; MUID:90039128; PMID:2478651

A;Accession: G61458

A;Molecule type: protein

A;Residues: 1-13 <BRO>

C;Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycop
C;Keywords: heterotetramer; immunoglobulin

Query Match 23.5%; Score 23; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPDV 6
| | | | |
Db 6 QPPSV 10

```
RESULT 17
PA0088
Protein QP200051 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0088
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A:Reference number: PA0051
A:Accession: PA0088
A:Molecule type: protein
A:Residues: 1-15 <CHO>

Query Match 23.5%; Score 23; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QPPDVEKPD 10
Db 1 QKPDIPXDD 9

RESULT 18
A60915
enkephalin-degrading aminopeptidase (EC 3.4.11.1), puromycin-sensitive - rat (fragment)
N:Alternate names: aminoenkephalinase; aminopeptidase MII
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A60915
R:Dyer, S.H.; Slaughter, C.A.; Orth, K.; Moonaw, C.R.; Herish, L.B.
J. Neurochem. 54, 547-554, 1990
A:Title: Comparison of the soluble and membrane-bound forms of the puromycin-sensitive enzyme
A:Reference number: A60915; MUID:90132681; PMID:2299352
A:Accession: A60915
A:Molecule type: protein
A:Residues: 1-18 <DYB>
A:Cross-references: UNIPROT:Q7M076
A:Note: this sequence represents the N-terminus of both soluble and membrane-associated
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: hydrolase

Query Match 23.5%; Score 23; DB 2; Length 18;
Best Local Similarity 42.9%; Pred. No. 2e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
Db 1 PEKPFPE 7

RESULT 19
S07436
tachykinin - African tree frog (Kassina maculata)
N:Alternate names: hylambatin
C:Species: Kassina maculata
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C:Accession: S07436
R:Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.
Biomed. Res. 2, 613-617, 1981
A:Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, in tachykinin
A:Reference number: S07436
A:Accession: S07436
A:Molecule type: protein
A:Residues: 1-12 <YAS>
A:Cross-references: UNIPROT:P08614
A:Experimental source: skin
A:Note: the source is designated as Hylambates maculatus
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 22.4%; Score 22; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
```

```
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPDVEK 8
Db 2 PPDPDR 7

RESULT 20
JH0517
insulin-like growth factor-binding protein 4 - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JH0517
R:Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.
Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991
A:Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth factor-binding proteins
A:Reference number: JH0515; MUID:92109718; PMID:1722398
A:Accession: JH0517
A:Molecule type: protein
A:Residues: 1-16 <COL>
A:Cross-references: UNIPROT:P24854
A:Experimental source: serum
C:Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat h

Query Match 22.4%; Score 22; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPDVEK 8
Db 8 PPSEK 13

RESULT 21
S78765
ribosomal protein MRP-S24, mitochondrial - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: S78765
R:Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A:Reference number: S78760
A:Accession: S78765
A:Molecule type: protein
A:Residues: 1-11 <GRA>
A:Cross-references: UNIPROT:Q7M374
C:Keywords: mitochondrion
F:1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Query Match 21.4%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DQPPDVEK 8
Db 4 DVPKDLTK 11

RESULT 22
S10059
tachykinin - African tree frog (Kassina maculata)
N:Alternate names: hylambates-kassinin
C:Species: Kassina maculata
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C:Accession: S10059
R:Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.
Biomed. Res. 2, 613-617, 1981
A:Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, in tachykinin
A:Reference number: S07436
A:Accession: S10059
A:Molecule type: protein
A:Residues: 1-12 <YAS>
A:Cross-references: UNIPROT:P08613
```

A:Experimental source: skin
A:Note: the source is designated as Hylambates maculatus
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 21.4%; Score 21; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 DVKPKD 10
| | | |
Db 1 DEPKPD 6

RESULT 23

PN0665

dystrophin-associated glycoprotein A3a-IV - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

C:Accession: PN0665

R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in Duchenne type muscular dystrophy muscle.

A:Reference number: PN0662; MUID:94156881; PMID:8113213

A:Accession: PN0665

A:Molecule type: protein

A:Residues: 1-15 <POS>

C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C:Keywords: glycoprotein; skeletal muscle

Query Match 21.4%; Score 21; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 3.4e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 9 PDLPQFQ 15
| | | |
Db 9 PNAPPYQ 15

RESULT 24

A60551

leukocyte elastase (EC 3.4.21.37) - dog (fragment)

C:Species: Canis lupus familiaris (dog)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C:Accession: A60551

R:Axelsson, L.; Bergengfeldt, M.; Bjoerk, P.; Olsson, R.; Ohlsson, K.

Scand. J. Clin. Lab. Invest. 50, 35-42, 1990

A:Title: Release of immunoreactive canine leukocyte elastase normally and in endotoxin a

A:Reference number: A60551; MUID:90193608; PMID:1690443

A:Accession: A60551

A:Molecule type: protein

A:Residues: 1-16 <AXE>

A:Cross-references: UNIPROT:Q8MJD1

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; leukocyte; lysosome; serine proteinase

Query Match 21.4%; Score 21; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 3.6e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 8 KPDLPQFQ 16
| | | |
Db 8 QPHAWPFQ 16

RESULT 25

B44873

caldesmon - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: B44873

R:Ikebe, M.; Hornick, T.

Arch. Biochem. Biophys. 288, 538-542, 1991

A:Title: Determination of the phosphorylation sites of smooth muscle caldesmon by protei
A:Reference number: A44873; MUID:91378498; PMID:1898046
A:Accession: B44873
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <IKE>
A:Cross-references: UNIPROT:Q9TRW1
A:Experimental source: skeletal myosin
A:Note: sequence extracted from NCBI backbone (NCBIP:63202)
C:Superfamily: caldesmon

Query Match 21.4%; Score 21; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEKP 9
| | | |
Db 8 VEKP 11

RESULT 26

S26664

microtubule-associated protein tau - human

C:Species: Homo sapiens (man)

C:Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995

C:Accession: S26664

R:Andreadis, A.; Brown, W.M.; Kosik, K.S.

Biochemistry 31, 10626-10633, 1992

A:Title: Structure and novel exons of the human tau gene.

A:Reference number: S26662; MUID:93041757; PMID:1420178

A:Accession: S26664

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-18 <AND>

A:Cross-references: EMBL:X61375

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991

Query Match 21.4%; Score 21; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 4.1e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DDPDVEKPDQ 12
| | | |
Db 8 DHP--LQGPDLR 17

RESULT 27

I57532

gene TnIslow protein - rat (fragment)

C:Species: Rattus sp. (rat)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Feb-1997

C:Accession: I57532

R:Banerjee-Basu, S.; Buonanno, A.

Mol. Cell. Biol. 13, 7019-7028, 1993

A:Title: cis-acting sequences of the rat troponin I slow gene confer tissue- and develop

A:Reference number: I57532; MUID:94019373; PMID:8413291

A:Accession: I57532

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-8 <RES>

A:Cross-references: GB:S66172; NID:g432603

C:Genetics:

A:Gene: TnIslow

Query Match 20.4%; Score 20; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PDVEK 8
| | | |
Db 2 PEVER 6

RESULT 28
S65433
bradykinin - horn fly (fragment)
C:Species: Haematobia irritans (horn fly)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65433
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, E.
Eur. J. Biochem. 237, 414-423, 1996
A>Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran
A:Reference number: S65431; MUID:96215437; PMID:8647080
A:Accession: S65433
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <WIJ>
A>Note: the source is designated as Haematobia irritans exigua

Query Match 20.4%; Score 20; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLOPFQ 15
| | |
Db 3 PGFSPPR 9

RESULT 29
D48186
ATPase R1 subunit - wood tobacco (fragment)
C:Species: Nicotiana sylvestris (wood tobacco)
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: D48186
R:De Paeppe, R.; Forchioni, A.; Chetrit, P.; Vedel, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993
A>Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase
A:Reference number: A48186; MUID:93317598; PMID:8327463
A:Accession: D48186
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DEI>
A:Cross-references: UNIPROT:Q9T2T4
A:Experimental source: pollen
A>Note: sequence extracted from NCBI backbone (NCBI:P134871)

Query Match 20.4%; Score 20; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 10 DLQPFQ 15
| | |
Db 4 DLAPYK 9

RESULT 30
A43065
hydroxyproline-3-bradykinin - frog (Helleophryne purcellii)
C:Species: Helleophryne purcellii
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A43065
R:Nakajima, T.; Yasuhara, T.; Erspamer, G.F.; Visser, J.
Experientia 35, 1133, 1979
A>Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of the South A
A:Reference number: A43065; MUID:80024576; PMID:488255
A:Accession: A43065
A:Molecule type: protein
A:Residues: 1-9 <NAK>
A:Cross-references: UNIPROT:Q7LZ17
C:Keywords: bradykinin; hydroxyproline; skin
F:3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 31
A61363
bradykinin - common frog
C:Species: Rana temporaria (common frog)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A61363
R:Anastasi, A.; Erspamer, V.; Bertaccini, G.
Comp. Biochem. Physiol. A 14, 43-52, 1965
A>Title: Occurrence of bradykinin in the skin of Rana temporaria.
A:Reference number: A61363
A:Accession: A61363
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <ANA>
A:Cross-references: UNIPROT:Q7LZJ8
C:Superfamily: unassigned animal peptides
C:Keywords: skin

Query Match 20.4%; Score 20; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLOPFQ 15
| | |
Db 3 PGFSPPR 9

RESULT 32
A60476
S-layer protein - Bacillus thuringiensis (fragment)
C:Species: Bacillus thuringiensis
C>Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 09-Jul-2004
C:Accession: A60476
R:Luckevich, M.D.; Beveridge, T.J.
J. Bacteriol. 171, 6656-6667, 1989
A>Title: Characterization of a dynamic S layer on Bacillus thuringiensis.
A:Reference number: A60476; MUID:90078111; PMID:2592346
A:Accession: A60476
A:Molecule type: protein
A:Residues: 1-10 <LUC>
A:Cross-references: UNIPROT:P49325
C:Comment: The S-layer, or surface array, is the outermost component of several archaea

Query Match 20.4%; Score 20; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PDLOP 13
| | |
Db 6 PDVXP 10

RESULT 33
S13279
Ile-Ser-bradykinin - human (fragment)
N:Alternate names: T-kinin
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S13279
R:Wunderer, G.; Walter, I.; Eschenbacher, B.; Lang, M.; Kellermann, J.; Kindermann, G.
Biol. Chem. Hoppe-Seyler 371, 977-981, 1990
A>Title: Ile-Ser-bradykinin is an aberrant permeability factor in various human malignan
A:Reference number: S13279; MUID:91166748; PMID:2076202
A:Accession: S13279
A:Molecule type: protein
A:Residues: 1-11 <WUN>
A:Cross-references: UNIPROT:Q7M4P1
C:Keywords: bradykinin

Query Match 20.4%; Score 20; DB 2; Length 11;
 Best Local Similarity 42.9%; Pred. No. 3.4e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
 Db 5 PGFSFPR 11

RESULT 34

YHJFY
 morphogenetic neuropeptide - human
 C:Species: Homo sapiens (man)
 C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
 C:Accession: B01427; A01427
 R:Schaller, H.C.; Bodenmuller, H.C.
 Nature 293, 579-580, 1981
 A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelestine
 A:Reference number: A93266; MUID:82035850; PMID:7290191
 A:Accession: B01427
 A:Molecule type: protein
 A:Residues: 1-11 <BOD>
 A:Cross-references: UNIPROT:P01163
 R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A:Reference number: A91296; MUID:82050803; PMID:7297679
 A:Contents: annotation; synthesis
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator
 C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide
 F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8
 Db 1 QPPGSK 7

RESULT 35

YHBO
 morphogenetic neuropeptide - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
 C:Accession: C01427; A01427
 R:Bodenmuller, H.; Schaller, H.C.
 Nature 293, 579-580, 1981
 A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelestine
 A:Reference number: A93266; MUID:82035850; PMID:7290191
 A:Accession: C01427
 A:Molecule type: protein
 A:Residues: 1-11 <BOD>
 A:Cross-references: UNIPROT:P01163
 R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A:Reference number: A91296; MUID:82050803; PMID:7297679
 A:Contents: annotation; synthesis
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator
 C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide
 F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8
 Db 1 QPPGSK 7

RESULT 36

YHJFY
 morphogenetic neuropeptide - Hydra attenuata
 N:Alternate names: head activator
 C:Species: Hydra attenuata
 C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
 C:Accession: B93900; A01427
 R:Schaller, H.C.; Bodenmuller, H.
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
 A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
 A:Reference number: A93900
 A:Accession: B93900
 A:Molecule type: protein
 A:Residues: 1-11 <SCH>
 A:Cross-references: UNIPROT:P01163
 R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A:Reference number: A91296; MUID:82050803; PMID:7297679
 A:Contents: annotation; synthesis
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator
 C:Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8
 Db 1 QPPGSK 7

RESULT 37

YHXAE
 morphogenetic neuropeptide - sea anemone (Anthopleura elegantissima)
 N:Alternate names: head activator
 C:Species: Anthopleura elegantissima
 C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
 C:Accession: A93900; A01427
 R:Schaller, H.C.; Bodenmuller, H.
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
 A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
 A:Reference number: A93900
 A:Accession: A93900
 A:Molecule type: protein
 A:Residues: 1-11 <SCH>
 A:Cross-references: UNIPROT:P01163
 R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A:Reference number: A91296; MUID:82050803; PMID:7297679
 A:Contents: annotation; synthesis
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator
 C:Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8
 Db 1 QPPGSK 7

RESULT 38

YHRT

morphogenetic neuropeptide - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004

C:Accession: A01427

R:Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coele

A:Reference number: A93266; MUID:82035850; PMID:7290191

A:Accession: A01427

A:Molecule type: protein

A:Residues: 1-11 <BOD>

A:Cross-references: UNIPROT:P01163

R:Birt, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A:Title: Synthesis of a new neuropeptide, the head activator from hydra.

A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Contents: annotation; synthesis

A:Note: the synthetic peptide was identical with the natural peptide in chemical structu

C:Comment: This peptide was first isolated from nerve cells of hydra and was called head

C:Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;

Best Local Similarity 57.1%; Pred. No. 3.4e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QPPDVEK 8

Db 1 QPPGSK 7

RESULT 39

C64030

hypothetical protein H11451 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 10-Oct-1997

C:Accession: C64030

R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman, J

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: C64030

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-12 <TIGR>

A:Cross-references: GB:U32823; GB:L42023; MUID:91574281; PID:91574296; TIGR:H11451

Query Match 20.4%; Score 20; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPD 5

Db 9 PPD 11

RESULT 40

S15755

actin 7 - soybean (fragment)

C:Species: Glycine max (soybean)

C:Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C:Accession: S15755

R:Pearson, L.; Meagher, R.B.

Plant Mol. Biol. 14, 513-526, 1990

A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated

A:Reference number: S15754; MUID:91346640; PMID:2102831

A:Accession: S15755

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-13 <PEAS>

A:Cross-references: UNIPROT:P15987; EMBL:X17120; MUID:918527; PID:918528

C:Superfamily: actin

C:Keywords: cytoskeleton; structural protein

Query Match 20.4%; Score 20; DB 2; Length 13;

Best Local Similarity 75.0%; Pred. No. 4.1e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLOP 13

Db 6 DLOP 9

Search completed: June 7, 2005, 23:20:37

Job time : 17.6909 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 79.2 seconds
(without alignments)
116.382 Million cell updates/sec

Title: US-10-691-157-3

Perfect score: 98
Sequence: 1 DQPPVEXKPDLPQGVQS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	31.6	15	1 MK1_PALPR	P80408 palomena pr
2	31	31.6	15	2 MK2_PALPR	P80410 palomena pr
3	31	31.6	16	1 MK2B_PALPR	P80410 palomena pr
4	31	31.6	16	1 MK3_PALPR	P80411 palomena pr
5	31	31.6	18	2 P82674	P82674 bos taurus
6	30	30.6	10	1 URE3_MORMO	P17339 morganella
7	29	29.6	15	2 Q9T2K8	Q9T2K8 spinacia ol
8	29	29.6	17	2 Q8UT86	Q8UT86 human immun
9	28.5	29.1	17	2 Q9UND6	Q9UND6 homo sapien
10	28	28.6	18	2 Q6ICE7	Q6ICE7 homo sapien
11	28	28.6	18	2 Q9R4E0	Q9R4E0 pseudomonas
12	28	28.6	18	2 O13167	O13167 xiphias gla
13	27	27.6	10	2 Q9PRV8	Q9PRV8 triakis scy
14	27	27.6	12	2 P82325	P82325 pium sativ
15	27	27.6	15	2 Q6WFA4	Q6WFA4 sturnus vul
16	27	27.6	15	2 Q6WFA5	Q6WFA5 anas platyr
17	27	27.6	15	2 Q6WFA6	Q6WFA6 podager nac
18	27	27.6	15	2 Q6WFA7	Q6WFA7 falco pereg
19	27	27.6	15	2 Q6WFA8	Q6WFA8 strix urale
20	27	27.6	15	2 Q6WFA9	Q6WFA9 surina ulul
21	27	27.6	15	2 Q6WFA0	Q6WFA0 tyco alba (
22	27	27.6	16	2 Q9UC12	Q9UC12 homo sapien
23	27	27.6	18	2 Q8MNX0	Q8MNX0 bombyx mori
24	27	27.6	18	2 Q9S8G8	Q9S8G8 psophocarpu
25	26.5	26.5	13	2 Q9UWH3	Q9UWH3 homo sapien
26	26.5	26.5	15	2 Q9UWH3	Q9UWH3 thermococu
27	26.5	26.5	15	2 Q9TR14	Q9TR14 bos taurus
28	26.5	26.5	17	2 Q9JX08	Q9JX08 mus musculu
29	26.5	26.5	17	2 P90402	P90402 human immun
30	26.5	26.5	17	2 Q9Q709	Q9Q709 human immun
31	26.5	26.5	18	2 Q9TWL5	Q9TWL5 lucilia cup

32	26	26.5	18	2 Q9X3E9	Q9X3E9 prochloroco
33	25.5	26.0	17	2 P83061	P83061 spinacia ol
34	25	25.5	15	2 Q7L245	Q7L245 cyprinus ca
35	25	25.5	18	2 Q9UCT9	Q9UCT9 homo sapien
36	24	24.5	10	2 Q7M1P6	Q7M1P6 haynaldia v
37	24	24.5	11	2 Q9S618	Q9S618 prochloroco
38	24	24.5	12	2 P82328	P82328 pium sativ
39	24	24.5	13	2 Q9R3R6	Q9R3R6 prochloroco
40	24	24.5	12	2 Q9R3R6	Q9R3R6 rana nigrom
41	24	24.5	14	1 BRK3_RANNI	BRK3_RANNI
42	24	24.5	17	2 Q6Y1B2	Q6Y1B2
43	24	24.5	17	2 Q9IB06	Q9IB06 prochloroco
44	24	24.5	18	2 Q7M1Z6	Q7M1Z6 aegilops lo
45	23.5	24.0	18	2 Q6Y971	Q6Y971 synchococc
46	23.5	24.0	9	2 Q9UCS8	Q9UCS8 homo sapien
47	23.5	24.0	14	2 Q6JVP2	Q6JVP2 ottopappus e
48	23.5	24.0	14	2 Q6JVP4	Q6JVP4 jefeca ping
49	23	23.5	14	2 Q6JVP6	Q6JVP6 angeliptyum
50	23	23.5	9	1 COXE_THUOB	COXE_THUOB
51	23	23.5	9	2 Q9R735	Q9R735
52	23	23.5	11	1 BRKP_PHYRO	BRKP_PHYRO
53	23	23.5	12	1 VESP_VESMA	VESP_VESMA
54	23	23.5	12	1 VESP_VESXA	VESP_VESXA
55	23	23.5	12	2 Q6EFAS	Q6EFAS chlamydomon
56	23	23.5	14	2 Q6JVP7	Q6JVP7 elaphandra
57	23	23.5	14	2 Q6JVP7	Q6JVP7 dimerostemm
58	23	23.5	14	2 Q6JVP1	Q6JVP1 blattvillia
59	23	23.5	14	2 Q6JVP2	Q6JVP2 baltimora r
60	23	23.5	14	2 Q6JVP4	Q6JVP4 angeliptyum
61	23	23.5	15	1 PBI_PROTR	PBI_PROTR
62	23	23.5	15	1 PBI_PROTR	PBI_PROTR
63	23	23.5	15	2 Q6JVP9	Q6JVP9 protocentru
64	23	23.5	17	2 P97135	P97135 mycobacteri
65	23	23.5	18	2 Q7SMCS	Q7SMCS neurospora
66	23	23.5	18	2 Q7M076	Q7M076 ractus norv
67	22	22.4	10	2 Q9LSW6	Q9LSW6 liberibacte
68	22	22.4	11	2 Q8HYM4	Q8HYM4 felis silve
69	22	22.4	12	1 PPK4_PERAM	PPK4_PERAM
70	22	22.4	12	1 TKN2_KASMA	TKN2_KASMA
71	22	22.4	13	2 Q6PF73	Q6PF73
72	22	22.4	14	2 Q9RIU3	Q9RIU3 ractus norv
73	22	22.4	15	2 Q08936	Q08936 nicotiana t
74	22	22.4	15	2 Q69142	Q69142 streptococc
75	22	22.4	16	1 IBP4_PIG	IBP4_PIG
76	22	22.4	16	2 Q6SFI7	Q6SFI7
77	22	22.4	16	2 Q9QV12	Q9QV12 mus sp. mep
78	22	22.4	17	2 Q7S179	Q7S179 neurospora
79	22	22.4	17	2 Q9SM99	Q9SM99 equus cabal
80	22	22.4	17	2 Q9EUP4	Q9EUP4 thermus the
81	22	22.4	17	2 Q9QVC2	Q9QVC2 ractus sp.
82	22	22.4	17	2 Q9QVC6	Q9QVC6 ractus norv
83	22	22.4	17	2 Q9QVC6	Q9QVC6 ractus norv
84	22	22.4	17	2 Q9QVC6	Q9QVC6 ractus norv
85	22	22.4	17	2 Q9QVC6	Q9QVC6 ractus norv
86	22	22.4	17	2 Q9QVC6	Q9QVC6 ractus norv
87	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv
88	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv
89	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv
90	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv
91	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv
92	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv
93	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv
94	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv
95	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv
96	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv
97	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv
98	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv
99	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv
100	22	22.4	18	2 Q9QVC6	Q9QVC6 ractus norv

ALIGNMENTS

RESULT 1

MK1_PALPR STANDARD; PRT; 15 AA.
 ID MK1_PALPR
 AC P80408;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Metalnikowin I.
 OS Palomena prasina (Green shield bug).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
 OC Panheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;
 OC Pentatominae; Palomena.
 CC NCBI_TaxID=55431;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RA Chernysh S., Cocciandich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 RT Palomena prasina: identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin."
 RL J. Insect Physiol. 42:81-89(1996).
 CC -1- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -1- INDUCTION: By bacterial infection.
 CC Antibiotic: Direct protein sequencing. Insect immunity.
 KW SEQUENCE 15 AA; 1838 MW; 21407B663C8A6299 CRC64;
 SQ

Query Match

Best Local Similarity 31.6%; Score 31; DB 1; Length 15;
 Pred. No. 7.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VEKPDLP 13
 DB 1 VDKPDYP 8

RESULT 2

MK2_PALPR STANDARD; PRT; 15 AA.
 ID MK2_PALPR
 AC P80409;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Metalnikowin IIA.
 OS Palomena prasina (Green shield bug).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
 OC Panheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;
 OC Pentatominae; Palomena.
 CC NCBI_TaxID=55431;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RA Chernysh S., Cocciandich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 RT Palomena prasina: identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin."
 RL J. Insect Physiol. 42:81-89(1996).
 CC -1- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -1- INDUCTION: By bacterial infection.
 CC Antibiotic: Direct protein sequencing. Insect immunity.
 KW SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;
 SQ

Query Match

Best Local Similarity 31.6%; Score 31; DB 1; Length 15;
 Pred. No. 7.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VEKPDLP 13
 DB 1 VDKPDYP 8

RESULT 3

MK2B_PALPR STANDARD; PRT; 16 AA.
 ID MK2B_PALPR
 AC P80410;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Metalnikowin IIB.
 OS Palomena prasina (Green shield bug).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
 OC Panheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;
 OC Pentatominae; Palomena.
 CC NCBI_TaxID=55431;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RA Chernysh S., Cocciandich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 RT Palomena prasina: identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin."
 RL J. Insect Physiol. 42:81-89(1996).
 CC -1- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -1- INDUCTION: By bacterial infection.
 CC Antibiotic: Direct protein sequencing. Insect immunity.
 KW SEQUENCE 16 AA; 2040 MW; AF21407D063B9462 CRC64;
 SQ

Query Match

Best Local Similarity 31.6%; Score 31; DB 1; Length 16;
 Pred. No. 7.6e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VEKPDLP 13
 DB 1 VDKPDYP 8

RESULT 4

MK3_PALPR STANDARD; PRT; 16 AA.
 ID MK3_PALPR
 AC P80411;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Metalnikowin III.
 OS Palomena prasina (Green shield bug).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
 OC Panheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;
 OC Pentatominae; Palomena.
 CC NCBI_TaxID=55431;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RA Chernysh S., Cocciandich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 RT Palomena prasina: identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin."
 RL J. Insect Physiol. 42:81-89(1996).
 CC -1- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -1- INDUCTION: By bacterial infection.
 CC Antibiotic: Direct protein sequencing. Insect immunity.
 KW SEQUENCE 16 AA; 2024 MW; A9E3835D063B9462 CRC64;
 SQ

Query Match

Best Local Similarity 31.6%; Score 31; DB 1; Length 16;
 Pred. No. 7.6e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VEKPDLP 13
 DB 1 VDKPDYP 8

Db 1 VDKPYRP 8

RESULT 5

PRELIMINARY; PRT; 18 AA.

AC P82674; PRELIMINARY; PRT; 18 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE Mitochondrial 28S ribosomal protein S5 (MRP-S5) (Fragments).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

OC Bovinae; Bos.

OX NCBI_TaxId=9913;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Liver;

RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Koc H., Sprenull L.L.;

RT "Identification of four proteins from the small subunit of the mammalian mitochondrial ribosome using a proteomics approach.";

RL Submitted (JUN-2000) to Swiss-Prot.

CC -1- SUBCELLULAR LOCATION: Mitochondrial.

CC -1- MASS SPECTROMETRY: MW=974.58; METHOD=Electrospray; RANGE=1-8.

CC -1- SIMILARITY: BELONGS TO THE S5P FAMILY OF RIBOSOMAL PROTEINS.

DR GO; GO:0005739; C:mitochondrion; IEA.

DR GO; GO:0003735; F:structural constituent of ribosome; IEA.

DR InterPro; IPR000851; Ribosomal_S5.

DR PROSITE; PS00585; RIBOSOMAL_S5; PARTIAL.

KM PROSITE; PS00585; RIBOSOMAL_S5; PARTIAL.

FT NON_TER 1 1

FT NON_CONS 6 9

FT UNSTRE 17 17 OR I.

FT NON_TER 18 18

FT SEQUENCE 18 AA; 2127 MW; 199BC913E25FAR CRC64;

Query Match

Best Local Similarity 31.6%; Score 31; DB 2; Length 18;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PDKPYRPDLQ 12

Db 10 PDKPYRPDLQ 18

RESULT 6

URE3 MORMO

ID URE3 MORMO STANDARD; PRT; 10 AA.

AC P17339;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DE 25-OCT-2004 (Rel. 15, Last annotation update)

DE Urease gamma subunit (EC 3.5.1.5) (Urease amidohydrolase gamma subunit)

DE (Urease 6 kDa subunit) (Fragment).

GN Name=urea; morganii (Proteus morganii).

OS Morganella morganii (Proteus morganii).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Morganella.

OX NCBI_TaxId=582;

RN [1]

RP SEQUENCE.

RP MEDLINE=90264298; PubMed=2345135;

RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;

RT "Morganella morganii urease: purification, characterization, and isolation of gene sequences.";

RT J. Bacteriol. 172:3073-3080(1990).

CC -1- CATALYTIC ACTIVITY: Urea + H(2O) = CO(2) + 2 NH(3).

CC -1- SUBUNIT: (Alpha, beta, gamma) (3) (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: Belongs to the urease gamma subunit family.

DR PIR; C35389; C35389.

DR HAMAP; MF_00739; -, 1.

KM Direct protein sequencing; Hydrolase.

FT NON_TER 10 10

FT SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match

Best Local Similarity 30.6%; Score 30; DB 1; Length 10;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDKPYRP 8

Db 5 PDKPYRP 10

RESULT 7

PRELIMINARY; PRT; 15 AA.

AC Q972K8; PRELIMINARY; PRT; 15 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE LHCII kinase, 64 kDa kinase (Fragment).

OS Spinacia oleracea (Spinach).

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Caryophyllales; Magnoliophyta; eudicotyledons; core eudicots; OC Caryophyllales; Amaranthaceae; Spinacia.

OX NCBI_TaxId=3562;

RN [1]

RP SEQUENCE.

RP MEDLINE=92183823; PubMed=1544419; DOI=10.1016/0014-5793(92)80016-A;

RA Gal A., Herrmann R.G., Lottepeich F., Ohad I.;

RT "Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cytochrome complex.";

RL FEBS Lett. 298:33-35(1992).

DR PIR; S20410; S20410.

DR PIR; S66419; S66419.

FT NON_TER 1 1

FT NON_TER 15 15

FT SEQUENCE 15 AA; 1556 MW; 6E00A4F917DDF33B CRC64;

Query Match

Best Local Similarity 29.6%; Score 29; DB 2; Length 15;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PDKPYRPDL 11

Db 5 PDKPYRPDL 12

RESULT 8

PRELIMINARY; PRT; 17 AA.

AC Q8UT86; PRELIMINARY; PRT; 17 AA.

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Vpr protein.

GN Name=vpr;

OS Human immunodeficiency virus 1.

OC Viruses; Retrovirus; Retroviridae; Lentivirus.

OX NCBI_TaxId=11676;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=21988475; PubMed=11991972;

RA DOI=10.1128/JVI.76.11.5435-5451.2002;

RA Novitsky V., Smith U.R., Gilbert P., McLane M.F., Chigwedere P., Williamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T., Thior I., Foley B.T., Golekwe S., Rybak N., Gasetlaine S., Vamberg P., Marink R., Lee T.-H., Essex M.;

RT "Human immunodeficiency virus type 1 subtype C molecular phylogeny: consensus sequence for an AIDS vaccine design?";

RT J. Virol. 76:5435-5451(2002).

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RN [2]
RP SEQUENCE FROM N.A.
RA Novitsky V.A., McInane M.F., Chigwedere P., Ndung'u T., Klein I.,
RA Chang S.-Y., Peter T., Thior I., Rybak N., Gassettswe S., Vannberg F.,
RA Marlink R., Lee T.-H., Essex M.;
RL Submitted (JUL-2004) to the EMBL/Genbank/DBD databases.
DR EMBL; AF443097; ALU34763.1; -.
DR HSSP; Q73369; IESX.
DR Pfam; PF00522; VPR; 1.
KM AIDS.
SQ SEQUENCE 17 AA; 2018 MW; 58CA6A463F4457C7 CRC64;

Query Match 29.6%; Score 29; DB 2; Length 17;
Best Local Similarity 28.6%; Pred. No. 1.6e+03;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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QY 1 DQPPVEXKPDLP 14
DB 2 EQAPEDQGFQREPY 15

RESULT 9
Q9UND6 PRELIMINARY; PRT; 17 AA.
AC Q9UND6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fatty acid ETHYL ester synthase-II, FAEE synthase-II (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92317032; PubMed=1618826;
RA Bora P.S., Wu X., Spilburg C.A., Lange L.G.;
RT "Purification and characterization of fatty acid ethyl ester synthase-
RT I from human myocardium."
RL J. Biol. Chem. 267:13217-13221(1992).
DR PIR; A42920; A42920.
DR GO; GO:0005829; C:cytosol; NAS.
DR GO; GO:0003039; F:fatty-acyl-ethyl-ester synthase activity; NAS.
DR GO; GO:0006067; P:ethanol metabolism; NAS.
DR GO; GO:0006331; P:fatty acid metabolism; NAS.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 17 AA; 1755 MW; 3456973BF1B39273 CRC64;

Query Match 29.1%; Score 28.5; DB 2; Length 17;
Best Local Similarity 46.2%; Pred. No. 1.9e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

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QY 1 DQPPVEXKPDLP 13
DB 1 EDPDPD---PDTPP 10

RESULT 10
Q6LCE7 PRELIMINARY; PRT; 18 AA.
AC Q6LCE7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Cycloxygenase-1 (EC 1.14.99.1) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=97056106; PubMed=8900446; DOI=10.1016/0090-6980(95)00158-1;
RA Hla T.;
RT "Molecular characterization of the 5.2 KB isoform of the human
RT cyclooxygenase-1 transcript."
RL Prostaglandin 51:81-85(1996).
DR EMBL; U63846; AAC50632.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004666; F:prostaglandin-endoperoxide synthase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 1884 MW; AFCIED7AA764188D CRC64;

Query Match 28.6%; Score 28; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 2.5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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QY 1 DQPPVEXKPDLP 12
DB 6 DDGPAVERPSTE 17

RESULT 11
Q9RAE0 PRELIMINARY; PRT; 18 AA.
AC Q9RAE0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Dipeptidyl aminopeptidase type I (Fragment).
OS Pseudomonas.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae.
ON NCB1_TaxID=286;
RN [1]
RP SEQUENCE.
RA MEDLINE=96200096; PubMed=8631703;
RA Ogasawara W., Ochiai K., Ando K., Yano K., Yamasaki M., Okada H.,
RA Morikawa Y.;
RT "A novel dipeptidyl aminopeptidase from Pseudomonas sp. strain WO24."
RL J. Bacteriol. 178:1283-1286(1996).
SQ SEQUENCE 18 AA; 1813 MW; 369B0388C394A737 CRC64;

Query Match 28.6%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 3 PPDVEX 8
DB 5 PPDVAK 10

RESULT 12
Q13167 PRELIMINARY; PRT; 18 AA.
AC Q13167;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Ribosomal protein S7 (Fragment).
OS Xiphias gladius (swordfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Scombroidei;
OC Xiphiidae; Xiphias.
ON NCB1_TaxID=8245;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Brazil116D, J26B, Peru9C, Peru9A, Peru5C, Peru5B, Japan26C, and
RC Brazil116B;
RA Chow S., Takeyama H.;
RT "Intron length variation observed in the creatine kinase and ribosomal
RT protein genes of the swordfish Xiphias gladius."
RL Fisheries Sci. 64:397-402(2000).

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DR EMBL; U95521; AAB58281.1; -
DR EMBL; U89244; AAB58379.1; -
DR EMBL; U95515; AAB58275.1; -
DR EMBL; U95516; AAB58276.1; -
DR EMBL; U95517; AAB58277.1; -
DR EMBL; U95518; AAB58278.1; -
DR EMBL; U95519; AAB58279.1; -
DR EMBL; U95520; AAB58280.1; -
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON TER 18 18
SQ SEQUENCE 18 AA; 1978 MW; E716F226CC5BEB15 CRC64;

Query Match 27.6%; Score 28; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PDVEKPD 10
|:|:|
Db 11 PNGEKPD 17

RESULT 13
Q9PRY8 PRELIMINARY; PRT; 10 AA.
ID Q9PRY8
AC Q9PRY8; PRELIMINARY; PRT; 10 AA.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Angiotensin I.
OS Triakis scyllium (Leopard shark) (Triakis scyllia).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
OC Triakis.
OX NCBI_TaxID=30494;
RN [1]
RP SEQUENCE.
RX MEDLINE=94141412; PubMed=8308464;
RA Takai Y., Hasegawa Y., Watanabe T.X., Nakajima K., Hazon N.;
RT "A novel angiotensin I isolated from an elasmobranch fishn.";
RL J. Endocrinol. 139:281-285(1993).
SQ SEQUENCE 10 AA; 1284 MW; 20F02PD761B04B47 CRC64;

Query Match 27.6%; Score 27; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KPDLOPFQV 16
|:|:|
Db 2 RYVHPFQL 10

RESULT 14
P82325 PRELIMINARY; PRT; 12 AA.
ID P82325
AC P82325; PRELIMINARY; PRT; 12 AA.
DT 01-JUN-2000 (TREMBlrel. 14, Created)
DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 24, Last annotation update)
DE Unknown protein from 2D-page of thylakoid (SPOT106) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eucoside I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Pelletier J.-B., Fritso G., Kallme D.E., Roepstorff P., Nilsson F.,
RA Adamka I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
targeting analysis of lumenal and peripheral thylakoid proteins.";

RL Plant Cell 12:319-341(2000).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
CC PERIPHERY.
CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.3, ITS MW IS: 18.2 kDa.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0009579; C:thylakoid; IEA.
KW Chloroplast; Thylakoid.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1236 MW; CEAC7ADC02633452 CRC64;

Query Match 27.6%; Score 27; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 2.3e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 VEKPDLP 13
|:|:|
Db 5 VNKPELIP 12

RESULT 15
Q6WFA4 PRELIMINARY; PRT; 15 AA.
ID Q6WFA4
AC Q6WFA4; PRELIMINARY; PRT; 15 AA.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE BMAL1 (Fragment).
GN Name=Bmal1;
OS Sturnus vulgaris (Starling).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Sturnidae; Sturnus.
OX NCBI_TaxID=9172;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14662308; DOI=10.1016/S1096-4959(03)00276-8;
RA Fidler A.E., Gwinner E.;
RT "Comparative analysis of avian BMAL1 and CLOCK protein sequences: a
search for features associated with owl nocturnal behaviour.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003).
DR EMBL; AY291073; AAC55074.1; -
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1457 MW; 83226D2D37373AAS CRC64;

Query Match 27.6%; Score 27; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVDEKP 9
|:|:|
Db 5 PPDTSSP 11

RESULT 16
Q6WFA5 PRELIMINARY; PRT; 15 AA.
ID Q6WFA5
AC Q6WFA5; PRELIMINARY; PRT; 15 AA.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE BMAL1 (Fragment).
GN Name=Bmal1;
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14662308; DOI=10.1016/S1096-4959(03)00276-8;
RA Fidler A.E., Gwinner E.;
RT "Comparative analysis of avian BMAL1 and CLOCK protein sequences: a

RT search for features associated with owl nocturnal behaviour."
 DR Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003).
 RL EMBL; AY291072; AAQ55073.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 15 AA; 1514 MW; 832261D37373AAS CRC64;

Query Match 27.6%; Score 27; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 PPDVEKP 9
 Db 5 PPDTRSP 11

RESULT 17

ID Q6WFA6 PRELIMINARY; PRT; 15 AA.
 AC Q6WFA6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE BMA1 (Fragment).
 GN Name=Bma1;
 OS Podager nacunda (nacunda nighthawk).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Caprimulgiformes; Caprimulgidae;
 OC Chordellinae; Podager.
 OK NCBI_TaxID=135181;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=14662308; DOI=10.1016/S1096-4959(03)00276-8;
 RA Fidler A.E., Gwinner E.;
 RT "Comparative analysis of avian BMA1 and CLOCK protein sequences: a
 search for features associated with owl nocturnal behaviour.";
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003).
 DR EMBL; AY291071; AAQ55072.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 15 AA; 1457 MW; 83226D2D37373AAS CRC64;

Query Match 27.6%; Score 27; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 PPDVEKP 9
 Db 5 PPDTRSP 11

RESULT 18

ID Q6WFA7 PRELIMINARY; PRT; 15 AA.
 AC Q6WFA7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE BMA1 (Fragment).
 GN Name=Bma1;
 OS Falco peregrinus (Peregrine falcon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Falconiformes; Falconidae; Falco.
 OK NCBI_TaxID=8954;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=14662308; DOI=10.1016/S1096-4959(03)00276-8;
 RA Fidler A.E., Gwinner E.;
 RT "Comparative analysis of avian BMA1 and CLOCK protein sequences: a
 search for features associated with owl nocturnal behaviour.";
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003).
 DR EMBL; AY291070; AAQ55071.1; -.
 FT NON_TER 1 1

FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1457 MW; 83226D2D37373AAS CRC64;
 Query Match 27.6%; Score 27; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 PPDVEKP 9
 Db 5 PPDTRSP 11

RESULT 19

ID Q6WFA8 PRELIMINARY; PRT; 15 AA.
 AC Q6WFA8;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE BMA1 (Fragment).
 GN Name=Bma1;
 OS Strix uralensis (Ural owl).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Strigiformes; Strigidae; Strix.
 OK NCBI_TaxID=36305;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=14662308; DOI=10.1016/S1096-4959(03)00276-8;
 RA Fidler A.E., Gwinner E.;
 RT "Comparative analysis of avian BMA1 and CLOCK protein sequences: a
 search for features associated with owl nocturnal behaviour.";
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003).
 DR EMBL; AY291069; AAQ55070.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 15 AA; 1457 MW; 83226D2D37373AAS CRC64;

Query Match 27.6%; Score 27; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 PPDVEKP 9
 Db 5 PPDTRSP 11

RESULT 20

ID Q6WFA9 PRELIMINARY; PRT; 15 AA.
 AC Q6WFA9;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE BMA1 (Fragment).
 GN Name=Bma1;
 OS Sturnia ulula (Northern hawk owl).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Strigiformes; Strigidae; Sturnia.
 OK NCBI_TaxID=69940;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=14662308; DOI=10.1016/S1096-4959(03)00276-8;
 RA Fidler A.E., Gwinner E.;
 RT "Comparative analysis of avian BMA1 and CLOCK protein sequences: a
 search for features associated with owl nocturnal behaviour.";
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003).
 DR EMBL; AY291068; AAQ55069.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 15 AA; 1457 MW; 83226D2D37373AAS CRC64;

Query Match 27.6%; Score 27; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 2.9e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PDVDEKP 9
| | | | |
DB 5 PPDITSSP 11

RESULT 21

Q6WFB0 PRELIMINARY; PRT; 15 AA.

AC Q6WFB0; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE BMA11 (Fragment).

OS Tyto alba (Barn owl).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Strigiformes; Tytonidae; Tyto.

OX NCBI_TaxID=56313;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed:14662308; DOI=10.1016/S1096-4959(03)00276-8;

RA Fidler A.E., Gwinner E.;

RT "Comparative analysis of avian BMA11 and CLOCK protein sequences: a search for features associated with owl nocturnal behaviour";

RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003).

DR EMBL: AY291067; AA05068.1; -.

FT NON_TER 1 15

SQ SEQUENCE 15 AA; 1457 MW; 83226D2D37373AA5 CRC64;

Query Match 27.6%; Score 27; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PDVDEKP 9
| | | | |
DB 5 PPDITSSP 11

RESULT 22

Q9UC12 PRELIMINARY; PRT; 16 AA.

AC Q9UC12; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Tropomyosin (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=93195352; PubMed=8450225;

RA Dae K.M., Dasgupta A., Mandal A., Geng X.;

RT "Autoimmunity to cytoskeletal protein tropomyosin. A clue to the pathogenetic mechanism for ulcerative colitis.";

RL J. Immunol. 150:2487-2493(1993).

SQ SEQUENCE 16 AA; 1960 MW; 7A26C49A1E0A335E CRC64;

Query Match 27.6%; Score 27; DB 2; Length 16;
Best Local Similarity 38.5%; Pred. No. 3.1e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 5 DVEKDPQFQVQ 17
| | | | |
DB 4 DEKMEIQEIQLK 16

RESULT 23

Q8MNX0

ID Q8MNX0 PRELIMINARY; PRT; 18 AA.

AC Q8MNX0; 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DE Hypothetical protein (Fragment).

OS Bombyx mori (Silk moth).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;

OC Bombycidae; Bombyx.

OX NCBI_TaxID=7091;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=ovary;

RX MEDLINE=22316879; PubMed=12429116; DOI=10.1016/S0965-1748(02)00104-2;

RA Swever L., Bystrachioy T., Iatrou K.;

RT "The orphan nuclear receptors Bme75A and Bme75C of the silkworm Bombyx mori: hormonal control and ovarian expression.";

RL Insect Biochem. Mol. Biol. 32:1643-1652(2002).

DR EMBL: AF332552; AAM43817.1; -.

KW Hypothetical protein.

FT NON_TER 1 18

SQ SEQUENCE 18 AA; 2012 MW; 072C6D18DF0E0D5E CRC64;

Query Match 27.6%; Score 27; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QPDVDEKP 9
| | | | |
DB 4 KPDSFEP 11

RESULT 24

Q9S8G8 PRELIMINARY; PRT; 18 AA.

AC Q9S8G8; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE Proline-rich protein (Fragment).

OS Psophocarpus tetragonolobus (Goa bean) (Asparagaceae).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosils 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

OX NCBI_TaxID=3891;

RN [1]

RP SEQUENCE.

RX MEDLINE=95277008; PubMed=7757337;

RA Esaka M., Hayakawa H.;

RT "Specific secretion of proline-rich proteins by salt-adapted winged bean cells.";

RL Plant Cell Physiol. 36:441-446(1995).

SQ SEQUENCE 18 AA; 2252 MW; 4FD7D1DA1B85D94A CRC64;

Query Match 27.6%; Score 27; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PDVDEKP 9
| | | | |
DB 9 FKVEKP 14

RESULT 25

Q9UEE2 PRELIMINARY; PRT; 13 AA.

AC Q9UEE2; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)


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DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Vpr protein.
GN Name=Vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2321B;
RX MEDLINE=97225063; PubMed=9071436;
RA Choi D.J., Dube S., Spicer T.P., Slade H.B., Jensen F.C., Polesz B.J.;
RT "HIV type 1 isolate 2321, the strain used to make a therapeutic HIV
type 1 immunogen, is intersubtype recombinant."
RL AIDS Res. Hum. Retroviruses 13:357-361(1997).
DR EMBL; U76035; AAB54106.1; -.
DR HSP; Q73369; 1ESX.
DR InterPro; IPR000012; Retrov_vpr/X.
DR Pfam; PF00522; VPR; 1.
KM AIDS.
SQ SEQUENCE 17 AA; 1969 MW; 58CA75563F4457C7 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 17;
Best Local Similarity 30.8%; Pred. No. 4.7e+03;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DQPPVEKPDLOP 13
DB 2 EQAPEDQGFQREP 14

RESULT 30
ID 09Q709 PRELIMINARY; PRT; 17 AA.
AC 09Q709;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Truncated Vpr.
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20436917; PubMed=10983640;
RA Janssens W., Laukkanen T., Salminen M.O., Carr J.K., McCutchan F.E.;
RT "HIV-1 subtype H near-full length genome reference strains and
RT analysis of subtype-H-containing inter-subtype recombinants."
RL AIDS 14:1533-1543(2000).
DR EMBL; AF190128; AAF18410.1; -.
DR HSP; Q73369; 1ESX.
DR InterPro; IPR000012; Retrov_vpr/X.
DR Pfam; PF00522; VPR; 1.
KM AIDS.
SQ SEQUENCE 17 AA; 1992 MW; 58CA70F63F4457C7 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 17;
Best Local Similarity 30.8%; Pred. No. 4.7e+03;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DQPPVEKPDLOP 13
DB 2 EQAPEDQGFQREP 14

RESULT 31
ID 09TWL5 PRELIMINARY; PRT; 18 AA.
AC 09TWL5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

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DE 24 kDa chymotrypsin-like enzyme (Fragment).
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Lucilia.
OC NCBI_TaxId=7375;
RN [1]
RP SEQUENCE.
RX MEDLINE=95219141; PubMed=7704304;
RA Casu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Riding G.A.,
RA Tellam R.L.;
RT "Excretory/secretory chymotrypsin from Lucilia cuprina: purification,
RT enzymatic specificity and amino acid sequence deduced from mRNA."
RL Insect Mol. Biol. 3:201-211(1994).
SQ SEQUENCE 18 AA; 2002 MW; AC29200B9B184300 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 5e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 PDLOPPOV 16
DB 9 PGLPPYQV 16

RESULT 32
ID 09X3B9 PRELIMINARY; PRT; 18 AA.
AC 09X3B9;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
GN Name=petd;
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OC NCBI_TaxId=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream."
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070147; AAD20766.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2029 MW; BBF8A4E54FDCDE56 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 PDVEKPDLOPQ 15
DB 7 PDLSDPKLRATQ 18

RESULT 33
ID P83061 PRELIMINARY; PRT; 17 AA.
AC P83061;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Putative FK506-binding protein (FKBP) (peptidyl-prolyl cis-trans
DE isomerase) (PPIase) (EC 5.2.1.8) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amarantaceae; Spinacia.
OC NCBI_TaxId=3562;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.

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RA Schubert M., Peterson U., Funk C., Haas B., Schroeder W.P.,
RA Kieselbach T.;
CC Submitted (JUN-2001) to Swiss-Prot.
CC -1- FUNCTION: PPIases accelerate the folding of proteins (By
CC similarity)
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
DR GO: GO:0009507; C:chloroplast; IEA.
DR GO: GO:0016853; F:isomerase activity; IEA.
DR GO: GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO: GO:0006457; P:protein folding; IEA.
DR InterPro: IPR001179; FKBP PPIase.
KW Chloroplast; Isomerase; Rotamase.
FT NON_TER
SQ SEQUENCE 17 AA; 1771 MW; E2013F998FBF908 CRC64;

Query Match
Best Local Similarity 26.0%; Score 25.5; DB 2; Length 17;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 3 PDVXKPDL 11
DB 4 PPE-EKPKL 11

RESULT 34
ID Q7LZ45 PRELIMINARY; PRT; 15 AA.
AC Q7LZ45;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE.
RX MEDLINE=90376100; PubMed=2118944;
RA Harel A., Faimaru M., Rubinstein M., Tal N., Schwartz M.;
RT "Fish apolipoprotein-A-I has heparin binding activity: implication for
RT nerve regeneration."
RL J. Neurochem. 55:1237-1243(1990).
DR PIR; A60221; A60221.
FT NON_TER
SQ SEQUENCE 15 AA; 1649 MW; 69B5C5F6B6320BF CRC64;

Query Match
Best Local Similarity 25.5%; Score 25; DB 2; Length 15;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPP 4
DB 1 DQPP 4

RESULT 35
ID Q9UCT9 PRELIMINARY; PRT; 18 AA.
AC Q9UCT9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE PRG-PROLINE-rich glycoprotein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Plimates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

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```

RN [1]
RX SEQUENCE.
RX MEDLINE=91373355; PubMed=1894623;
RA Gillece-Castro B.L., Prakobphol A., Burlingame A.L., Loeffler H.,
RA Fisher S.J.;
RT "Structure and bacterial receptor activity of a human salivary
RT proline-rich glycoprotein."
RT J. Biol. Chem. 266:17358-17368(1991).
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0008368; F:Gram-negative bacterial binding; NAS.
DR GO: GO:0009618; P:response to pathogenic bacteria; NAS.
FT NON_TER
SQ SEQUENCE 18 AA; 1780 MW; 961F6B0A83D2E40 CRC64;

Query Match
Best Local Similarity 25.5%; Score 25; DB 2; Length 18;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 PDVXKPDLPQ 15
DB 5 PPRGKPEGPPQ 17

RESULT 36
ID Q7MIF6 PRELIMINARY; PRT; 10 AA.
AC Q7MIF6;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Alpha-glucan 6Ha (Fragment).
OS Haynaldia villosa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticaceae; Haynaldia.
OX NCBI_TaxID=40247;
RN [1]
RP SEQUENCE.
RX MEDLINE=91315394; PubMed=1859356;
RA Shewry P.R., Sabelli P.A., Parmar S., Lafandra D.;
RT "alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha
RT of Haynaldia villosa Schur (syn. Daasytrum villosum L.)."
RL Biochem. Genet. 29:207-211(1991).
DR PIR; B61218; B61218.
FT NON_TER
SQ SEQUENCE 10 AA; 1132 MW; DEAE5936C772D772 CRC64;

Query Match
Best Local Similarity 24.5%; Score 24; DB 2; Length 10;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 VEKPDLP 13
DB 3 VPVQDLP 10

RESULT 37
ID Q9S618 PRELIMINARY; PRT; 11 AA.
AC Q9S618;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
OS Name=petD;
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.

```

RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in *Prochlorococcus* populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070133; AAD20740.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B763337 CRC64;

Query Match 24.5%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 5.9e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKPD 11
Db 4 LKPPDL 9

RESULT 38

ID P82328 PRELIMINARY; PRT; 12 AA.
AC P82328;
DT 01-JUN-2000 (TRENBLREL. 14, Created)
DT 01-JUN-2000 (TRENBLREL. 14, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT110) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid 1; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN (1)
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.

RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Pelletier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 21.3 kDa.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0009579; C:thylakoid; IEA.
KW Chloroplast; Thylakoid.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1264 MW; 96691CB663B1B01 CRC64;

Query Match 24.5%; Score 24; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 6.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 PDVEKPD 11
Db 4 PTEBKPP 11

RESULT 39

ID Q9R3R6 PRELIMINARY; PRT; 13 AA.
AC Q9R3R6;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
GN Name=petd;
OS *Prochlorococcus* sp.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC *Prochlorococcus*.
OX NCBI_TaxID=1220;
RN (1)
RP SEQUENCE FROM N.A.

RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in *Prochlorococcus* populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070222; AAD23275.1; -.
DR EMBL; AF070221; AAD23273.1; -.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1522 MW; 4CDE4C38013B763 CRC64;

Query Match 24.5%; Score 24; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 7.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKPD 11
Db 4 LKPPDL 9

RESULT 40

ID BRK3_RANNI STANDARD; PRT; 14 AA.
AC 07LZ53;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bradykinin-like peptide III.
OS *Rana nigromaculata* (Japanese pond frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8409;
RN (1)
RP SEQUENCE.

RC TISSUE=skin;
RX MEDLINE=69117202; PubMed=5751736;
RA Nakajima T.;
RT "On the third active peptide on smooth muscle in the skin of *Rana*
RT *nigromaculata* hallowell.";
RL Chem. Pharm. Bull. 16:2088-2089(1968).
CC -1- FUNCTION: Induces smooth muscle contraction.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the bradykinin family.
DR PIR; A61362; A61362.
KW Bradykinin; Direct protein sequencing; Vasodilator.
SQ SEQUENCE 14 AA; 1486 MW; 33344EB3978393D7 CRC64;

Query Match 24.5%; Score 24; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 PDLOPFOV 16
Db 3 PGFSPFRV 10

Search completed: June 7, 2005, 23:18:54
Job time : 82.2 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 64.5818 Seconds
(without alignments)
71.864 Million cell updates/sec

Title: US-10-691-157-4
Perfect score: 62
Sequence: 1 LFFFLPVNVLP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	62	100.0	12 4 AAB72503	Aab72503 Colostrien
2	62	100.0	12 4 AAB59323	Aab59323 Ewe colob
3	62	100.0	12 4 AAB72249	Aab72249 Colostrien
4	62	100.0	12 4 AAB72535	Aab72535 Colostrien
5	62	100.0	12 5 AAO14580	Aao14580 Neural ce
6	62	100.0	12 5 AAM51039	Aam51039 Colostrien
7	62	100.0	12 5 AAE20231	Aae20231 Colostrien
8	62	100.0	12 8 ADN60298	Adn60298 Constricti
9	62	100.0	12 8 ADS74339	Ads74339 Ovine col
10	62	100.0	14 4 AAB59353	Aab59353 Ewe colob
11	35	56.5	14 4 AAM96786	Aam96786 Human pep
12	33	53.2	9 2 AAY21194	Aay21194 Human bcl
13	33	53.2	9 8 ADR84035	Adr84035 Human 191
14	33	53.2	9 8 ADR84519	Adr84519 Human 191
15	33	53.2	9 8 ADR85026	Adr85026 Human 191
16	33	53.2	9 8 ADR85074	Adr85074 Human 191
17	33	53.2	9 8 ADR87550	Adr87550 Human 191
18	33	53.2	9 8 ADR88447	Adr88447 Human 191
19	33	53.2	9 8 ADR84560	Adr84560 Human 191
20	33	53.2	9 8 ADR85620	Adr85620 Human 191
21	33	53.2	9 8 ADR86086	Adr86086 Human 191
22	33	53.2	9 8 ADR86641	Adr86641 Human 191
23	33	53.2	9 8 ADR87058	Adr87058 Human 191
24	33	53.2	9 8 ADR86146	Adr86146 Human 191
25	33	53.2	9 8 ADR86653	Adr86653 Human 191

26	33	53.2	9 8	ADR83459	Adr83459 Human 191
27	33	53.2	9 8	ADR85080	Adr85080 Human 191
28	33	53.2	9 8	ADR86684	Adr86684 Human 191
29	33	53.2	9 8	ADR87195	Adr87195 Human 191
30	33	53.2	9 8	ADR84539	Adr84539 Human 191
31	33	53.2	9 8	ADR88123	Adr88123 Human 191
32	33	53.2	9 8	ADR88312	Adr88312 Human 191
33	33	53.2	9 8	ADR88446	Adr88446 Human 191
34	33	53.2	9 8	ADR83504	Adr83504 Human 191
35	33	53.2	9 8	ADR83957	Adr83957 Human 191
36	33	53.2	9 8	ADR87688	Adr87688 Human 191
37	33	53.2	9 8	ADR87898	Adr87898 Human 191
38	33	53.2	9 8	ADR83493	Adr83493 Human 191
39	33	53.2	9 8	ADR84019	Adr84019 Human 191
40	33	53.2	9 8	ADR83977	Adr83977 Human 191
41	33	53.2	9 8	ADR85541	Adr85541 Human 191
42	33	53.2	9 8	ADR87676	Adr87676 Human 191
43	33	53.2	9 8	ADR88134	Adr88134 Human 191
44	33	53.2	9 8	ADR84504	Adr84504 Human 191
45	33	53.2	9 8	ADR85539	Adr85539 Human 191
46	33	53.2	9 8	ADR85041	Adr85041 Human 191
47	33	53.2	10 8	ADR84805	Adr84805 Human 191
48	33	53.2	10 8	ADR89332	Adr89332 Human 191
49	33	53.2	10 8	ADR84236	Adr84236 Human 191
50	33	53.2	10 8	ADR86947	Adr86947 Human 191
51	33	53.2	10 8	ADR88864	Adr88864 Human 191
52	33	53.2	10 8	ADR86378	Adr86378 Human 191
53	33	53.2	10 8	ADR86940	Adr86940 Human 191
54	33	53.2	10 8	ADR85840	Adr85840 Human 191
55	33	53.2	10 8	ADR84256	Adr84256 Human 191
56	33	53.2	10 8	ADR85286	Adr85286 Human 191
57	33	53.2	10 8	ADR88890	Adr88890 Human 191
58	33	53.2	10 8	ADR89485	Adr89485 Human 191
59	33	53.2	10 8	ADR83714	Adr83714 Human 191
60	33	53.2	10 8	ADR84737	Adr84737 Human 191
61	33	53.2	10 8	ADR89186	Adr89186 Human 191
62	33	53.2	10 8	ADR89336	Adr89336 Human 191
63	33	53.2	10 8	ADR89660	Adr89660 Human 191
64	33	53.2	10 8	ADR85806	Adr85806 Human 191
65	33	53.2	10 8	ADR83774	Adr83774 Human 191
66	33	53.2	10 8	ADR85814	Adr85814 Human 191
67	33	53.2	10 8	ADR86405	Adr86405 Human 191
68	33	53.2	10 8	ADR89640	Adr89640 Human 191
69	33	53.2	10 8	ADR83723	Adr83723 Human 191
70	33	53.2	10 8	ADR84297	Adr84297 Human 191
71	33	53.2	10 8	ADR84802	Adr84802 Human 191
72	33	53.2	10 8	ADR86336	Adr86336 Human 191
73	33	53.2	10 8	ADR86874	Adr86874 Human 191
74	33	53.2	10 8	ADR84273	Adr84273 Human 191
75	33	53.2	10 8	ADR85316	Adr85316 Human 191
76	33	53.2	10 8	ADR89476	Adr89476 Human 191
77	33	53.2	10 8	ADR84214	Adr84214 Human 191
78	33	53.2	10 8	ADR84762	Adr84762 Human 191
79	33	53.2	10 8	ADR85358	Adr85358 Human 191
80	33	53.2	10 8	ADR88719	Adr88719 Human 191
81	33	53.2	10 8	ADR83780	Adr83780 Human 191
82	33	53.2	10 8	ADR85298	Adr85298 Human 191
83	33	53.2	10 8	ADR85881	Adr85881 Human 191
84	33	53.2	10 8	ADR85559	Adr85559 Human 191
85	33	53.2	10 8	ADR86913	Adr86913 Human 191
86	33	53.2	15 8	ADR90296	Adr90296 Human 191
87	33	53.2	15 8	ADR90299	Adr90299 Human 191
88	33	53.2	15 8	ADR90535	Adr90535 Human 191
89	33	53.2	15 8	ADR89879	Adr89879 Human 191
90	33	53.2	15 8	ADR89884	Adr89884 Human 191
91	33	53.2	15 8	ADR90058	Adr90058 Human 191
92	33	53.2	15 8	ADR89878	Adr89878 Human 191
93	33	53.2	15 8	ADR90051	Adr90051 Human 191
94	33	53.2	15 8	ADR89885	Adr89885 Human 191
95	33	53.2	15 8	ADR90278	Adr90278 Human 191
96	33	53.2	15 8	ADR90286	Adr90286 Human 191
97	33	53.2	15 8	ADR90298	Adr90298 Human 191
98	33	53.2	15 8	ADR89858	Adr89858 Human 191

99 33 53.2 15 8 ADK90044
100 33 53.2 15 8 ADK89868

AdK90044 Human 191
AdK89868 Human 191

ALIGNMENTS

RESULT 1

AAB72503

ID AAB72503 standard; peptide; 12 AA.

XX AAB72503;

XX 09-MAY-2001 (first entry)

XX Colostriin peptide #4.

XX Dermatological; oxidative stress regulator; colostriin.

XX Unidentified.

XX WO200112650-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US022665.

XX 17-AUG-1999; 99US-0149310P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I,

XX MPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the cell

XX with an oxidative stress regulator selected from colostriin, its

XX constituent peptide, analog or their combinations.

XX Claim 6; Page 25; 48pp; English.

XX The present invention relates to a method for modulating the oxidative

XX stress level in a cell or a patient, comprising contacting the cell with,

XX or administering to the patient, an oxidative stress regulator selected

XX from colostriin, or its constituent peptide (e.g. the present peptide),

XX to change the level of an oxidizing species in the cell. The method can

XX be used to treat oxidative damage to skin, by decreasing or preventing an

XX increase in the level of damage to a biomolecule of the patient

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 4; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00054;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVVNVLP 12

DB 1 LFFFLPVVNVLP 12

RESULT 2

ID AAB59323 standard; peptide; 12 AA.

XX AAB59323;

XX 21-MAR-2001 (first entry)

XX Ewe colostriin peptide fragment B-8.

XX Sheep; colostriin; proline rich polypeptide; colostrum; immune disorder;

XX central nervous system disorder; dietary supplement; beta-amyloid plaque.

OS Ovis sp.

XX WO200075173-A2.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-GB002128.

XX 02-JUN-1999; 99GB-00012852.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX MPI; 2001-071058/08.

XX Peptides having an N-terminal amino acid sequence isolated from

XX colostriin for treating e.g. disorders of the central nervous system and

XX immune system, viral and bacterial infections, and diseases characterized

XX by amyloid plaques.

XX Claim 7; Page 27; 63pp; English.

XX The present invention provides the sequences of a number of peptides

XX found in ewe's colostriin. Colostriin is the proline-rich polypeptide

XX fragment of colostrum. These peptides can be used in the treatment of

XX central nervous system disorders such as senile dementia, Parkinson's

XX disease, Alzheimer's disease, psychosis and neurosis, immune system

XX disorders such as bacterial and viral infections, to improve the

XX development of a child's immune system, as a dietary supplement, and to

XX promote the dissolution of beta-amyloid plaques

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 4; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00054;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVVNVLP 12

DB 1 LFFFLPVVNVLP 12

RESULT 3

ID AAB72249 standard; peptide; 12 AA.

XX AAB72249;

XX 14-MAY-2001 (first entry)

XX Colostriin derived cytokine inducing peptide SEQ ID 4.

XX Colostriin; immune response; cytokine; blood cell proliferation;

XX central nervous system disorder; neurological disorder; mental disorder;

XX dementia; neurodegenerative disease; Alzheimer's disease; psychosis;

XX neurosis; infection.

XX Synthetic.

XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US022818.

XX 17-AUG-1999; 99US-0149311P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2001-202804/20.
 XX Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator.
 XX
 XX Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides
 CC have immune response modulatory activity, and are capable of inducing
 CC cytokines. Colostrinin and its derived peptides are useful for inducing
 CC cytokine production, for modulating an immunological response and for
 CC inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 100.0%; Score 62; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00054;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LFFFLPVNVLP 12
 DB 1 LFFFLPVNVLP 12
 RESULT 4
 AAB72535
 ID AAB72535 standard; peptide; 12 AA.
 XX
 XX AAB72535;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #4.
 XX
 KM Neuroprotective; neural cell differentiation regulator; colostrinin;
 KM colostrum.
 XX
 OS Unidentified.
 XX
 PN WO200112651-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US022774.
 XX
 PR 17-AUG-1999; 99US-0149633P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I;
 XX
 DR WPI; 2001-226545/23.
 XX
 PT Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating damaged
 PT neural cells in a patient.
 XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
 XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00054;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LFFFLPVNVLP 12
 DB 1 LFFFLPVNVLP 12
 RESULT 5
 AAO14580
 ID AAO14580 standard; peptide; 12 AA.
 XX
 XX AAO14580;
 XX
 DT 27-MAY-2002 (first entry)
 XX
 DE Neural cell regulatory colostrinin peptide 4.
 XX
 KM Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KM neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KM neural cell treatment.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 12 /note="Optional C-terminal amide"
 FT
 PN WO200213851-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022777.
 XX
 PR 17-AUG-2000; 2000WO-US022777.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I, Stanton JG, Hughes TK;
 XX
 DR WPI; 2002-269152/31.
 XX
 PT Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 7; Page 21; 37pp; English.
 XX
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 62; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00054;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LFFFLPVNVLP 12
 DB 1 LFFFLPVNVLP 12
 RESULT 6
 AAM51039

ID AAM51039 standard; peptide; 12 AA.
 XX AAM51039;
 AC
 XX
 XX
 DT 30-MAY-2002 (first entry)
 XX
 DE Colostriin constituent peptide.
 XX
 XX Colostriin; colostrum; immunomodulator; cardiovascular;
 KM blood cell regulator; cytokine inducer; beta-casein; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 12 /note="optional C-terminal amidation"
 FT
 XX
 PN WO200213849-A1.
 PD
 XX 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022775.
 XX
 PR 17-AUG-2000; 2000WO-US022775.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA (REGG-) REGEN THERAPEUTICS PLC.
 XX
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 PI WPI; 2002-269150/31.
 DR
 XX
 XX
 PT Modulation of blood cell proliferation in a patient involves use of blood
 PT cell regulator selected from colostriin, its constituent peptide and/or
 PT analog.
 PS
 XX Claim 1; Page 34; 54pp; English.
 XX
 XX The present sequence is that of a colostriin constituent peptide that is
 CC preferred for use as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified as having
 CC a beta-casein homologue precursor. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator, where the
 CC cell is present in a cell culture, a tissue, an organ or an organism, and
 CC the cell is mammalian, including human; modulating an immune response in
 CC a cell by contact with the immunological regulator under conditions
 CC effective to induce a cytokine; modulating an immune response in a
 CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator is
 CC administered topically or as part of a dietary supplement, and where the
 CC immune response is specific or non specific, an interferon response or an
 CC antibody response; modulating blood cell proliferation by contacting
 CC blood cells with a blood cell regulator, where the blood cells are
 CC present in a cell culture or an organism, are mammalian or human, and
 CC where the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patient. A claimed
 CC cytokine-inducing composition comprises a pharmaceutical carrier and an
 CC active agent such as the present peptide. Cytokines induced by this
 CC peptide in human leucocyte cultures include interferon-gamma, tumour
 CC necrosis factor-alpha, interleukin-6 and interleukin-10
 CC
 XX
 SQ Sequence 12 AA;
 XX
 XX
 Query Match 100.0%; Score 62; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00054;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LFFFLPVVNVLP 12
 |||||
 |||||
 DB 1 LFFFLPVVNVLP 12

RESULT 7

AAE20231
 ID AAE20231 standard; peptide; 12 AA.
 XX
 AC AAE20231;
 XX
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Colostriin constituent peptide #4.
 XX
 XX Blood cell regulator; colostriin; constituent peptide; oxidative stress;
 KM therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KM tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KM transplantation; implantation; dermatological; veterinary.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 12 /note="Optionally C-terminal amide"
 FT
 XX
 PN WO200213850-A1.
 PD
 XX 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022776.
 XX
 PR 17-AUG-2000; 2000WO-US022776.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Stanton GJ, Hughes TK, Boldogh I;
 PI WPI; 2002-269151/31.
 DR
 XX
 XX
 PT Composition useful for the modulation of blood cell proliferation in a
 PT patient comprising a blood cell regulator selected from colostriin, its
 PT constituent peptide and/or analog.
 PS
 XX Claim 6; Page 25; 51pp; English.
 XX
 XX The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostriin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress level
 CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
 CC organ, or organism; or for treating oxidative damage to the skin of a
 CC patient e.g. animal or human; to modulate oxidative stress during/ after
 CC a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostriin constituent peptide
 CC
 XX
 SQ Sequence 12 AA;
 XX
 XX
 Query Match 100.0%; Score 62; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00054;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LFFFLPVVNVLP 12
 |||||
 |||||
 DB 1 LFFFLPVVNVLP 12

RESULT 8
 ADN60298
 ID ADN60298 standard; peptide; 12 AA.


```

XX AC ADN60298;
XX XX
XX DT 29-JUL-2004 (first entry)
XX DE Constituent peptide of colostrinin SEQ ID NO:4.
XX XX
XX KW modulator; colostrinin; intracellular signaling molecule modulator;
XX KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibitor;
XX KW DNA damage; beta-amyloid; retinoic acid; cytoskeletal; 4HNE inhibitor;
XX KW 4HNE-protein adduct formation reduction;
XX KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;
XX KW c-Jun NH2-terminal Kinase inhibition.
XX OS
XX OS Synthetic.
XX PN WO2004037851-A2.
XX PD
XX PD 06-MAY-2004.
XX PF 22-OCT-2003; 2003WO-US033423.
XX PR 22-OCT-2002; 2002US-0420369P.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PA (BOLD/) BOLDOGH I.
XX PA (STAN/) STANTON J G.
XX PA (GEOR/) GEORGIADDES J A.
XX PA (HUGH/) HUGHES T K.
XX PA (KRUZ/) KRUZEL M.
XX PI Bolldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;
XX WPI; 2004-365494/34.
XX DR
XX PT Use of colostrinin for e.g. modulating an intracellular signaling
XX PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a
XX PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
XX PT a cell.
XX XX
XX PS Claim 6; SEQ ID NO 4; 46pp; English.
XX XX
XX CC The present invention describes the use of a modulator selected from
XX CC colostrinin, its constituent peptide, its active analogue, and a
XX CC combination of these, for modulating an intracellular signaling molecule
XX CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,
XX CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
XX CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
XX CC The modulator has cytoskeletal activity, and can be used as a 4HNE
XX CC inhibitor. The modulator is useful in the manufacture of a medicament for
XX CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated
XX CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,
XX CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.
XX CC Colostrinin, or its constituent peptide or active analogue is useful for
XX CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
XX CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
XX CC The present sequence represents a synthetic constituent peptide of
XX CC colostrinin, which can be used as a modulator in the present invention.
XX SQ
SQ Sequence 12 AA;

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Query Match 100.0%; Score 62; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LFFFLPVNVNLP 12
   |||||
Db 1 LFFFLPVNVNLP 12

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RESULT 9
ADS74399
ID ADS74399 standard; peptide; 12 AA.

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XX AC ADS74399;
XX XX
XX DT 16-DEC-2004 (first entry)
XX DE Ovine colostrinin peptide.
XX XX
XX KW Colostrum; colostrinin; sheep; peptide purification.
XX KW Ovis aries.
XX OS
XX OS WO2004081038-A1.
XX PN
XX PD 23-SEP-2004.
XX PF 10-MAR-2004; 2004WO-GB001014.
XX PR 11-MAR-2003; 2003GB-00005552.
XX PR 08-MAR-2004; 2004GB-00005190.
XX PA (REGE-) REGEN THERAPEUTICS PLC.
XX PA Georgiades JA, Polanowski A, Wilusz T, Kruzel ME;
XX WPI; 2004-677519/66.
XX DR
XX PT Recovering peptides such as colostrinin from mammalian colostrum, by
XX PT mixing colostrum with alcohol to form alcohol phase containing peptides
XX PT and precipitate, separating alcohol phase from precipitate, and
XX PT recovering alcohol phase.
XX XX
XX PS Example; SEQ ID NO 16; 41pp; English.
XX XX
XX CC The present sequence is that of a peptide that can be recovered from
XX CC ovine colostrinin using the method of the invention. The invention
XX CC provides a method for the recovery of peptides (especially colostrinin)
XX CC from colostrum in substantially pure, biologically active form and in
XX CC high yield. The method involves mixing the colostrum with an alcohol to
XX CC form an alcohol phase containing the colostrinin and a precipitate
XX CC containing higher molecular weight caseins and other proteins. Best
XX CC results are obtained using methanol or ethanol of at least 80%, and
XX CC preferably up to 100%, purity. The alcohol phase is then separated from
XX CC the precipitate, and the colostrinin is separated from the alcohol,
XX CC preferably by evaporation, to form a colostrinin-rich phase, which is
XX CC recovered. A precipitation agent, such as ammonium sulfate, may be added
XX CC either to the alcohol phase or, preferably, to the colostrinin-rich phase
XX CC to induce precipitation of the colostrinin peptides. The method is
XX CC generally applicable to the separation of peptides from fluids containing
XX CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic
XX CC acids. In an example from the invention, the antigenic profile of
XX CC peptides recovered from sheep colostrum using the alcohol precipitation
XX CC methods was determined by ELISA using antibodies prepared against 9
XX CC synthetic peptides, including a peptide having the present sequence
XX CC (denoted antigen class B-9).
XX XX
XX SQ
SQ Sequence 12 AA;

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Query Match 100.0%; Score 62; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LFFFLPVNVNLP 12
   |||||
Db 1 LFFFLPVNVNLP 12

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RESULT 10
AAB59353
ID AAB59353 standard; peptide; 14 AA.

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XX AC AAB59353;
XX XX
XX DT 21-MAR-2001 (first entry)

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XX DE Ewe colostrinin peptide fragment derived sequence #13.
XX PF
XX XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX XX
XX OS Ovis sp.
XX XX
XX PN WO20075173-A2.
XX XX
XX PD 14-DEC-2000.
XX XX
XX PF 02-JUN-2000; 2000WO-GB002128.
XX XX
XX PR 02-JUN-1999; 99GB-00012852.
XX XX
XX PA (REGG-) REGEN THERAPEUTICS PLC.
XX XX
XX PI Georgiades JA;
XX XX
XX DR WPI; 2001-071058/08.
XX XX
XX PT Peptides having an N-terminal amino acid sequence isolated from
XX PT colostrinin for treating e.g. disorders of the central nervous system and
XX PT immune system, viral and bacterial infections, and diseases characterized
XX PT by amyloid plaques.
XX XX
XX PS Claim 8; Page 27; 63pp; English.
XX XX
XX CC The present invention provides the sequences of a number of peptides
XX CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
XX CC fragment of colostrum. These peptides can be used in the treatment of
XX CC central nervous system disorders such as senile dementia, Parkinson's
XX CC disease, Alzheimer's disease, psychosis and neurosis, immune system
XX CC disorders such as bacterial and viral infections, to improve the
XX CC development of a child's immune system, as a dietary supplement, and to
XX CC promote the dissolution of beta-amyloid plaques
XX CC
XX SQ Sequence 14 AA;
XX XX
XX Query Match 100.0%; Score 62; DB 4; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0.00063;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LFFFLPVNVLP 12
XX |||||||||
XX 2 LFFFLPVNVLP 13
XX
XX DB
XX
XX RESULT 11
XX ID AAM96786
XX AC AAM96786 standard; peptide; 14 AA.
XX XX
XX AC AAM96786;
XX XX
XX DT 24-JAN-2002 (first entry)
XX XX
XX DE Human peptide #61 encoded by a SNP oligonucleotide.
XX XX
XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX KW complement related protein; cytochrome; kinesin; cytokine; interferon;
XX KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX KW multifactorial disease; autoimmune disease; infection;
XX KW nervous system disease.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200147944-A2.
XX XX
XX PD 05-JUL-2001.

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XX XX
XX XX 28-DEC-2000; 2000WO-US035498.
XX PF
XX XX 28-DEC-1999; 99US-0173419P.
XX PR 27-DEC-2000; 2000US-00173419.
XX XX
XX PA (CURA-) CURAGEN CORP.
XX XX
XX PI Shinkets RA, Leach M;
XX XX
XX DR WPI; 2001-465210/50.
XX XX
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX PT autoimmune diseases and infections.
XX XX
XX PS Disclosure; Page 3681; 4143pp; English.
XX XX
XX CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
XX CC encoding polymorphic variants of proteins related to amylases, amyloid
XX CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
XX CC polymerase, oncogene, histones, kinases, colony stimulating factors,
XX CC complement related proteins, cytochromes, kinesins, cytokines,
XX CC interferons, interleukins, G-protein coupled receptors and thioesterases.
XX CC The present sequence is a peptide encoded by one such oligonucleotide.
XX CC The oligonucleotides and the peptides encoded by them may be used in the
XX CC prevention, diagnosis and treatment of diseases associated with
XX CC inappropriate expression of the proteins listed above. Disorders that may
XX CC be prevented, diagnosed and/or treated include multifactorial diseases
XX CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
XX CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
XX CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
XX CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
XX CC system and an infection of pathogenic organisms
XX CC
XX SQ Sequence 14 AA;
XX XX
XX Query Match 56.5%; Score 35; DB 4; Length 14;
XX Best Local Similarity 66.7%; Pred. No. 30;
XX Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 2 FFFLPVNVN 10
XX |::|||
XX 2 FFFLPVNVN 10
XX
XX DB
XX
XX RESULT 12
XX ID AAY21194
XX AC AAY21194 standard; protein; 9 AA.
XX XX
XX AC AAY21194;
XX XX
XX DT 22-JUL-1999 (first entry)
XX XX
XX DE Human bcl2 proto-oncogene mutant protein fragment 42.
XX XX
XX KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
XX KW frameshift mutation; age-related disease; neurodegenerative disorder;
XX KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
XX KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
XX KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
XX KW ubiquitin B; apolipoprotein B; MAP2; neurofilament-L; neurofilament-M;
XX KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
XX KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
XX KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
XX KW high mobility group protein-C; neuroendocrine specific protein A.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX PN WO9845322-A2.
XX XX
XX PD 15-OCT-1998.

```

XX 02-APR-1998; 98WO-1B000705.
 PF 10-APR-1997; 97US-0043163P.
 XX
 PR
 XX
 PA (ROYA-) ROYAL NETHERLANDS ACADEMY OF SCI.
 PA (UYUO-) UNIV ROTTERDAM ERASMUS.
 PA (UYUT-) RIJKSUNIV UTRECHT.
 XX
 PI Van Leeuwen FM, Grosveld FG, Burbach JPH;
 DR WPI, 1998-609901/51.
 DR N-PSDB; AAX75766.
 XX
 PT Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also for
 PT treatment and prevention with specific ribozymes or wild-type RNA.
 PS Disclosure, Fig 15; 258pp; English.
 XX
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-ApP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein B, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin 1, presenilin 2, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HMPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A
 CC
 XX
 SQ Sequence 9 AA;
 Query Match 53.2%; Score 33; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FFFFLPV 7
 DB 4 FFFFLPV 9
 RESULT 13
 ID ADR84035 standard; peptide; 9 AA.
 AC ADR84035;
 DT 20-MAY-2004 (first entry)
 DE Human 191PAD12(b) peptide fragment #736.
 XX
 KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191PAD12(b); cancer;
 KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
 KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
 KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
 KW Suppression Subtractive Hybridisation; SSH.
 XX
 OS Homo sapiens.
 XX
 PN WO2004016799-A2.
 XX
 PD 26-FEB-2004.
 XX

PF 23-APR-2003; 2003WO-US013013.
 XX
 PR 16-AUG-2002; 2002US-0404306P.
 PR 01-NOV-2002; 2002US-0423290P.
 XX
 PA (AGEN-) AGENSYS INC.
 PA Raitano AB, Challita-Bid PM, Jakobovits A, Faris M, Ge W;
 PI WPI, 2004-203808/19.
 DR
 XX
 PT New composition comprising 191PAD12(b) proteins and polynucleotides,
 PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
 PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
 PT humoral or cellular immune response.
 XX
 PS Claim 1; Page 149; 443pp; English.
 XX
 CC The present invention relates to novel compositions comprising peptides
 CC (ADR83300-ADR90584) from 191PAD12(b) and related proteins. It was found
 CC that 191PAD12(b), which maps to chromosome 1q22-q23.2, is aberrantly
 CC expressed in a number of cancers and so the compositions of the invention
 CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
 CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
 CC uterus or cervix and in eliciting a humoral or cellular immune response.
 CC To isolate genes that are overexpressed in prostate cancer, the
 CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
 CC derived from prostate cancer tissues.
 CC
 XX
 SQ Sequence 9 AA;
 Query Match 53.2%; Score 33; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LFFFLPV 6
 DB 4 LFFFLPV 9
 RESULT 14
 ID ADR84519 standard; peptide; 9 AA.
 AC ADR84519;
 DT 20-MAY-2004 (first entry)
 DE Human 191PAD12(b) peptide fragment #1220.
 XX
 KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191PAD12(b); cancer;
 KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
 KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
 KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
 KW Suppression Subtractive Hybridisation; SSH.
 XX
 OS Homo sapiens.
 XX
 PN WO2004016799-A2.
 XX
 PD 26-FEB-2004.
 XX
 PF 23-APR-2003; 2003WO-US013013.
 PR 16-AUG-2002; 2002US-0404306P.
 PR 01-NOV-2002; 2002US-0423290P.
 XX
 PA (AGEN-) AGENSYS INC.
 PA Raitano AB, Challita-Bid PM, Jakobovits A, Faris M, Ge W;
 PI WPI, 2004-203808/19.
 DR

PT New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.

PS Claim 1; Page 155; 443pp; English.

XX The present invention relates to novel compositions comprising peptides
XX (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.

XX Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LFFFLP 6
|||
3 LFFFLP 8

RESULT 15
ADK85026
ID ADK85026 standard; peptide; 9 AA.

AC ADK85026;

DT 20-MAY-2004 (first entry)

DE Human 191P4D12(b) peptide fragment #1727.

XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KM prostate cancer; bladder cancer; kidney cancer; colon cancer;
KM lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KM cervix cancer; immune response; human; chromosome 1q22-q23.2;
KM Suppression Subtractive Hybridisation; SSH.

OS Homo sapiens.

PN WO2004016799-A2.

PD 26-FEB-2004.

PF 23-APR-2003; 2003WO-US013013.

PR 16-AUG-2002; 2002US-0404306P.

PR 01-NOV-2002; 2002US-0423290P.

PS (AGEN-) AGENSYS INC.

PI Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
DR WPI; 2004-203808/19.

XX The present invention relates to novel compositions comprising peptides
XX expressed in a number of cancers and so the compositions of the invention
XX are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX uterus or cervix and in eliciting a humoral or cellular immune response.

PS Claim 1; Page 161; 443pp; English.

XX The present invention relates to novel compositions comprising peptides
XX (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention

CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.

XX Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LFFFLP 6
|||
1 LFFFLP 6

RESULT 16
ADK85074
ID ADK85074 standard; peptide; 9 AA.

AC ADK85074;

DT 20-MAY-2004 (first entry)

DE Human 191P4D12(b) peptide fragment #1725.

XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KM prostate cancer; bladder cancer; kidney cancer; colon cancer;
KM lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KM cervix cancer; immune response; human; chromosome 1q22-q23.2;
KM Suppression Subtractive Hybridisation; SSH.

OS Homo sapiens.

PN WO2004016799-A2.

PD 26-FEB-2004.

PF 23-APR-2003; 2003WO-US013013.

PR 16-AUG-2002; 2002US-0404306P.

PR 01-NOV-2002; 2002US-0423290P.

PS (AGEN-) AGENSYS INC.

PI Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
DR WPI; 2004-203808/19.

XX The present invention relates to novel compositions comprising peptides
XX expressed in a number of cancers and so the compositions of the invention
XX are useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX humoral or cellular immune response.

PS Claim 1; Page 162; 443pp; English.

XX The present invention relates to novel compositions comprising peptides
XX (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.

XX Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;

```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LFFFLP 6
   |||||
Db 4 LFFFLP 9

RESULT 17
ADK87550
ID ADK87550 standard; peptide; 9 AA.
AC ADK87550;
XX
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX
DE Human 191P4D12(b) peptide fragment #4251.
XX
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.
XX
XX
XX Homo sapiens.
OS
XX
XX WO2004016799-A2.
XX
XX 26-FEB-2004.
XX
XX 23-APR-2003; 2003WO-US013013.
XX
XX 16-AUG-2002; 2002US-0404306P.
XX
XX 01-NOV-2002; 2002US-0423290P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Raitano AB, Challita-Bid PM, Jakobovits A, Paris M, Ge W;
XX
XX WPI; 2004-203808/19.
XX
XX New composition comprising 191P4D12(b) proteins and polynucleotides,
XX useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX humoral or cellular immune response.
XX
XX Claim 1; Page 192; 443pp; English.
XX
XX The present invention relates to novel compositions comprising peptides
XX (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
XX that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
XX expressed in a number of cancers and so the compositions of the invention
XX are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX uterus or cervix and in eliciting a humoral or cellular immune response.
XX To isolate genes that are overexpressed in prostate cancer, the
XX Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
XX derived from prostate cancer tissues.
XX
XX Sequence 9 AA;
SQ
Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LFFFLP 6
   |||||
Db 1 LFFFLP 6

RESULT 18
ADK88447
ID ADK88447 standard; peptide; 9 AA.
XX

```

```

AC ADK88447;
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human 191P4D12(b) peptide fragment #5148.
XX
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.
XX
XX
XX Homo sapiens.
OS
XX
XX WO2004016799-A2.
XX
XX 26-FEB-2004.
XX
XX 23-APR-2003; 2003WO-US013013.
XX
XX 16-AUG-2002; 2002US-0404306P.
XX
XX 01-NOV-2002; 2002US-0423290P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Raitano AB, Challita-Bid PM, Jakobovits A, Paris M, Ge W;
XX
XX WPI; 2004-203808/19.
XX
XX New composition comprising 191P4D12(b) proteins and polynucleotides,
XX useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX humoral or cellular immune response.
XX
XX Claim 1; Page 204; 443pp; English.
XX
XX The present invention relates to novel compositions comprising peptides
XX (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
XX that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
XX expressed in a number of cancers and so the compositions of the invention
XX are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX uterus or cervix and in eliciting a humoral or cellular immune response.
XX To isolate genes that are overexpressed in prostate cancer, the
XX Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
XX derived from prostate cancer tissues.
XX
XX Sequence 9 AA;
SQ
Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LFFFLP 6
   |||||
Db 1 LFFFLP 6

RESULT 19
ADK84560
ID ADK84560 standard; peptide; 9 AA.
XX
XX ADK84560;
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human 191P4D12(b) peptide fragment #1261.
XX
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.
XX

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XX OS Homo sapiens.
XX PN WO2004016799-A2.
XX PD 26-FEB-2004.
XX PF 23-APR-2003; 2003WO-US013013.
XX PR 16-AUG-2002; 2002US-0404306P.
XX PR 01-NOV-2002; 2002US-0423290P.
XX PA (AGEN-) AGENSYS INC.
XX PI Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
XX DR WPI; 2004-203808/19.
XX CC The present invention relates to novel compositions comprising peptides
XX CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
XX CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
XX CC expressed in a number of cancers and so the compositions of the invention
XX CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX CC uterus or cervix and in eliciting a humoral or cellular immune response.
XX CC To isolate genes that are overexpressed in prostate cancer, the
XX CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
XX CC derived from prostate cancer tissues.
XX SQ Sequence 9 AA;
XX
XX Query Match          53.2%; Score 33; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LFFFLP 6
XX      |||||
XX DB 4 LFFFLP 9
XX
XX RESULT 20
XX ADK85620
XX ID ADK85620 standard; peptide; 9 AA.
XX AC ADK85620;
XX XX
XX DT 20-MAY-2004 (first entry)
XX DE Human 191P4D12(b) peptide fragment #2321.
XX XX
XX KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX KW Suppression Subtractive Hybridisation; SSH.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO2004016799-A2.
XX PD 26-FEB-2004.
XX PF 23-APR-2003; 2003WO-US013013.
XX PR 16-AUG-2002; 2002US-0404306P.
XX PR 01-NOV-2002; 2002US-0423290P.

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XX PA (AGEN-) AGENSYS INC.
XX XX
XX PI Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
XX XX
XX DR WPI; 2004-203808/19.
XX CC The present invention relates to novel compositions comprising peptides
XX CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
XX CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
XX CC expressed in a number of cancers and so the compositions of the invention
XX CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX CC uterus or cervix and in eliciting a humoral or cellular immune response.
XX CC To isolate genes that are overexpressed in prostate cancer, the
XX CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
XX CC derived from prostate cancer tissues.
XX SQ Sequence 9 AA;
XX
XX Query Match          53.2%; Score 33; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LFFFLP 6
XX      |||||
XX DB 4 LFFFLP 9
XX
XX RESULT 21
XX ADK86086
XX ID ADK86086 standard; peptide; 9 AA.
XX AC ADK86086;
XX XX
XX DT 20-MAY-2004 (first entry)
XX DE Human 191P4D12(b) peptide fragment #2787.
XX XX
XX KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX KW Suppression Subtractive Hybridisation; SSH.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO2004016799-A2.
XX PD 26-FEB-2004.
XX PF 23-APR-2003; 2003WO-US013013.
XX PR 16-AUG-2002; 2002US-0404306P.
XX PR 01-NOV-2002; 2002US-0423290P.
XX PA (AGEN-) AGENSYS INC.
XX XX
XX PI Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
XX XX
XX DR WPI; 2004-203808/19.
XX CC New composition comprising 191P4D12(b) proteins and polynucleotides,
XX CC useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX CC bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX CC humoral or cellular immune response.
XX PS Claim 1; Page 168; 443pp; English.
XX XX
XX CC The present invention relates to novel compositions comprising peptides
XX CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
XX CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
XX CC expressed in a number of cancers and so the compositions of the invention
XX CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX CC uterus or cervix and in eliciting a humoral or cellular immune response.
XX CC To isolate genes that are overexpressed in prostate cancer, the
XX CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
XX CC derived from prostate cancer tissues.

```


Db 3 LFFFLP 8

RESULT 24
ADK86146
ID ADK86146 standard; peptide; 9 AA.
XX
AC ADK86146;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human 191P4D12(b) peptide fragment #2847.
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
KW Suppression Subtractive Hybridisation; SSH.
XX
OS Homo sapiens.
XX
PN WO2004016799-A2.
XX
PD 26-FEB-2004.
XX
PF 23-APR-2003; 2003WO-US013013.
XX
PR 16-AUG-2002; 2002US-0404306P.
XX
PR 01-NOV-2002; 2002US-0423290P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Raitano AB, Challita-Bid PM, Jakobovits A, Faris M, Ge W;
XX
DR MPI; 2004-203808/19.
XX
DT MPI; 2004-203808/19.
XX
PT New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.
XX
PS Claim 1; Page 174; 443pp; English.
XX
XX The present invention relates to novel compositions comprising peptides
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.
XX
SQ Sequence 9 AA;
XX

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6
XX |||||
XX
DB 2 LFFFLP 7
XX

RESULT 25
ADK86653
ID ADK86653 standard; peptide; 9 AA.
XX
AC ADK86653;
XX
DT 20-MAY-2004 (first entry)
XX

DE Human 191P4D12(b) peptide fragment #3354.
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
KW Suppression Subtractive Hybridisation; SSH.
XX
OS Homo sapiens.
XX
PN WO2004016799-A2.
XX
PD 26-FEB-2004.
XX
PF 23-APR-2003; 2003WO-US013013.
XX
PR 16-AUG-2002; 2002US-0404306P.
XX
PR 01-NOV-2002; 2002US-0423290P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Raitano AB, Challita-Bid PM, Jakobovits A, Faris M, Ge W;
XX
DR MPI; 2004-203808/19.
XX
DT MPI; 2004-203808/19.
XX
PT New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.
XX
PS Claim 1; Page 180; 443pp; English.
XX
XX The present invention relates to novel compositions comprising peptides
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.
XX
SQ Sequence 9 AA;
XX

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6
XX |||||
XX
DB 3 LFFFLP 8
XX

RESULT 26
ADK83459
ID ADK83459 standard; peptide; 9 AA.
XX
AC ADK83459;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human 191P4D12(b) peptide fragment #160.
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
KW Suppression Subtractive Hybridisation; SSH.
XX
OS Homo sapiens.
XX
PN WO2004016799-A2.

XX 26-FEB-2004.
PD 23-APR-2003; 2003WO-US013013.
XX
PF 16-AUG-2002; 2002US-0404306P.
XX PR 01-NOV-2002; 2002US-0423290P.
XX
XX (AGEN-) AGENSYS INC.
XX
PI Raitano AB, Challita-Bid PM, Jakobovits A, Faris M, Ge W;
XX WPI; 2004-203808/19.
DR
XX
XX New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.
XX
XX Claim 1; Page 142; 443pp; English.
XX
XX The present invention relates to novel compositions comprising peptides
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.
XX
XX Sequence 9 AA;
SQ

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6
XX |||||
XX 3 LFFFLP 8
DB

RESULT 27
ADK85080
ID ADK85080 standard; peptide; 9 AA.
XX
XX ADR85080;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human 191P4D12(b) peptide fragment #1781.
DE
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
KW Suppression Subtractive Hybridisation; SSH.
XX
XX Homo sapiens.
OS
XX
XX WO2004016799-A2.
PN
XX
XX 26-FEB-2004.
PD
XX
XX 23-APR-2003; 2003WO-US013013.
PF
XX 16-AUG-2002; 2002US-0404306P.
PR
XX 01-NOV-2002; 2002US-0423290P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX Raitano AB, Challita-Bid PM, Jakobovits A, Faris M, Ge W;
PI

XX WPI; 2004-203808/19.
DR
XX
XX New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.
XX
XX Claim 1; Page 162; 443pp; English.
XX

XX The present invention relates to novel compositions comprising peptides
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.
XX

SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6
XX |||||
XX 2 LFFFLP 7
DB

RESULT 28
ADK86684
ID ADK86684 standard; peptide; 9 AA.
XX
XX ADR86684;
AC
XX
XX 20-MAY-2004 (first entry)
DT

XX Human 191P4D12(b) peptide fragment #3385.
DE
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
KW Suppression Subtractive Hybridisation; SSH.
XX
XX Homo sapiens.
OS
XX
XX WO2004016799-A2.
PN
XX
XX 26-FEB-2004.
PD
XX
XX 23-APR-2003; 2003WO-US013013.
PF

XX 16-AUG-2002; 2002US-0404306P.
PR
XX 01-NOV-2002; 2002US-0423290P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX
XX Raitano AB, Challita-Bid PM, Jakobovits A, Faris M, Ge W;
PI

XX WPI; 2004-203808/19.
DR
XX
XX New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.
XX
XX Claim 1; Page 180; 443pp; English.
XX

XX The present invention relates to novel compositions comprising peptides
CC

CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.

XX
XX
SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6
|||
2 LFFFLP 7

DB

RESULT 29
ADK87195
ID ADK87195 standard; peptide; 9 AA.

XX ADR87195;

XX 20-MAY-2004 (first entry)

XX Human 191P4D12(b) peptide fragment #3896.

XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.

XX Homo sapiens.

XX WO2004016799-A2.

XX 26-FEB-2004.

XX 23-APR-2003; 2003WO-US013013.

XX 16-AUG-2002; 2002US-0404306P.

XX 01-NOV-2002; 2002US-0423290P.

XX (AGEN-) AGENSYS INC.

XX Raitano AB, Challita-Bid PM, Jakobovits A, Paris M, Ge W;

XX MPI; 2004-203808/19.

XX New composition comprising 191P4D12(b) proteins and polynucleotides,
XX useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX humoral or cellular immune response.

XX Claim 1; Page 187; 443pp; English.

XX The present invention relates to novel compositions comprising peptides
XX (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
XX that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
XX expressed in a number of cancers and so the compositions of the invention
XX are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX uterus or cervix and in eliciting a humoral or cellular immune response.
XX To isolate genes that are overexpressed in prostate cancer, the
XX Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
XX derived from prostate cancer tissues.

XX Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6
|||
2 LFFFLP 7

DB

RESULT 30
ADK84539
ID ADK84539 standard; peptide; 9 AA.

XX ADR84539;

XX 20-MAY-2004 (first entry)

XX Human 191P4D12(b) peptide fragment #1240.

XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.

XX Homo sapiens.

XX WO2004016799-A2.

XX 26-FEB-2004.

XX 23-APR-2003; 2003WO-US013013.

XX 16-AUG-2002; 2002US-0404306P.

XX 01-NOV-2002; 2002US-0423290P.

XX (AGEN-) AGENSYS INC.

XX Raitano AB, Challita-Bid PM, Jakobovits A, Paris M, Ge W;

XX MPI; 2004-203808/19.

XX New composition comprising 191P4D12(b) proteins and polynucleotides,
XX useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX humoral or cellular immune response.

XX Claim 1; Page 155; 443pp; English.

XX The present invention relates to novel compositions comprising peptides
XX (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
XX that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
XX expressed in a number of cancers and so the compositions of the invention
XX are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX uterus or cervix and in eliciting a humoral or cellular immune response.
XX To isolate genes that are overexpressed in prostate cancer, the
XX Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
XX derived from prostate cancer tissues.

XX Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6
|||
1 LFFFLP 6

DB

RESULT 31

ADK88123
ID ADK88123 standard; peptide; 9 AA.
XX
AC ADK88123;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human 191P4D12(b) peptide fragment #4824.
XX
KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
KW Suppression Subtractive Hybridisation; SSH.
XX
OS Homo sapiens.
XX
PN WO2004016799-A2.
XX
PD 26-FEB-2004.
XX
PF 23-APR-2003; 2003WO-US013013.
XX
PR 16-AUG-2002; 2002US-0404306P.
PR 01-NOV-2002; 2002US-0423290P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Raitano AB, Challita-Bid PM, Jakobovits A, Faris M, Ge W;
XX
DR WPI; 2004-203808/19.
XX
PT New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.
XX
PS Claim 1; Page 200; 443pp; English.
XX
SQ The present invention relates to novel compositions comprising peptides
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.
XX
SQ Sequence 9 AA:
XX
Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 LFFFLP 6
XX
DB 1 LFFFLP 6
XX
RESULT 32
ADK88312
ID ADK88312 standard; peptide; 9 AA.
XX
AC ADK88312;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human 191P4D12(b) peptide fragment #5013.
XX
KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;

KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
KW Suppression Subtractive Hybridisation; SSH.
XX
OS Homo sapiens.
XX
PN WO2004016799-A2.
XX
PD 26-FEB-2004.
XX
PF 23-APR-2003; 2003WO-US013013.
XX
PR 16-AUG-2002; 2002US-0404306P.
PR 01-NOV-2002; 2002US-0423290P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Raitano AB, Challita-Bid PM, Jakobovits A, Faris M, Ge W;
XX
DR WPI; 2004-203808/19.
XX
PT New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.
XX
PS Claim 1; Page 202; 443pp; English.
XX
SQ The present invention relates to novel compositions comprising peptides
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.
XX
SQ Sequence 9 AA:
XX
Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 LFFFLP 6
XX
DB 1 LFFFLP 6
XX
RESULT 33
ADK88446
ID ADK88446 standard; peptide; 9 AA.
XX
AC ADK88446;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human 191P4D12(b) peptide fragment #5147.
XX
KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
KW Suppression Subtractive Hybridisation; SSH.
XX
OS Homo sapiens.
XX
PN WO2004016799-A2.
XX
PD 26-FEB-2004.
XX
PF 23-APR-2003; 2003WO-US013013.

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XX 16-AUG-2002; 2002US-0404306P.  
PR 01-NOV-2002; 2002US-0423290P.  
XX  
XX (AGEN-) AGENSYS INC.  
XX  
XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;  
XX WPI; 2004-203808/19.  
XX  
XX  
XX New composition comprising 191P4D12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.  
XX  
XX  
XX Claim 1; Page 204; 443pp; English.  
XX  
XX The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.  
XX  
XX  
XX Sequence 9 AA;  
SQ  
XX  
XX Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LFFFLP 6  
DB 3 LFFFLP 8  
XX  
XX  
XX RESULT 34  
ADK83504  
ID ADK83504 standard; peptide; 9 AA.  
XX  
XX ADRK3504;  
AC  
XX  
XX 20-MAY-2004 (first entry)  
DT  
XX  
XX Human 191P4D12(b) peptide fragment #205.  
DE  
XX  
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;  
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;  
KW Suppression Subtractive Hybridisation; SSH.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004016799-A2.  
PN  
XX  
XX 26-FEB-2004.  
PD  
XX  
XX 23-APR-2003; 2003WO-US013013.  
PF  
XX  
XX 16-AUG-2002; 2002US-0404306P.  
PR  
XX  
XX 01-NOV-2002; 2002US-0423290P.  
PR  
XX  
XX (AGEN-) AGENSYS INC.  
PA  
XX  
XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;  
PI WPI; 2004-203808/19.  
XX  
XX New composition comprising 191P4D12(b) proteins and polynucleotides,  
PT
```

```
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.  
XX  
XX  
XX Claim 1; Page 143; 443pp; English.  
XX  
XX The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.  
XX  
XX  
XX Sequence 9 AA;  
SQ  
XX  
XX Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LFFFLP 6  
DB 2 LFFFLP 7  
XX  
XX  
XX RESULT 35  
ADK83957  
ID ADK83957 standard; peptide; 9 AA.  
XX  
XX ADRK3957;  
AC  
XX  
XX 20-MAY-2004 (first entry)  
DT  
XX  
XX Human 191P4D12(b) peptide fragment #658.  
DE  
XX  
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;  
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;  
KW Suppression Subtractive Hybridisation; SSH.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004016799-A2.  
PN  
XX  
XX 26-FEB-2004.  
PD  
XX  
XX 23-APR-2003; 2003WO-US013013.  
PF  
XX  
XX 16-AUG-2002; 2002US-0404306P.  
PR  
XX  
XX 01-NOV-2002; 2002US-0423290P.  
PR  
XX  
XX (AGEN-) AGENSYS INC.  
PA  
XX  
XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;  
PI WPI; 2004-203808/19.  
XX  
XX New composition comprising 191P4D12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.  
XX  
XX  
XX Claim 1; Page 148; 443pp; English.  
XX  
XX The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
```

CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.
XX

SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6
 |||||
 2 LFFFLP 7

RESULT 36
ADK87688
ID ADK87688 standard; peptide; 9 AA.
XX
XX ADK87688;
AC
XX 20-MAY-2004 (first entry)
DT
XX
XX Human 191P4D12(b) peptide fragment #4389.
DE

KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
KW Suppression Subtractive Hybridisation; SSH.
XX
XX Homo sapiens.
OS

XX WO2004016799-A2.
XX

XX 26-FEB-2004.
XX

XX 23-APR-2003; 2003WO-US013013.
XX

XX 16-AUG-2002; 2002US-0404306P.
XX

XX 01-NOV-2002; 2002US-0423290P.
XX

XX (AGEN-) AGENSYS INC.
XX

XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
XX

XX WPI; 2004-203808/19.
XX

XX New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.
XX

XX Claim 1; Page 194; 443pp; English.
XX

XX The present invention relates to novel compositions comprising peptides
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.
XX

SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6
 |||||
 3 LFFFLP 8

RESULT 37
ADK87898
ID ADK87898 standard; peptide; 9 AA.
XX
XX ADK87898;
AC

XX 20-MAY-2004 (first entry)
DT

XX Human 191P4D12(b) peptide fragment #4599.
DE

KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
KW Suppression Subtractive Hybridisation; SSH.
XX
XX Homo sapiens.
OS

XX WO2004016799-A2.
XX

XX 26-FEB-2004.
XX

XX 23-APR-2003; 2003WO-US013013.
XX

XX 16-AUG-2002; 2002US-0404306P.
XX

XX 01-NOV-2002; 2002US-0423290P.
XX

XX (AGEN-) AGENSYS INC.
XX

XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
XX

XX WPI; 2004-203808/19.
XX

XX New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.
XX

XX Claim 1; Page 197; 443pp; English.
XX

XX The present invention relates to novel compositions comprising peptides
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.
XX

SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6
 |||||
 1 LFFFLP 6

RESULT 38
ADK83493
ID ADK83493 standard; peptide; 9 AA.
XX
XX ADK83493;
AC

```

XX 20-MAY-2004 (first entry)
DT
XX
XX Human 191P4D12(b) peptide fragment #194.
DE
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.
XX
XX Homo sapiens.
OS
XX
XX WO2004016799-A2.
PN
XX
XX 26-FEB-2004.
PD
XX
XX 23-APR-2003; 2003WO-US013013.
PF
XX 16-AUG-2002; 2002US-0404306P.
XX PR 01-NOV-2002; 2002US-0423290P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX
XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
PI
XX WPI; 2004-203808/19.
DR
XX
XX New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.
XX
XX Claim 1; Page 142; 443pp; English.
PS
XX
XX The present invention relates to novel compositions comprising peptides
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.
XX
XX Sequence 9 AA:
SQ
XX
XX Query Match 53.2%; Score 33; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LFFFLP 6
XX |||||
DB 1 LFFFLP 6
XX
XX
XX RESULT 39
XX ADK84019
XX ID ADK84019 standard; peptide; 9 AA.
XX
XX
XX ADK84019;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human 191P4D12(b) peptide fragment #720.
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.
XX

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OS Homo sapiens.
XX
XX WO2004016799-A2.
XX
XX 26-FEB-2004.
XX
XX 23-APR-2003; 2003WO-US013013.
XX
XX 16-AUG-2002; 2002US-0404306P.
XX PR 01-NOV-2002; 2002US-0423290P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX
XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
PI
XX WPI; 2004-203808/19.
DR
XX
XX New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.
XX
XX Claim 1; Page 149; 443pp; English.
PS
XX
XX The present invention relates to novel compositions comprising peptides
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.
XX
XX Sequence 9 AA:
SQ
XX
XX Query Match 53.2%; Score 33; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LFFFLP 6
XX |||||
DB 3 LFFFLP 8
XX
XX
XX RESULT 40
XX ADK83977
XX ID ADK83977 standard; peptide; 9 AA.
XX
XX
XX ADK83977;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human 191P4D12(b) peptide fragment #678.
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.
XX
XX Homo sapiens.
OS
XX
XX WO2004016799-A2.
PN
XX
XX 26-FEB-2004.
PD
XX
XX 23-APR-2003; 2003WO-US013013.
XX
XX 16-AUG-2002; 2002US-0404306P.
XX PR 01-NOV-2002; 2002US-0423290P.
XX

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PA (AGEN-) AGENSYS INC.
XX
XX
PI Raitano AB, Challita-Eld PM, Jakobovits A, Faris M, Ge W;
XX
DR WPI; 2004-203808/19.
XX
XX New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.
XX
PS Claim 1; Page 149; 443pp; English.
XX
XX The present invention relates to novel compositions comprising peptides
CC (ADK83100-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues.
XX
SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LFFFLP 6
DB 1 LFFFLP 6

Search completed: June 7, 2005, 23:10:47
Job time : 66.5818 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:57:32 ; Search time 16.3636 Seconds
(without alignments)
54.743 Million cell updates/sec

Title: US-10-691-157-4
Perfect score: 62
Sequence: 1 LFFFLPVNVLP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 183464

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6CTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	12	4	US-09-641-803-4
2	29	46.8	11	2	US-08-464-531-57
3	29	46.8	11	2	US-08-461-598-57
4	29	46.8	11	3	US-08-322-137-57
5	29	46.8	11	3	US-08-582-333A-68
6	28	45.2	8	2	US-08-508-664-20
7	27	43.5	18	6	5185441-4
8	27	43.5	18	6	5185441-4
9	26	41.9	5	2	US-08-920-162A-30
10	26	41.9	5	2	US-09-356-931-30
11	26	41.9	5	4	US-09-895-443A-30
12	26	41.9	10	3	US-09-328-501-7
13	26	41.9	10	4	US-09-777-710A-7
14	26	41.9	16	4	US-09-009-953-15
15	25	40.3	10	3	US-08-159-339A-1023
16	25	40.3	13	2	US-08-194-981B-16
17	25	40.3	17	3	US-09-177-249-88
18	25	40.3	17	4	US-09-812-283-88
19	25	40.3	18	3	US-08-482-918-94
20	25	40.3	18	3	US-08-482-918-95
21	25	40.3	18	3	US-09-224-681-94
22	25	40.3	18	3	US-09-224-681-95
23	25	40.3	18	3	US-08-336-728A-94
24	25	40.3	18	3	US-08-336-728A-95
25	25	40.3	18	4	US-09-635-251-94
26	25	40.3	18	4	US-09-635-251-95
27	25	40.3	18	4	US-09-471-276-1473

28	24	38.7	7	3	US-09-103-478-5	Sequence 5, Appl
29	24	38.7	7	3	US-09-103-478-17	Sequence 17, Appl
30	24	38.7	7	3	US-09-193-931C-5	Sequence 5, Appl
31	24	38.7	7	3	US-09-193-931C-17	Sequence 17, Appl
32	24	38.7	7	4	US-09-026-221-5	Sequence 5, Appl
33	24	38.7	7	4	US-09-026-221-17	Sequence 17, Appl
34	24	38.7	7	4	US-09-516-052-17	Sequence 17, Appl
35	24	38.7	7	4	US-09-516-052-17	Sequence 17, Appl
36	24	38.7	9	2	US-08-934-222-106	Sequence 106, App
37	24	38.7	9	2	US-08-934-222-106	Sequence 106, App
38	24	38.7	9	2	US-09-933-402-106	Sequence 106, App
39	24	38.7	9	2	US-09-207-621-106	Sequence 106, App
40	24	38.7	9	2	US-08-532-818-106	Sequence 106, App
41	24	38.7	9	3	US-09-231-797-106	Sequence 106, App
42	24	38.7	9	3	US-08-934-224-106	Sequence 106, App
43	24	38.7	9	3	US-08-933-843-106	Sequence 106, App
44	24	38.7	9	3	US-08-934-223-106	Sequence 106, App
45	24	38.7	12	4	US-10-118-575A-7	Sequence 7, Appl
46	24	38.7	13	5	PCT-US94-10257A-16	Sequence 16, Appl
47	24	38.7	16	3	US-08-213-419B-7	Sequence 7, Appl
48	23	37.1	5	3	US-08-812-586-25	Sequence 25, Appl
49	23	37.1	5	3	US-08-812-586-35	Sequence 35, Appl
50	23	37.1	5	4	US-09-535-832A-26	Sequence 26, Appl
51	23	37.1	7	2	US-08-559-492-10	Sequence 10, Appl
52	23	37.1	8	3	US-09-171-337A-17	Sequence 17, Appl
53	23	37.1	8	4	US-09-631-022-17	Sequence 17, Appl
54	23	37.1	8	4	US-08-979-847B-150	Sequence 150, App
55	23	37.1	8	4	US-08-979-847B-151	Sequence 151, App
56	23	37.1	8	4	US-08-979-847B-152	Sequence 152, App
57	23	37.1	9	3	US-08-159-339A-1217	Sequence 1217, App
58	23	37.1	9	3	US-08-159-339A-1218	Sequence 1218, App
59	23	37.1	9	3	US-09-492-543-149	Sequence 149, App
60	23	37.1	9	3	US-09-492-543-159	Sequence 159, App
61	23	37.1	9	4	US-09-527-487-5	Sequence 5, Appl
62	23	37.1	9	4	US-09-239-043D-402	Sequence 402, App
63	23	37.1	9	4	US-09-462-453-20	Sequence 20, Appl
64	23	37.1	10	3	US-08-159-339A-1219	Sequence 1219, App
65	23	37.1	10	4	US-09-239-043D-403	Sequence 403, App
66	23	37.1	11	2	US-08-508-664-13	Sequence 13, Appl
67	23	37.1	11	4	US-09-239-043D-366	Sequence 366, App
68	23	37.1	11	4	US-09-239-043D-404	Sequence 404, App
69	23	37.1	11	4	US-09-239-043D-1657	Sequence 1657, App
70	23	37.1	14	3	US-09-082-420-16	Sequence 16, Appl
71	23	37.1	15	3	US-08-159-339A-1215	Sequence 1215, App
72	23	37.1	15	4	US-09-009-953-176	Sequence 176, App
73	23	37.1	15	4	US-09-148-545-224	Sequence 224, App
74	23	37.1	15	4	US-09-947-372A-28	Sequence 28, Appl
75	23	37.1	15	4	US-09-239-043D-2151	Sequence 2151, App
76	23	37.1	15	4	US-09-563-222C-63	Sequence 63, Appl
77	23	37.1	15	5	PCT-US93-06751-86	Sequence 86, Appl
78	23	37.1	16	4	US-09-009-953-25	Sequence 25, Appl
79	23	37.1	17	4	US-09-148-545-221	Sequence 221, App
80	23	37.1	18	1	US-08-451-472-48	Sequence 48, Appl
81	23	37.1	18	1	US-08-451-472-48	Sequence 48, Appl
82	23	37.1	18	1	US-08-451-472-68	Sequence 68, Appl
83	23	37.1	18	1	US-09-171-337A-16	Sequence 16, Appl
84	23	37.1	18	4	US-09-631-022-16	Sequence 16, Appl
85	23	37.1	18	4	US-09-471-276-863	Sequence 863, App
86	22.5	36.3	18	4	US-09-311-784A-554	Sequence 554, App
87	22.5	36.3	15	4	US-09-009-953-51	Sequence 51, Appl
88	22.5	36.3	15	4	US-09-009-953-54	Sequence 54, Appl
89	22.5	36.3	15	4	US-09-009-953-60	Sequence 60, Appl
90	22.5	36.3	15	4	US-09-009-953-63	Sequence 63, Appl
91	22	35.5	5	2	US-08-920-162A-24	Sequence 24, Appl
92	22	35.5	5	2	US-08-920-162A-25	Sequence 25, Appl
93	22	35.5	5	2	US-09-356-931-24	Sequence 24, Appl
94	22	35.5	5	3	US-09-356-931-25	Sequence 25, Appl
95	22	35.5	5	3	US-09-356-931-26	Sequence 26, Appl
96	22	35.5	5	3	US-08-703-675C-24	Sequence 24, Appl
97	22	35.5	5	3	US-08-703-675C-25	Sequence 25, Appl
98	22	35.5	5	3	US-08-703-675C-26	Sequence 26, Appl
99	22	35.5	5	4	US-09-895-443A-24	Sequence 24, Appl
100	22	35.5	5	4	US-09-895-443A-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-641-803-4
Sequence 4, Application US/09641803
Patent No. 6500798
GENERAL INFORMATION:
APPLICANT: STANTON, G. John
APPLICANT: HUGHES, Thomas K.
APPLICANT: BOLDOGH, Istvan
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
FILE REFERENCE: 265.00220101
CURRENT APPLICATION NUMBER: US/09/641,803
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 60/149,310
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 4
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-4

Query Match 100.0%; Score 62; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVNVLP 12
|||||
Db 1 LFFFLPVNVLP 12

RESULT 2
US-08-464-531-57
Sequence 57, Application US/08464531
Patent No. 5789184
GENERAL INFORMATION:
APPLICANT: FOMIKES, Dana M.
APPLICANT: BROACH, Jim
APPLICANT: MANFREDI, John
APPLICANT: KLEIN, Christine
APPLICANT: MURPHY, Andrew J.
APPLICANT: PAUL, Jeremy
APPLICANT: TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,531
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/322,137

FILING DATE: 13-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOMIKES-2G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-531-57

Query Match 46.8%; Score 29; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. .94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6
|||||
Db 6 FFFLP 10

RESULT 3
US-08-461-598-57
Sequence 57, Application US/08461598
Patent No. 5876951
GENERAL INFORMATION:
APPLICANT: FOMIKES, Dana M.
APPLICANT: BROACH, Jim
APPLICANT: MANFREDI, John
APPLICANT: KLEIN, Christine
APPLICANT: MURPHY, Andrew J.
APPLICANT: PAUL, Jeremy
APPLICANT: TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,598
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/322,137
FILING DATE: 13-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOLWKES=2F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-461-598-57

Query Match 46.8%; Score 29; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
Db 6 FFFLP 10

RESULT 4

US-08-322-137-57

Sequence 57, Application US/08322137
Patent No. 6100042
GENERAL INFORMATION:
APPLICANT: FOLWKES, Dana M.
APPLICANT: BROACH, Jim
APPLICANT: MANFREDI, John
APPLICANT: KLEIN, Christine
APPLICANT: MURPHY, Andrew J.
APPLICANT: PAUL, Jeremy
APPLICANT: TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
NUMBER OF SEQUENCES: 119
TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,137
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: FOLWKES=2C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-322-137-57

Query Match 46.8%; Score 29; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
Db 6 FFFLP 10

RESULT 5

US-08-582-333A-68

Sequence 68, Application US/08582333A
Patent No. 6255059

GENERAL INFORMATION:
APPLICANT: Klein, Christine A.
APPLICANT: Murphy, Andrew J. M.
TITLE OF INVENTION: Methods and Compositions for
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascii(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,333A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Catherine J. Kara
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: CPT-012CP5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-4214
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-582-333A-68

Query Match 46.8%; Score 29; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
Db 6 FFFLP 10

RESULT 6

US-08-508-664-20
; Sequence 20, Application US/08508664
; Patent No. 5840542
; GENERAL INFORMATION:
; APPLICANT: KANG, YUP
; APPLICANT: YOON, JI-WON
; TITLE OF INVENTION: METHOD FOR MANUFACTURE OF PROINSULIN
; TITLE OF INVENTION: WITH HIGH EXPORT YIELD
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,664
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0136/0B300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CONN PEPTIDE
; US-08-508-664-20

Query Match 45.2%; Score 28; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FFELPVV 8
|||:|
Db 1 FFYTPIV 7

RESULT 7
5185441-4
; Patent No. 5185441
; APPLICANT: WALINER, BARBARA P.; HESSIONS, CATHERINE
; TITLE OF INVENTION: DNA SEQUENCES, RECOMBINANT DNA
; MOLECULES AND PROCESSES FOR PRODUCING PI-LINKED LYMPHOCYTE
; FUNCTION ASSOCIATED ANTIGEN-3
; NUMBER OF SEQUENCES: 41
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/237,309
; FILING DATE: 26-AUG-1988
; SEQ ID NO: 4:
; LENGTH: 18
5185441-4

Query Match 43.5%; Score 27; DB 6; Length 18;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 FFELPVVNVLP 12
|||:|
Db 1 FFYLVLESIP 10

RESULT 8
5185441-4
; Patent No. 5185441
; APPLICANT: WALINER, BARBARA P.; HESSIONS, CATHERINE
; TITLE OF INVENTION: DNA SEQUENCES, RECOMBINANT DNA
; MOLECULES AND PROCESSES FOR PRODUCING PI-LINKED LYMPHOCYTE
; FUNCTION ASSOCIATED ANTIGEN-3
; NUMBER OF SEQUENCES: 41
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/237,309
; FILING DATE: 26-AUG-1988
; SEQ ID NO: 4:
; LENGTH: 18
5185441-4

Query Match 43.5%; Score 27; DB 6; Length 18;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 FFELPVVNVLP 12
|||:|
Db 1 FFYLVLESIP 10

RESULT 9
US-08-920-162A-30
; Sequence 30, Application US/08920162A
; Patent No. 5985242
; GENERAL INFORMATION:
; APPLICANT: Finkel, M. et al.
; TITLE OF INVENTION: Modulators of {SYMBOL} 98 {f "Symbol"}-Amyloid Peptide
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162A
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 21-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400

TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION: 1-5
OTHER INFORMATION: /note= D amino acid
US-09-920-162A-30

Query Match
Best Local Similarity 41.9%; Score 26; DB 2; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFL 5
Db 1 LFFFL 5

RESULT 10
US-09-356-931-30
Sequence 30, Application US/09356931
Patent No. 6277826
GENERAL INFORMATION:
APPLICANT: FIndeis, M. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide
TITLE OF INVENTION: Aggregation Comprising D-Amino Acids
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1784
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/356,931
FILING DATE: 19-JUL-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/920,162
FILING DATE: 27-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/897,342
FILING DATE: 21-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/703,675
FILING DATE: 27-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Jr., Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-016CP4CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION: 1-5
OTHER INFORMATION: /note= D amino acid
US-09-356-931-30

Query Match
Best Local Similarity 41.9%; Score 26; DB 3; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFL 5
Db 1 LFFFL 5

RESULT 11
US-09-895-443A-30
Sequence 30, Application US/09895443A
Patent No. 6689752
GENERAL INFORMATION:
APPLICANT: FIndeis, MARK A.
APPLICANT: GEFTER, MALCOLM L.
APPLICANT: MUSSO, GARY
APPLICANT: SIGNER, ETHAN R.
APPLICANT: WAKERFIELD, JAMES
APPLICANT: MOLINAUX, SUSAN
APPLICANT: CHIN, JOSEPH
APPLICANT: LEE, JUNG-JA
APPLICANT: KELLEY, MICHAEL
APPLICANT: KOMAR-PANICUCCI, SONJA
APPLICANT: ARICO-MUENDEL, CHRISTOPHER C.
APPLICANT: PHILLIPS, KATHRYN
APPLICANT: HAYWARD, NEIL J.
TITLE OF INVENTION: MODULATORS OF BETA-AMYLOID PEPTIDE
TITLE OF INVENTION: AGGREGATION COMPRISING D-AMINO ACIDS
FILE REFERENCE: PPI-0016CP4CN2
CURRENT APPLICATION NUMBER: US/09/895,443A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/356931
PRIOR FILING DATE: 1990-07-19
PRIOR APPLICATION NUMBER: 08/920162
PRIOR FILING DATE: 1997-08-27
PRIOR APPLICATION NUMBER: 08/548998
PRIOR FILING DATE: 1995-10-27
PRIOR APPLICATION NUMBER: 08/616081
PRIOR FILING DATE: 1996-03-14
PRIOR APPLICATION NUMBER: 08/703675
PRIOR FILING DATE: 1996-08-27
PRIOR APPLICATION NUMBER: 08/897342
PRIOR FILING DATE: 1997-07-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide
NAME/KEY: VARIANT
LOCATION: (1).....(5)
OTHER INFORMATION: Modified site; D amino acid
US-09-895-443A-30

Query Match
Best Local Similarity 41.9%; Score 26; DB 4; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFL 5
Db 1 LFFFL 5

```
RESULT 12
US-09-328-501-7
; Sequence 7, Application US/09328501A
; Patent No. 6258581
; GENERAL INFORMATION:
; APPLICANT: OKINO, No. 6258581omu
; APPLICANT: ITO, Makoto
; TITLE OF INVENTION: Ceramidase Gene
; FILE REFERENCE: 1422-0377P
; CURRENT APPLICATION NUMBER: US/09/328,501A
; CURRENT FILING DATE: 1999-06-09
; EARLIER APPLICATION NUMBER: 10-234769 JAPAN
; EARLIER FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; OTHER INFORMATION: any n or Xaa = Unknown
US-09-328-501-7

Query Match
Best Local Similarity 41.9%; Score 26; DB 3; Length 10;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 FLPVNV 10
   |||||
   :
Db 2 FLEVVNI 8

RESULT 13
US-09-777-710A-7
; Sequence 7, Application US/09777710A
; Patent No. 6489117
; GENERAL INFORMATION:
; APPLICANT: OKINO, No. 6489117omu et al.
; TITLE OF INVENTION: CERAMIDASE GENE
; FILE REFERENCE: 1422-0458P
; CURRENT APPLICATION NUMBER: US/09/777,710A
; CURRENT FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-777-710A-7

Query Match
Best Local Similarity 41.9%; Score 26; DB 4; Length 10;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 FLPVNV 10
   |||||
   :
Db 2 FLEVVNI 8

RESULT 14
US-09-009-953-15
; Sequence 15, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; Reactive DR Restricted Epitopes
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
```

```
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,953
; FILING DATE: 21-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,713
; FILING DATE: 23-JAN-1997
; APPLICATION NUMBER: US 60/037,432
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-011520US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-009-953-15

Query Match
Best Local Similarity 41.9%; Score 26; DB 4; Length 16;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 FFLPVNV 10
   |||||
   :
Db 5 FFLPALPV 12

RESULT 15
US-08-159-339A-1023
; Sequence 1023, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Bettean
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 1023:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-1023

Query Match
Best Local Similarity 40.3%; Score 25; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 3.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFLPVNV 11
Db 2 FLLRVVDIL 10

RESULT 16
US-08-194-981E-16
Sequence 16, Application US/08194981E
Patent No. 5886157
GENERAL INFORMATION:
APPLICANT: GUENGERICH, F. Peter
APPLICANT: GUO, Zuyun
APPLICANT: SANDHU, Punam
APPLICANT: GILLAM, Elizabeth M. J.
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF
TITLE OF INVENTION: HUMAN
TITLE OF INVENTION: CYTOCHROME P450
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street, NE
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,981E
FILING DATE: February 10, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Selby
REGISTRATION NUMBER: 38,298
REFERENCE/DOCKET NUMBER: 22000.0022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-194-981E-16

Query Match
Best Local Similarity 40.3%; Score 25; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LFFLPV 8
Db 5 LAVFLPVI 12

RESULT 17
US-09-177-249-88
Sequence 88, Application US/09177249
Patent No. 6229064
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Onad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramon
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
FILE REFERENCE: 023070-086120US
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US 09/071,838
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 88
LENGTH: 17
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-09-177-249-88

Query Match
Best Local Similarity 40.3%; Score 25; DB 3; Length 17;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFLPV 7
Db 9 WFLPL 14

RESULT 18
US-09-812-283-88
Sequence 88, Application US/09812283
Patent No. 6828477
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramon
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
FILE REFERENCE: 023070-086120US
CURRENT APPLICATION NUMBER: US/09/812,283
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/177,249
PRIOR FILING DATE: 1998-10-22

PRIOR APPLICATION NUMBER: US 09/071,838
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 88
LENGTH: 17
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-09-812-283-88

Query Match 40.3%; Score 25; DB 4; Length 17;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPLPV 7
DB 9 FFPLPL 14

RESULT 19

US-08-482-918-94
Sequence 94, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-94

Query Match 40.3%; Score 25; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FFPLPV 8
DB 10 FFMLPPV 16

RESULT 20

US-08-482-918-95
Sequence 95, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-95

Query Match 40.3%; Score 25; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FFPLPV 8
DB 10 FFMLPPV 16

RESULT 21

US-09-224-681-94
Sequence 94, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

Query Match 40.3%; Score 25; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-94

Query Match 40.3%; Score 25; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FFPLPV 8
DB 10 FFMLPV 16

RESULT 22
US-09-224-681-95
Sequence 95, Application US/09224681
GENERAL INFORMATION:
APPLICANT: Zeebo, Kriestina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CITY: Chicago
STATE: Illinois

COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-95

Query Match 40.3%; Score 25; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FFPLPV 8
DB 10 FFMLPV 16

RESULT 23
US-08-336-728A-94
Sequence 94, Application US/08336728A
GENERAL INFORMATION:
APPLICANT: Zeebo, Kriestina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: 07/982,255
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-94

Query Match 40.3%; Score 25; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 7e+02; 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2;

QY 2 PFELPV 8
Db 10 FFMALPV 16

RESULT 24
US-08-336-728A-95
Sequence 95, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: 07/982,255
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-95

Query Match 40.3%; Score 25; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 7e+02; 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2;

QY 2 PFELPV 8
Db 10 FFMALPV 16

RESULT 25
US-09-635-251-94
Sequence 94, Application US/09635251
Patent No. 6759215
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/635,251
; FILING DATE: 07-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,182
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: 08/172,329
; FILING DATE: 21-DEC-1993
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; APPLICATION NUMBER: 07/684,535
; FILING DATE: 04-OCT-1991
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32957A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-635-251-94

Query Match          40.3% Score 25; DB 4; Length 18;
Beet Local Similarity 71.4%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 FFFLPV 8
        |||||
Db       10 FFMLEPV 16

RESULT 26
US-09-635-251-95
; Sequence 95, Application US/09635251
; Patent No. 6759215
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristina M.
;              Bosselman, Robert A.
;              Suggs, Sidney V.
;              Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/635,251

```

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;
; FILING DATE: 07-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,182
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: 08/172,329
; FILING DATE: 21-DEC-1993
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; APPLICATION NUMBER: 07/684,535
; FILING DATE: 04-OCT-1991
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32957A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-09-635-251-95

Query Match          40.3% Score 25; DB 4; Length 18;
Beet Local Similarity 71.4%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 FFFLPV 8
        |||||
Db       10 FFMLEPV 16

RESULT 27
US-09-471-276-1473
; Sequence 1473, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: GENSER. 025CPI
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1473
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL

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/ LOCATION: -16...-1
US-09-471-276-1473

Query Match      40.3%; Score 25; DB 4; Length 18;
Best Local Similarity 75.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LFFVLPVV 8
      |||||
Db      11 LFFVFLGV 18

RESULT 28
US-09-103-478-5
; Sequence 5, Application US/09103478
; Patent No. 6235975
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,478
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,221
; FILING DATE: 19-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/804,534
; FILING DATE: 21-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-077611US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-103-478-5

Query Match      38.7%; Score 24; DB 3; Length 7;
Best Local Similarity 42.9%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
/ Sequence 17, Application US/09103478
; Patent No. 6235975
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,478
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,221
; FILING DATE: 19-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/804,534
; FILING DATE: 21-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-077611US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-103-478-17

Query Match      38.7%; Score 24; DB 3; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      5 LPPVNV 10
      |||||
Db      1 LPIANV 6

RESULT 30
US-09-193-931C-5
; Sequence 5, Application US/09193931C
; Patent No. 6320102
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-077620
; CURRENT APPLICATION NUMBER: US/09/193,931C
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 09/103,478
```

;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 09/026,221
;; PRIOR FILING DATE: 1998-02-19
;; PRIOR APPLICATION NUMBER: US 08/804,534
;; PRIOR FILING DATE: 1997-02-21
;; NUMBER OF SEQ ID NOS: 29
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 5
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:DNA binding
;; OTHER INFORMATION: region of HAP3 subunit of CCAAT box-binding factor
;; OTHER INFORMATION: (CBF) protein B domain homolog with transcription
;; OTHER INFORMATION: activation function
US-09-193-931C-5

Query Match 38.7%; Score 24; DB 3; Length 7;
Best Local Similarity 42.9%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPPVNV 11
Db 1 MPIANVI 7

RESULT 31
US-09-193-931C-17
; Sequence 17, Application US/09193931C
; Patent No. 6320102
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; FILE REFERENCE: 023070-077620
; CURRENT APPLICATION NUMBER: US/09/193,931C
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 09/103,478
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 09/026,221
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 08/804,534
; PRIOR FILING DATE: 1997-02-21
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNA binding
; OTHER INFORMATION: region of HAP3 subunit of CCAAT box-binding factor
; OTHER INFORMATION: (CBF-A) protein yeast homolog
US-09-193-931C-17

Query Match 38.7%; Score 24; DB 3; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPPVNV 10
Db 1 LPIANV 6

RESULT 32
US-09-026-221-5
; Sequence 5, Application US/09026221
; Patent No. 6545201

;; GENERAL INFORMATION:
;; APPLICANT: Harada, John J.
;; APPLICANT: Lotan, Tamar
;; APPLICANT: Ohto, Masa-aki
;; APPLICANT: Goldberg, Robert B.
;; APPLICANT: Fischer, Robert L.
;; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
;; NUMBER OF SEQUENCES: 18
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/026,221
;; FILING DATE: 19-FEB-1998
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/804,534
;; FILING DATE: 21-FEB-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bastian, Kevin L.
;; REGISTRATION NUMBER: 34,774
;; REFERENCE/DOCKET NUMBER: 023070-077610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-026-221-5

Query Match 38.7%; Score 24; DB 4; Length 7;
Best Local Similarity 42.9%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPPVNV 11
Db 1 MPIANVI 7

RESULT 33
US-09-026-221-17
; Sequence 17, Application US/09026221
; Patent No. 6545201
; GENERAL INFORMATION:
; APPLICANT: Harada, John J.
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,221
FILING DATE: 19-FEB-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-077610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-026-221-17

Query Match 38.7%; Score 24; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 LPVNV 10
||: ||
DB 1 LPINAV 6

RESULT 34
US-09-516-052-5
Sequence 5, Application US/09516052
Patent No. 6781035
GENERAL INFORMATION:
APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Ohto, Masa-Aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
APPLICANT: Bui, Anhthu
APPLICANT: Khong, Raymond
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
FILE REFERENCE: 023070-077630US
CURRENT APPLICATION NUMBER: US/09/516,052
CURRENT FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 09/193,931
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 09/103,478
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 09/026,221
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: US 08/804,534
PRIOR FILING DATE: 1997-02-21
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:DNA binding
OTHER INFORMATION: region of HAP3 subunit of CCAAT box-binding factor
OTHER INFORMATION: (CBF) protein B domain homolog with transcription
OTHER INFORMATION: activation function
US-09-516-052-5

Query Match 38.7%; Score 24; DB 4; Length 7;
Best Local Similarity 42.9%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 LPVNV 11
||: ||:
DB 1 LPINAV 7

RESULT 35
US-09-516-052-17
Sequence 17, Application US/09516052
Patent No. 6781035
GENERAL INFORMATION:
APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Ohto, Masa-Aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
APPLICANT: Bui, Anhthu
APPLICANT: Khong, Raymond
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
FILE REFERENCE: 023070-077630US
CURRENT APPLICATION NUMBER: US/09/516,052
CURRENT FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 09/193,931
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 09/103,478
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 09/026,221
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: US 08/804,534
PRIOR FILING DATE: 1997-02-21
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:DNA binding
OTHER INFORMATION: region of HAP3 subunit of CCAAT box-binding factor
OTHER INFORMATION: (CBF-A) protein yeast homolog
US-09-516-052-17

Query Match 38.7%; Score 24; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 LPVNV 10
||: ||
DB 1 LPINAV 6

RESULT 36
US-08-934-222-106
Sequence 106, Application US/08934222
Patent No. 5928896
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,222
FILING DATE: 19-SEPT-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ. ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-222-106
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Query Match      38.7%  Score 24; DB 2; Length 9;
Best Local Similarity 71.4%  Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      6 PVTNVL 12
        | |||
Db       2 PFGNVL 8
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RESULT 37
US-08-933-402-106
Sequence 106, Application US/08933402
Patent No. 594887
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,402
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
```

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NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ. ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-933-402-106
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Query Match      38.7%  Score 24; DB 2; Length 9;
Best Local Similarity 71.4%  Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      6 PVTNVL 12
        | |||
Db       2 PFGNVL 8
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RESULT 38
US-09-207-621-106
Sequence 106, Application US/09207621
Patent No. 5952465
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/207,621
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ. ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-207-621-106
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Query Match      38.7%  Score 24; DB 2; Length 9;
Best Local Similarity 71.4%  Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db       2 PFGNVL 8
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RESULT 39
US-08-532-818-106
; Sequence 106, Application US/08532818
; Patent No. 5965698
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Iacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-532-818-106

Query Match 38.7%; Score 24; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PVTNVLIP 12
| | | | |
DB 2 PFGNVLIP 8

RESULT 40
US-09-231-797-106
; Sequence 106, Application US/09231797
; Patent No. 6084066
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA

ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,797
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Iacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-231-797-106

Query Match 38.7%; Score 24; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PVTNVLIP 12
| | | | |
DB 2 PFGNVLIP 8

Search completed: June 7, 2005, 23:23:14
Job time : 18.3636 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 23:00:52 ; Search time 54 Seconds
(without alignments)
85.185 Million cell updates/sec

Title: US-10-691-157-4
Perfect score: 62
Sequence: 1 LFFFLPVNVLP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 309695

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	62	100.0	12	14	US-10-281-652-4	Sequence 4, Appl1
2	62	100.0	12	16	US-10-691-157-4	Sequence 4, Appl1
3	62	100.0	12	17	US-10-691-330-4	Sequence 4, Appl1
4	31	50.0	6	16	US-10-182-110-2	Sequence 2, Appl1
5	31	50.0	9	14	US-10-119-536A-89	Sequence 89, Appl1
6	29	46.8	9	14	US-10-119-536A-182	Sequence 182, Appl1
7	29	46.8	10	10	US-09-935-430-446	Sequence 446, Appl1
8	29	46.8	10	14	US-10-277-292-446	Sequence 446, Appl1
9	29	46.8	10	15	US-10-280-340-446	Sequence 446, Appl1
10	29	46.8	11	9	US-09-747-774A-68	Sequence 68, Appl1
11	29	46.8	11	10	US-09-309-196-57	Sequence 57, Appl1

12	29	46.8	11	10	US-09-201-396-38	Sequence 38, Appl
13	29	46.8	11	10	US-09-953-354-68	Sequence 68, Appl
14	29	46.8	11	14	US-10-277-607-38	Sequence 38, Appl
15	29	46.8	11	15	US-10-263-341-57	Sequence 57, Appl
16	29	46.8	11	15	US-10-600-003-57	Sequence 57, Appl
17	29	46.8	11	17	US-10-752-478-68	Sequence 68, Appl
18	29	46.8	11	17	US-10-116-252-22	Sequence 68, Appl
19	29	46.8	13	14	US-10-706-391-63	Sequence 63, Appl
20	29	46.8	14	14	US-10-014-340-611	Sequence 611, Appl
21	29	46.8	14	14	US-10-014-340-612	Sequence 612, Appl
22	29	46.8	18	14	US-10-084-813-249	Sequence 249, Appl
23	29	46.8	18	14	US-10-084-813-250	Sequence 250, Appl
24	28	45.2	9	14	US-10-119-536A-84	Sequence 84, Appl
25	28	45.2	9	14	US-10-119-536A-92	Sequence 92, Appl
26	27	43.5	9	15	US-10-447-161-61	Sequence 61, Appl
27	27	43.5	9	16	US-10-415-841A-38	Sequence 38, Appl
28	27	43.5	9	16	US-10-362-715-20	Sequence 20, Appl
29	27	43.5	10	17	US-10-475-049A-103	Sequence 103, Appl
30	27	43.5	11	10	US-09-201-396-6	Sequence 6, Appl
31	27	43.5	11	14	US-10-277-607-6	Sequence 6, Appl
32	27	43.5	14	14	US-10-269-171A-6	Sequence 6, Appl
33	27	43.5	15	15	US-10-149-135-1941	Sequence 1941, Ap
34	27	43.5	15	15	US-10-149-135-1950	Sequence 1950, Ap
35	27	43.5	15	15	US-10-149-135-2026	Sequence 2026, Ap
36	27	43.5	15	15	US-10-149-135-2412	Sequence 2412, Ap
37	26	41.9	5	9	US-09-895-443-30	Sequence 30, Appl
38	26	41.9	8	15	US-10-137-867-292	Sequence 292, App
39	26	41.9	9	14	US-10-119-536A-176	Sequence 176, App
40	26	41.9	9	14	US-10-119-536A-190	Sequence 190, App
41	26	41.9	9	15	US-10-057-475B-10903	Sequence 10903, A
42	26	41.9	9	15	US-10-057-475B-10956	Sequence 10956, A
43	26	41.9	9	15	US-10-154-884B-10903	Sequence 10903, A
44	26	41.9	9	15	US-10-154-884B-10956	Sequence 10956, A
45	26	41.9	17	17	US-10-705-459-281	Sequence 281, App
46	26	41.9	10	9	US-09-777-710A-7	Sequence 7, Appl
47	26	41.9	10	10	US-09-935-430-427	Sequence 427, App
48	26	41.9	10	10	US-09-935-430-503	Sequence 503, App
49	26	41.9	10	10	US-09-935-430-613	Sequence 613, App
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51	26	41.9	10	14	US-10-277-252-427	Sequence 427, App
52	26	41.9	10	14	US-10-277-252-503	Sequence 503, App
53	26	41.9	10	14	US-10-277-252-613	Sequence 613, App
54	26	41.9	10	15	US-10-280-340-427	Sequence 427, App
55	26	41.9	10	15	US-10-280-340-503	Sequence 503, App
56	26	41.9	10	15	US-10-280-340-613	Sequence 613, App
57	26	41.9	14	17	US-10-206-659-37	Sequence 37, Appl
58	26	41.9	14	17	US-10-700-922-39	Sequence 39, Appl
59	26	41.9	15	14	US-10-294-891-11	Sequence 11, Appl
60	26	41.9	15	17	US-10-920-313-11	Sequence 11, Appl
61	26	41.9	16	13	US-10-103-385-15	Sequence 15, Appl
62	26	41.9	16	16	US-10-771-931-22	Sequence 22, Appl
63	26	41.9	17	11	US-09-833-245-570	Sequence 570, App
64	26	41.9	18	14	US-10-084-813-248	Sequence 248, App
65	25	40.3	10	17	US-10-801-990-86	Sequence 86, Appl
66	25	40.3	11	14	US-10-119-528-31	Sequence 31, Appl
67	25	40.3	12	14	US-10-269-171A-5	Sequence 5, Appl
68	25	40.3	12	16	US-10-685-898-27	Sequence 27, Appl
69	25	40.3	12	17	US-10-801-990-370	Sequence 370, App
70	25	40.3	13	9	US-09-826-290-122	Sequence 122, App
71	25	40.3	13	15	US-10-264-309-305	Sequence 305, App
72	25	40.3	13	17	US-10-801-990-142	Sequence 142, App
73	25	40.3	14	14	US-10-261-798-40	Sequence 40, Appl
74	25	40.3	14	15	US-10-162-134A-6	Sequence 6, Appl
75	25	40.3	14	15	US-10-162-134A-10	Sequence 10, Appl
76	25	40.3	14	17	US-10-240-035-40	Sequence 40, Appl
77	25	40.3	16	10	US-09-880-748-2250	Sequence 2250, Ap
78	25	40.3	16	15	US-10-293-418-2250	Sequence 2250, Ap
79	25	40.3	17	9	US-09-071-838-88	Sequence 88, Appl
80	25	40.3	17	10	US-09-759-130B-354	Sequence 354, App
81	25	40.3	17	14	US-10-189-123-84	Sequence 84, Appl
82	25	40.3	17	14	US-10-213-512-88	Sequence 88, Appl
83	25	40.3	17	14	US-10-188-695-84	Sequence 84, Appl
84	25	40.3	17	16	US-10-741-790-354	Sequence 354, App

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85 25 40.3 18 9 US-09-005-243-94 Sequence 94, Appl
86 25 40.3 18 9 US-09-005-243-95 Sequence 95, Appl
87 25 40.3 18 9 US-09-224-683-94 Sequence 94, Appl
88 25 40.3 18 9 US-09-224-683-95 Sequence 95, Appl
89 25 40.3 18 9 US-10-175-608-94 Sequence 94, Appl
90 25 40.3 18 16 US-10-175-608-95 Sequence 95, Appl
91 25 40.3 18 17 US-10-620-642-94 Sequence 94, Appl
92 25 40.3 18 17 US-10-620-642-95 Sequence 95, Appl
93 25 40.3 18 17 US-10-926-683-1473 Sequence 1473, Ap
94 24 38.7 10 16 US-10-433-234A-187 Sequence 187, App
95 24 38.7 10 16 US-10-433-234A-188 Sequence 188, App
96 24 38.7 10 16 US-10-433-234A-189 Sequence 189, App
97 24 38.7 10 16 US-10-433-234A-190 Sequence 190, App
98 24 38.7 10 16 US-10-433-234A-191 Sequence 191, App
99 24 38.7 10 16 US-10-433-234A-192 Sequence 192, App
100 24 38.7 12 14 US-10-075-869-41 Sequence 41, Appl
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ALIGNMENTS

RESULT 1

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US-10-281-652-4
; Sequence 4, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265, 00220101
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/10/281,652
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-10-281-652-4
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Query Match 100.0%; Score 62; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00097;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 LFFFLPVNVLP 12
Db 1 LFFFLPVNVLP 12
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RESULT 2

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US-10-691-157-4
; Sequence 4, Application US/10691157
; Publication No. US2004026681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265, 00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; CURRENT FILING DATE: 2003-10-22
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; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
; US-10-691-157-4
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Query Match 100.0%; Score 62; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00097;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 LFFFLPVNVLP 12
Db 1 LFFFLPVNVLP 12
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RESULT 3

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US-10-691-330-4
; Sequence 4, Application US/10691330
; Publication No. US20050042500A1
; GENERAL INFORMATION:
; APPLICANT: Boldogh, Istvan
; APPLICANT: Stanton, G. John
; APPLICANT: Georgiades, Jerzy A.
; APPLICANT: Hughes, Thomas K., Jr.
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265, 00390101
; CURRENT APPLICATION NUMBER: US/10/691,330
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
; US-10-691-330-4
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Query Match 100.0%; Score 62; DB 17; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00097;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 LFFFLPVNVLP 12
Db 1 LFFFLPVNVLP 12
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RESULT 4

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US-10-182-110-2
; Sequence 2, Application US/10182110
; Publication No. US2004017153A1
; GENERAL INFORMATION:
; APPLICANT: Regen Therapeutics plc
; APPLICANT: Georgiades, Jerzy A
; TITLE OF INVENTION: Peptide Fragments of Colostrinin And Their Use
; FILE REFERENCE: AAT-14173
; CURRENT APPLICATION NUMBER: US/10/182,110
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; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: GB0001825.9
; PRIOR FILING DATE: 2000-01-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Truncated version of a peptide found in colostrin
US-10-182-110-2
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Query Match          50.0%; Score 31; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 FFLPVN 6
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; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandaal, Brian Berg
; TITLE OF INVENTION: Method for identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CPN0998 immunogenic peptide
US-10-119-536A-89
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Query Match          50.0%; Score 31; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Db      2 LFFFLPIL 9
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RESULT 6
US-10-119-536A-182
; Sequence 182, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandaal, Brian Berg
; TITLE OF INVENTION: Method for identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 182
; LENGTH: 9
```

```
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CT841 immunogenic peptide
US-10-119-536A-182
```

```
Query Match          46.8%; Score 29; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 LFFFLPV 8
        |||||
Db      2 LFFFLPIL 9
```

```
RESULT 7
US-09-935-430-446
; Sequence 446, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALITRA-ETD, PIA
; APPLICANT: JAKOBYTZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 446
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-446
```

```
Query Match          46.8%; Score 29; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      2 FFFFLPVNVL 11
        |||||
Db      1 FTHLPVSNIL 10
```

```
RESULT 8
US-10-277-292-446
; Sequence 446, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALITRA-ETD, PIA
; APPLICANT: JAKOBYTZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
```

FILE REFERENCE: 51158-20050.00
CURRENT APPLICATION NUMBER: US/10/277,292
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US/09/935,430
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,098
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/282,739
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 446
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-446

Query Match 46.8%; Score 29; DB 14; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FFELPVVNL 11
| | | | |
Db 1 FTHLPVSNIL 10

RESULT 9
US-10-280-340-446
Sequence 446, Application US/10280340
Publication No. US20030207835A1
GENERAL INFORMATION:
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RAITANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALILTA-EID, PIA
APPLICANT: JAKOBOVITZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
TITLE OF INVENTION: OTHER CANCERS
FILE REFERENCE: 51158-20050.00
CURRENT APPLICATION NUMBER: US/10/280,340
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US/09/935,430
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,098
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/282,739
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 446
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-446

Query Match 46.8%; Score 29; DB 15; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FFELPVVNL 11
| | | | |
Db 1 FTHLPVSNIL 10

RESULT 10
US-09-747-774A-68

Sequence 68, Application US/09747774A
Publication No. US20010026926A1
GENERAL INFORMATION:
APPLICANT: Klein, Christine A.
APPLICANT: Murphy, Andrew J. M.
APPLICANT: Broach, James R.
APPLICANT: Manfredi, John
APPLICANT: Paul, Jeremy
APPLICANT: Fowlkes, Dana M.
APPLICANT: Trueheart, Joshua
TITLE OF INVENTION: Methods and Compositions for Identifying
TITLE OF INVENTION: Receptor Effectors
FILE REFERENCE: CPT-012C95DV
CURRENT APPLICATION NUMBER: US/09/747,774A
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 08/582,333
PRIOR FILING DATE: 1996-01-17
PRIOR APPLICATION NUMBER: US 08/464,531
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/461,598
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/461,383
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/463,181
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/322,137
PRIOR FILING DATE: 1994-10-13
PRIOR APPLICATION NUMBER: US 08/309,313
PRIOR FILING DATE: 1994-09-20
PRIOR APPLICATION NUMBER: US 08/190,328
PRIOR FILING DATE: 1994-01-31
PRIOR APPLICATION NUMBER: US 08/041,431
PRIOR FILING DATE: 1993-03-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 68
LENGTH: 11
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-747-774A-68

Query Match 46.8%; Score 29; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFELP 6
| | | | |
Db 6 FFELP 10

RESULT 11
US-09-309-196-57
Sequence 57, Application US/09309196
Publication No. US20030008380A1
GENERAL INFORMATION:
APPLICANT: FOWLKES, Dana M.
APPLICANT: BROACH, Jim
APPLICANT: MANFREDI, John
APPLICANT: KLEIN, Christine
APPLICANT: MURPHY, Andrew J.
APPLICANT: PAUL, Jeremy
APPLICANT: TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHARMACEUTICAL SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/309,196
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/322,137
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOLMKS=2C
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-309-196-57

Query Match 46.8%; Score 29; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFPLP 6
Db 6 PFPLP 10

RESULT 12
US-09-201-396-38
Sequence 38, Application US/09201396A
Publication No. US2003009022A1
GENERAL INFORMATION:
APPLICANT: Klein, Christine A.
APPLICANT: Murphy, Andrew J.
APPLICANT: Paul, Jeremy
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR
TITLE OF INVENTION: EFFECTORS
FILE REFERENCE: CPI-012CP9
CURRENT APPLICATION NUMBER: US/09/201,396A
CURRENT FILING DATE: 1998-11-30
EARLIER APPLICATION NUMBER: 08/582,333
EARLIER FILING DATE: 1996-01-17
EARLIER APPLICATION NUMBER: 08/322,137
EARLIER FILING DATE: 1994-10-13
EARLIER APPLICATION NUMBER: 08/309,313
EARLIER FILING DATE: 1994-09-20
EARLIER APPLICATION NUMBER: 08/190,328
EARLIER FILING DATE: 1994-01-31
EARLIER APPLICATION NUMBER: 08/041,431
EARLIER FILING DATE: 1993-03-31
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 38
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic

OTHER INFORMATION: construct
US-09-201-396-38

Query Match 46.8%; Score 29; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFPLP 6
Db 6 PFPLP 10

RESULT 13
US-09-953-354-68
Sequence 68, Application US/09953354
Publication No. US20030054402A1
GENERAL INFORMATION:
APPLICANT: Klein, Christine A.
APPLICANT: Murphy, Andrew J. M.
TITLE OF INVENTION: Methods and Compositions for
Identifying Receptor Effectors
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascii(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,354
FILING DATE: 13-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/689,172
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CPI-012CP7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-953-354-68

Query Match 46.8%; Score 29; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFPLP 6
Db 6 PFPLP 10

RESULT 14
US-10-277-607-38
Sequence 38, Application US/10277607
Publication No. US20030166143A1
GENERAL INFORMATION:
APPLICANT: Klein, Christine A.
APPLICANT: Murphy, Andrew J.

APPLICANT: Paul, Jeremy I.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR
FILE REFERENCE: CPI-012CP9CN
CURRENT APPLICATION NUMBER: US/10/277,607
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: 09/201,396
PRIOR FILING DATE: 1998-11-30
PRIOR APPLICATION NUMBER: 60/109,902
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: PCT/US98/21168
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 08/946,298
PRIOR FILING DATE: 1997-10-07
PRIOR APPLICATION NUMBER: 08/689,172
PRIOR FILING DATE: 1996-08-06
PRIOR APPLICATION NUMBER: 08/582,333
PRIOR FILING DATE: 1996-01-17
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 38
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-277-607-38

Query Match 46.8%; Score 29; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFPLP 6
Db 6 FFPLP 10

RESULT 15
US-10-263-341-57
Sequence 57, Application US/10263341
Publication No. US20030203417A1
GENERAL INFORMATION:
APPLICANT: FOWLKES, Dana M.
BROACH, Jim
MANFREDI, John
KLEIN, Christine
MURPHY, Andrew J.
PAUL, Jeremy
TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/263,341
FILING DATE: 01-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/322,137
FILING DATE: 13-Oct-1994
APPLICATION NUMBER: US 08/309,313

FILING DATE: 20-SEP-1994
APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994
APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOLWKES=2C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-263-341-57

Query Match 46.8%; Score 29; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFPLP 6
Db 6 FFPLP 10

RESULT 16
US-10-600-003-57
Sequence 57, Application US/10600003
Publication No. US20040197840A1
GENERAL INFORMATION:
APPLICANT: FOWLKES, Dana M.
BROACH, Jim
MANFREDI, John
KLEIN, Christine
MURPHY, Andrew J.
PAUL, Jeremy
TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE AND COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/600,003
FILING DATE: 18-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/266,166
FILING DATE: 05-APR-1999
APPLICATION NUMBER: US 08/461,383
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/322,137
FILING DATE: 13-Oct-1994
APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994

APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CPI-012CP4B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-227-7400
TELEFAX: 617-227-5941
TELEX: 752806
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-600-003-57

Query Match 46.8%; Score 29; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6
| | | | |
DB 6 FFFLP 10

RESULT 17
US-10-752-478-68
; Sequence 68, Application US/10752478
; Publication No. US20050059135A1
GENERAL INFORMATION:
APPLICANT: Klein, Christine A.
Murphy, Andrew J. M.
TITLE OF INVENTION: Methods and Compositions for
Identifying Receptor Effectors
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascii(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/752,478
FILING DATE: 05-Jan-2004
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CPI-012CP7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-10-752-478-68

Query Match 46.8%; Score 29; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6
| | | | |
DB 6 FFFLP 10

RESULT 18
US-10-116-252-22
; Sequence 22, Application US/10116252
; Publication No. US20030028008A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: Seven Transmembrane Receptor Polynucleotides,
File Reference: PT007P1
CURRENT APPLICATION NUMBER: US/10/116,252
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US/09/711,909
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: PCT/US00/13737
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 60/135,167
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 60/143,616
PRIOR FILING DATE: 1999-07-13
PRIOR APPLICATION NUMBER: 60/152,934
PRIOR FILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: 60/189,029
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-252-22

Query Match 46.8%; Score 29; DB 14; Length 13;
Best Local Similarity 54.5%; Pred. No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LFFFLPVVNVL 11
| | | | | : |
DB 2 LFFFLPLALIL 12

RESULT 19
US-10-706-391-63
; Sequence 63, Application US/10706391
; Publication No. US20040137482A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: WASHINGTON DENTAL SERVICE
APPLICANT: Eckert, Randal
APPLICANT: Qi, Fengxia
APPLICANT: Shi, Wenyan
APPLICANT: Anderson, Maxwell H.
TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
FILE REFERENCE: 2101363-991600
CURRENT APPLICATION NUMBER: US/10/706,391
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 10/077,624
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 09/910,358
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.1
SEQ ID NO 63
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial sequence

```
; FEATURE:
; OTHER INFORMATION: Design peptide
US-10-706-391-63

Query Match
Best Local Similarity 46.8%; Score 29; DB 16; Length 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 LPVVNVL 12
   |||: |||
Db 4 LPVLEVL 11

RESULT 20
US-10-014-340-611
; Sequence 611, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 611
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-611

Query Match
Best Local Similarity 46.8%; Score 29; DB 14; Length 14;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PVVNVL 12
   | : |||
Db 4 PPINVL 10

RESULT 21
US-10-014-340-612
; Sequence 612, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 612
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-612

Query Match
Best Local Similarity 46.8%; Score 29; DB 14; Length 14;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PVVNVL 12
   | : |||
Db 4 PPINVL 10

RESULT 22
US-10-084-813-249
; Sequence 249, Application US/10084813
; Publication No. US20030068615A1
```

```
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 249
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-249

Query Match
Best Local Similarity 46.8%; Score 29; DB 14; Length 18;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LFFLPVVNVL 11
   | |||: :
Db 6 LGFPLPLTLMI 16

RESULT 23
US-10-084-813-250
; Sequence 250, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 250
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-250

Query Match
Best Local Similarity 46.8%; Score 29; DB 14; Length 18;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LFFLPVVNVL 11
   | |||: :
Db 2 LGFPLPLTLMI 12

RESULT 24
US-10-119-536A-84
; Sequence 84, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/1091US1
```


; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CPN0998 immunogenic peptide
US-10-119-536A-84

Query Match 45.2%; Score 28; DB 14; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.5e+06;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PFLPVNVY 10
| | | | |
Db 1 FTFLPIIVL 9

RESULT 25
; Sequence 92, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for identification of proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/J09JUS1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CPN0998 immunogenic peptide
US-10-119-536A-92

Query Match 45.2%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLFVVNVL 11
| | | | |
Db 1 FLFPIIVL 8

RESULT 26
US-10-447-161-61
; Sequence 61, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-61

Query Match 43.5%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFLP 6
: | | | |
Db 1 VYFFLP 6

RESULT 27
US-10-415-841A-38
; Sequence 38, Application US/10415841A
; Publication No. US20040131598A1
; GENERAL INFORMATION:
; APPLICANT: Tatufo, Sabrina
; APPLICANT: Meier, Ute-Christiane
; APPLICANT: McMichael, Andrew James
; APPLICANT: Bell, John Irving
; APPLICANT: Layton, Guy
; APPLICANT: Hunter, Michael
; TITLE OF INVENTION: Cancer Therapy
; FILE REFERENCE: 3547.1001.000
; CURRENT APPLICATION NUMBER: US/10/415,841A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: PCT/GB01/04844
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-841A-38

Query Match 43.5%; Score 27; DB 16; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFLP 6
: | | | |
Db 1 VYFFLP 6

RESULT 28
US-10-362-715-20
; Sequence 20, Application US/10362715
; Publication No. US20040253574A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: Schuler-Thurner, Beatrice
; TITLE OF INVENTION: METHOD FOR READY-TO-USE, ANTIGEN LOADED OR UNLOADED,
; FILE REFERENCE: 1430/12
; CURRENT APPLICATION NUMBER: US/10/362,715
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-715-20

Query Match 43.5%; Score 27; DB 16; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.5e+06;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFLP 6
:|||||
Db 1 VFFFLP 6

RESULT 29
US-10-475-049A-103
; Sequence 103, Application US/10475049A
; Publication No. US20050019854A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Rene
; APPLICANT: Lajoix, Anne-Dominique
; APPLICANT: Ribes, Gerard
; TITLE OF INVENTION: Novel Method For Screening Inhibitors of
; TITLE OF INVENTION: the Linkage Between the Neuronal Nitric Oxide Synthase
; TITLE OF INVENTION: Associated Protein and the Protein Inhibiting Neuronal
; FILE REFERENCE: 50319/005001
; CURRENT APPLICATION NUMBER: US/10/475,049A
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/FR02/01327
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: FR 01/05248
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 103
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nNOS mutated protein fragment
US-10-475-049A-103

Query Match 43.5%; Score 27; DB 17; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PYYVNLIP 12
||:|||||
Db 4 PVLSTLP 10

RESULT 30
US-09-201-396-6
; Sequence 6, Application US/09201396A
; Publication No. US20030009022A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; APPLICANT: Murphy, Andrew J.
; APPLICANT: Paul, Jeremy
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR
; TITLE OF INVENTION: EFFECTORS
; FILE REFERENCE: CPI-012CP9
; CURRENT APPLICATION NUMBER: US/09/201,396A
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: 08/582,333
; PRIOR FILING DATE: 1996-01-17
; PRIOR APPLICATION NUMBER: 08/322,137
; PRIOR FILING DATE: 1994-10-13
; PRIOR APPLICATION NUMBER: 08/309,313
; PRIOR FILING DATE: 1994-09-20
; PRIOR APPLICATION NUMBER: 08/190,328
; PRIOR FILING DATE: 1994-01-31
; PRIOR APPLICATION NUMBER: 08/041,431
; PRIOR FILING DATE: 1993-03-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 6
; LENGTH: 11
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-201-396-6

Query Match 43.5%; Score 27; DB 10; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLPV 7
|||||
Db 3 FFFRPV 8

RESULT 31
US-10-277-607-6
; Sequence 6, Application US/10277607
; Publication No. US20030166143A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; APPLICANT: Murphy, Andrew J.
; APPLICANT: Paul, Jeremy I.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR
; TITLE OF INVENTION: EFFECTORS
; FILE REFERENCE: CPI-012CP9CN
; CURRENT APPLICATION NUMBER: US/10/277,607
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/109,902
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: 60/109,902
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: PCT/US98/21168
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 08/946,298
; PRIOR FILING DATE: 1997-10-07
; PRIOR APPLICATION NUMBER: 08/689,172
; PRIOR FILING DATE: 1996-08-06
; PRIOR APPLICATION NUMBER: 08/582,333
; PRIOR FILING DATE: 1996-01-17
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-10-277-607-6

Query Match 43.5%; Score 27; DB 14; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLPV 7
|||||
Db 3 FFFRPV 8

RESULT 32
US-10-269-171A-6
; Sequence 6, Application US/10269171A
; Publication No. US20030095979A1
; GENERAL INFORMATION:
; APPLICANT: Frank Matner
; APPLICANT: Wolfgang Zauner
; APPLICANT: Walter Schmidt
; APPLICANT: Michael Buschle
; TITLE OF INVENTION: Pharmaceutical preparations comprising modified
; TITLE OF INVENTION: peptides
; FILE REFERENCE: SONN-02005
; CURRENT APPLICATION NUMBER: US/10/269,171A

```
/ CURRENT FILING DATE: 2002-10-11
/ PRIOR APPLICATION NUMBER: PCT/EP01/04313
/ PRIOR FILING DATE: 2001-04-17
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-269-171A-6
```

```
Query Match          43.5%; Score 27; DB 14; Length 14;
Best Local Similarity 33.3%; Pred. No. 8.4e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 LFFPLPVNVLP 9
        | | | | |
Db       2 LVFGLEVEVVP 10
```

```
RESULT 33
US-10-149-135-1941
/ Sequence 1941, Application US/10149135
/ Publication No. US20040053822A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0130001
/ CURRENT APPLICATION NUMBER: US/10/149,135
/ CURRENT FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: PCT/US00/33545
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,298
/ PRIOR FILING DATE: 1999-12-10
/ PRIOR APPLICATION NUMBER: US 09/189,702
/ PRIOR FILING DATE: 1998-11-10
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ NUMBER OF SEQ ID NOS: 2479
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1941
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificial Peptide
US-10-149-135-1941
```

```
Query Match          43.5%; Score 27; DB 15; Length 15;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 LFFPLPVNVLP 12
        | | | | |
Db       3 LVFGLEVEVVP 14
```

RESULT 34

```
US-10-149-135-1950
/ Sequence 1950, Application US/10149135
/ Publication No. US20040053822A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Elissa
```

```
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0130001
/ CURRENT APPLICATION NUMBER: US/10/149,135
/ CURRENT FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: PCT/US00/33545
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,298
/ PRIOR FILING DATE: 1999-12-10
/ PRIOR APPLICATION NUMBER: US 09/189,702
/ PRIOR FILING DATE: 1998-11-10
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ NUMBER OF SEQ ID NOS: 2479
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1950
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificial Peptide
US-10-149-135-1950
```

```
Query Match          43.5%; Score 27; DB 15; Length 15;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 LFFPLPVNVLP 12
        | | | | |
Db       2 LVFGLEVEVVP 13
```

```
RESULT 35
US-10-149-135-2026
/ Sequence 2026, Application US/10149135
/ Publication No. US20040053822A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0130001
/ CURRENT APPLICATION NUMBER: US/10/149,135
/ CURRENT FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: PCT/US00/33545
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,298
/ PRIOR FILING DATE: 1999-12-10
/ PRIOR APPLICATION NUMBER: US 09/189,702
/ PRIOR FILING DATE: 1998-11-10
/ PRIOR APPLICATION NUMBER: US 08/205,713
```

PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2026
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-2026

Query Match 43.5%; Score 27; DB 15; Length 15;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LFFFLPVNVLP 12
| | | | |
Db 2 LVFGIEVEVVP 13

RESULT 36
US-10-149-135-2412
Sequence 2412, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2412
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-2412

Query Match 43.5%; Score 27; DB 15; Length 15;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LFFFLPVNVLP 12
| | | | |

Db 2 LVFGIEVEVVP 13

RESULT 37
US-09-895-443-30
Sequence 30, Application US/09895443
Patent No. US20020103134A1
GENERAL INFORMATION:
APPLICANT: Finkelstein, M. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide
Aggregation Comprising D-Amino Acids
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1784
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/895,443
FILING DATE: 29-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/356,931
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/897,342
FILING DATE: 21-JUL-1997
APPLICATION NUMBER: USSN 08/703,675
FILING DATE: 27-AUG-1996
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Jr., Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PFI-016CP4CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION: 1-5
OTHER INFORMATION: /note= D amino acid
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-895-443-30

Query Match 41.9%; Score 26; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFL 5
| | | | |
Db 1 LFFFL 5

RESULT 38
US-10-137-867-292
Sequence 292, Application US/10137867
Publication No. US20030207349A1
GENERAL INFORMATION:

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 292
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-292
```

```
Query Match          41.9%; Score 26; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 LFFFL 5
        |||||
Db       1 LFFFL 5
```

```
RESULT 39
US-10-119-536A-176
; Sequence 176, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/1J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9) <223> CT841 immunogenic peptide
US-10-119-536A-176
```

```
Query Match          41.9%; Score 26; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.5e+06;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 FFELPVNV 10
        ||::||
Db       1 FFMPIVLV 9
```

RESULT 40

```
US-10-119-536A-190
; Sequence 190, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/1J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 190
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CT841 immunogenic peptide
US-10-119-536A-190
```

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Query Match          41.9%; Score 26; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 FLEPVNVL 11
        ||::||
Db       1 FMPPIVLV 8
```

```
Search completed: June 7, 2005, 23:31:36
Job time : 56 secs
```

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ALIGNMENTS

RESULT 1

hypothetical protein SCU30.08 - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C/Accession: T37075

R/Sander, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1999

A/Reference number: T21621

A/Accession: T37075

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-16 <S>

A/Cross-references: EMBL:AL109973; PIDN:CAM53303.1; GSPDB:GN00070; SCODEB:SCU30.08

A/Experimental source: strain A3(2)

A/Genetic8:

A/Genes: SCODEB:SCU30.08

Query Match

Best Local Similarity 37.1%; Score 23; DB 2; Length 16;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LPVNVLP 12

Db 1 MPVIRMP 8

RESULT 2

cysteine-rich secretory protein-3 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999

C/Accession: S53123; S56161

R/Schwidetzky, U.; Haendler, B.; Schlenning, W.D. submitted to the EMBL Data Library, March 1995

A/Description: Isolation and characterization of the androgen-dependent mouse cysteine-X

A/Reference number: S53125

A/Accession: S53125

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-18 <SCH>

A/Cross-references: EMBL:X85321

R/Schwidetzky, U.; Haendler, B.; Schlenning, W.D. Blochm. J. 309, 831-836, 1995

A/Title: Isolation and characterization of the androgen-dependent mouse cysteine-rich se

A/Reference number: S56161; MUID:95366959; PMID:7639699

A/Accession: S56161

A/Status: preliminary; translation not shown

A/Molecule type: DNA

A/Residues: 1-18 <SC2>

A/Cross-references: EMBL:X85321

Query Match

Best Local Similarity 100.0%; Score 22; DB 2; Length 18;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFPL 5

Db 4 PFPL 7

RESULT 3

hemolytic protein B9 - edible frog (fragment)

C/Species: Rana esculenta (edible frog)

C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C/Accession: S09019

R/Simmaco, M.; De Biase, D.; Severini, C.; Aita, M.; Erpamer, G.F.; Barra, D.; Bossa, F. Blochm. Biophys. Acta 1033, 318-323, 1990

A/Title: Purification and characterization of bioactive peptides from skin extracts of R

Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 14;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

A/Reference number: S09018; MUID:90198965; PMID:2317508
A/Accession: S09019
A/Molecule type: protein
A/Residues: 1-13 <SIM>
A/Cross-references: UNIPROT:P32416

Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 13;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPPV 8

Db 1 FLPLI 5

RESULT 4

crabrolin - European hornet

C/Species: Vespa crabro (European hornet)

C/Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004

C/Accession: A01781

R/Argolas, A.; Pisano, J.J. J. Biol. Chem. 259, 10106-10111, 1984

A/Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin,

A/Reference number: A92441; MUID:84289390; PMID:6206053

A/Accession: A01781

A/Molecule type: protein

A/Residues: 1-13 <ARG>

A/Cross-references: UNIPROT:P01518

A/Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.

C/Keywords: amidated carboxyl end; venom

F/13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 13;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPPV 8

Db 1 FLPLI 5

RESULT 5

histamine-releasing peptide II - oriental hornet

N/Alternate names: venom protein HR-2

C/Species: Vespa orientalis (oriental hornet)

C/Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 09-Jul-2004

C/Accession: JN0390; S10919

R/Miroshnikov, A.I.; Snezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Gus

Bilovoy, Khim. 7, 1467-1477, 1981

A/Title: Structure and properties of histamine releasing peptides from the venom of Vesp

A/Reference number: JN0389

A/Accession: JN0390

A/Molecule type: protein

A/Residues: 1-14 <MIR>

A/Cross-references: UNIPROT:P17236

R/Tulchibaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I. Biochemistry (N.Y.) 53, 183-190, 1968

A/Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. St

A/Reference number: S06445

A/Accession: S10919

A/Molecule type: protein

A/Residues: 1-14 <TVLI>

C/Superfamily: crabrolin

C/Keywords: amidated carboxyl end; venom

F/14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 14;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPPV 8

Db 1 FLPLI 5

RESULT 6

S62374
alpha-1-antichymotrypsin - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S62374
R:Tsuda, M.; Sei, Y.; Ohkubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.; Tsuda, T.;
Eur. J. Biochem. 235, 821-827, 1996
A:Title: The defective secretion of a naturally occurring alpha-1-antichymotrypsin varia
A:Reference number: S62374; PMID:96184564; PMID:8654434
A:Accession: S62374
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-14 <TSU>
A:Cross-references: UNIPROT:Q9UNU9; UNIPROT:Q96DM8; UNIPROT:Q8N177

Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 14;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFFLPVVN 9
| | | | |
Db 2 IFMSKVTN 10

RESULT 7

S15778
Insulin chain B - bovine (fragments)
C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: S15778; S15779
R:Berghman, T.; Agerbergh, B.; Joernvall, H.
FEBS Lett. 283, 100-103, 1991
A:Title: Direct analysis of peptides and amino acids from capillary electrophoresis.
A:Reference number: S15778; PMID:91243852; PMID:2037061
A:Accession: S15778
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <FEH1>
A:Accession: S15779
A:Status: preliminary
A:Molecule type: protein
A:Residues: 9-17 <FEH2>
C:Superfamily: Insulin
C:Keywords: hormone; pancreas

Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 17;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLP 6
| | | |
Db 11 FFYTP 15

RESULT 8

S09731
Photosystem I protein psal - spinach chloroplast (fragment)
C:Species: chloroplast Spinacia oleracea (spinach)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 19-Jan-1996
C:Accession: S09731
R:Ikeuchi, M.; Hirano, A.; Hiyaama, T.; Inoue, Y.
FEBS Lett. 263, 274-276, 1990
A:Title: Polypeptide composition of higher plant photosystem I complex. Identification
A:Reference number: S09730; PMID:90242987; PMID:2185553
A:Accession: S09731
A:Molecule type: protein
A:Residues: 1-18 <IKE>
C:Genetics:

A:Gene: psal
A:Genome: chloroplast
C:Superfamily: photosystem I protein psal
C:Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem I; thyl

Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 18;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPLVNL 11
| | | | |
Db 7 FVLVLGLV 14

RESULT 9

I40062
Shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C:Species: Buchnera aphidicola
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999
C:Accession: I40062
R:Roubabkeh, D.; Baumann, P.
Gene 155, 107-112, 1995
A:Title: Characterization of a putative 238-SS rRNA operon of Buchnera aphidicola (endos
A:Reference number: I40061; PMID:95212914; PMID:7535281
A:Accession: I40062
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18 <RBS>
A:Cross-references: EMBL:U10496; NID:9854711; PIDN:AAA79125.1; PID:9854712
C:Genetics:
A:Gene: aroB
C:Keywords: oxidoreductase

Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12
| | | | |
Db 7 NVLP 10

RESULT 10

S6636
alpha-2-macroglobulin isoform 2 - bovine (fragment)
C:Species: Bos primigenius indicus (zebu cattle)
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S6636
R:Polmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottoru
FEBS Lett. 372, 93-95, 1995
A:Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain o
A:Reference number: S6634; PMID:96032553; PMID:7556651
A:Accession: S6636
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DOB>
A:Cross-references: UNIPROT:Q7M2N7

Query Match 32.3%; Score 20; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12
| | | | |
Db 2 NVLP 5

RESULT 11

S65715
aryl hydrocarbon (benzo[a]pyrene) hydroxylase (EC 1.14.14.-) cytochrome P450 K(Ah) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 29-Oct-1999
C:Accession: S65715

R.Obgitya, N.; Yokota, H.; Takahashi, M.; Komoro, S.; Yuasa, A.
 Biochim. Biophys. Acta 1289, 122-130, 1996
 A>Title: Purification and properties of a new beta-naphthoflavone inducible cytochrome P
 A:Reference number: S65715; MUID:96195850; PMID:6605221
 A:Accession: S65715
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <OHG>
 C:Keywords: monooxygenase; oxidoreductase

Query Match 32.3%; Score 20; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 LPVNVLP 12
 |||:
 Db 3 VPVXLLP 10

RESULT 12
 S09018
 hemolytic protein A1 - edible frog (fragment)
 C:Species: Rana esculenta (edible frog)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: S09018
 R:Simmaco, M.; De Biase, D.; Severini, C.; Alta, M.; Erepamer, G.F.; Barra, D.; Bossa, F
 Biochim. Biophys. Acta 1033, 318-323, 1990
 A>Title: Purification and characterization of bioactive peptides from skin extracts of R
 A:Reference number: S09018; MUID:90198965; PMID:2317508
 A:Accession: S09018
 A:Molecule type: protein
 A:Residues: 1-13 <SIM>
 A:Cross-references: UNIPROT:P32415

Query Match 32.3%; Score 20; DB 2; Length 13;
 Best Local Similarity 60.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 FLPPV 8
 |||:
 Db 1 FLDPAL 5

RESULT 13
 AF0832
 phe leader peptide [imported] - Salmonella enterica subsp. enterica serovar Typhi (strai
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A>Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AF0832
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A>Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AF0832
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-15 <PBR>
 A:Cross-references: GB:AL513382; PIDN:CAD05845.1; PID:g16503820; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY2853a

Query Match 32.3%; Score 20; DB 2; Length 15;
 Best Local Similarity 75.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPFL 5
 |||:
 Db 10 PPFL 13

RESULT 14
 A39040
 calsequesterin, cardiac muscle - dog (fragments)
 C:Species: Canis lupus familiaris (dog)
 C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 09-Jul-2004
 C:Accession: A39040
 R:Gala, S.E.; Jones, L.R.
 J. Biol. Chem. 266, 391-398, 1991
 A>Title: Phosphorylation of cardiac and skeletal muscle calsequesterin isoforms by casein
 A:Reference number: A39040; MUID:91093153; PMID:1985907
 A:Accession: A39040
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-18 <CAL>
 A:Cross-references: UNIPROT:P12637
 C:Keywords: cardiac muscle; heart; phosphoprotein

Query Match 32.3%; Score 20; DB 2; Length 18;
 Best Local Similarity 60.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 LPVNV 9
 |||:
 Db 8 LPTIN 12

RESULT 15
 S04229
 N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24k chain - rat (fragment)
 N:Alternate names: glycosylasparaginase
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
 C:Accession: S04229
 R:Tollersrud, O.K.; Aronson, Jr., N.N.
 Biochem. J. 260, 101-108, 1989
 A>Title: Purification and characterization of rat liver glycosylasparaginase.
 A:Reference number: S04229; MUID:89374025; PMID:2775174
 A:Accession: S04229
 A:Molecule type: protein
 A:Residues: 1-18 <ROL>
 C:Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase
 C:Keywords: hydrolase

Query Match 31.5%; Score 19.5; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 3.8e+03;
 Matches 6; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 5 LP-VNVNLP 12
 |||:
 Db 4 LPLVNVNLP 12

RESULT 16
 S01119
 photosystem II protein pbxk - spinach chloroplast (fragment)
 C:Species: chloroplast *Spinacia oleracea* (spinach)
 C:Date: 30-Jun-1989 #sequence_revision 31-Dec-1990 #text_change 19-Jan-1996
 C:Accession: S01119
 R:Murai, N.; Miyao, M.; Hayashida, N.; Hidaka, T.; Sugiura, M.
 FEBS Lett. 235, 283-288, 1988
 A>Title: Identification of a new gene in the chloroplast genome encoding a low-molecular
 A:Reference number: S01119
 A:Accession: S01119
 A:Molecule type: protein
 A:Residues: 1-13 <MOR>
 C:Genetics:
 A:Gene: pbxk
 A:Genome: chloroplast
 C:Superfamily: photosystem II protein pbxk
 C:Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem II; th

Query Match 30.6%; Score 19; DB 2; Length 13;

Best Local Similarity 50.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 FFLPVV 8
| : | : |
Db 8 FLXPV 13

RESULT 17

170076

glycophorin B/glycophorin A mutant fusion protein St-a (miscellaneous) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-May-1996 #sequence_revision 14-Aug-1997 #text_change 09-Jul-2004

C:Accession: I70076

R:Rearden, A.; Phan, H.; Dubnicoff, T.; Kudo, S.; Fukuda, M.

J. Biol. Chem. 265, 9259-9263, 1990

A:Title: Identification of the crossing-over point of a hybrid gene encoding human glyco

A:Reference number: I55334; PMID:90264417; PMID:1971625

A:Accession: I70076

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-13 <REA>

A:Cross-references: UNIPROT:Q14462; GB:M33507; GB:J05465; NID:9183743; PIDD:AAA35942.1;

A:Note: The translation is from an incorrect reading frame

C:Genetics:

A:Gene: GYPB/GYPB

C:Keywords: fusion protein

Query Match 30.6%; Score 19; DB 4; Length 13;
Best Local Similarity 33.3%; Pred. No. 3.4e+03;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVNVV 10
| : | : | : | : |
Db 6 LPVNVV 11

RESULT 18

PA0029

protein QAL00012 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997

C:Accession: PA0029

R:Kam, M.; Kawakami, T.; Miyake, N.; Tsugita, A.

submitted to JIPID July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensiona

A:Reference number: PA0001

A:Accession: PA0029

A:Molecule type: protein

A:Residues: 1-15 <KAM>

A:Experimental source: callus

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 3.9e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 FLVNVV 12
| : | : | : | : |
Db 7 FLVNVV 15

RESULT 19

S13973

chlorophyll a/b-binding protein type II - garden pea (fragment)

C:Species: Pisum sativum (garden pea)

C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

C:Accession: S13973

R:Jahn, P.; Junge, W.

Bur. J. Biochem. 193, 731-736, 1990

A:Title: Dicyclohexylcarbodiimide-binding proteins related to the short circuit of the P

A:Reference number: S13973; PMID:91065379; PMID:2174365

A:Accession: S13973

A:Molecule type: protein

A:Residues: 1-15 <JAH>

C:Genetics:

A:Genome: nuclear

C:Keywords: chlorophyll; chloroplast; light-harvesting complex; thylakoid; transmembrane

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 30.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 LFFPLPVNV 10
| : | : | : | : |
Db 5 VFTSIGIIV 14

RESULT 20

S54712

zein Zp22/6 protein - maize

C:Species: Zea mays (maize)

C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C:Accession: S54712

R:Chaudhuri, S.; Messing, J.

Mol. Gen. Genet. 246, 707-715, 1995

A:Title: RFLP mapping of the maize dz1 locus, which regulates methionine-rich 10 kDa ze

A:Reference number: S54712; PMID:95206245; PMID:7898438

A:Accession: S54712

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <CHA>

A:Cross-references: UNIPROT:Q7M1P8

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 30.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 FFLPVNVV 12
| : | : | : | : |
Db 1 FFLPVNVV 10

RESULT 21

T09741

photosystem I chain psal - upland cotton chloroplast (fragment)

C:Species: chloroplast Gossypium hirsutum (upland cotton)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T09741

R:Small, R.L.; Ryburn, J.A.; Cronm, R.C.; Seelanan, T.; Wendel, J.F.

Am. J. Bot. 85, 1301-1315, 1998

A:Title: The tortoise and the hare: choosing between noncoding plastome and nuclear Adh

A:Reference number: Z16323

A:Accession: T09741

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-16 <SMA>

A:Cross-references: UNIPROT:O19971; EMBL:AF031581; NID:92623684; PID:G3723945

C:Genetics:

A:Gene: psal

A:Genome: chloroplast

C:Keywords: chloroplast; photosynthesis; photosystem I

Query Match 30.6%; Score 19; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLVNV 8
| : | : | : | : |
Db 11 FLVNV 15

RESULT 22

T44936

calmodulin kinase 2 - fission yeast (Schizosaccharomyces pombe) (fragment)

C:Species: Schizosaccharomyces pombe

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T44936
 R:Alamy, V.; Alique, R.
 submitted to the EMBL Data Library, May 1996
 C:Reference number: Z22873
 A:Accession: T44936
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-16 <ALE>
 A:Cross-references: UNIPROT:O94554; EMBL:U57982; PDB:AA09466.1

Query Match
 Best Local Similarity 30.6%; Score 19; DB 2; Length 16;
 57.1%; Pred. No. 4.1e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 FFLPVVN 9
 : |||
 Db 10 FFLVVTN 16

RESULT 23
 C37520
 glutathione transferase (BC 2.5.1.18) MII - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 30-Sep-1993
 C:Accession: C37520; N24735
 R:Mannerlyk, B.; Alin, P.; Gutheberg, C.; Jensen, H.; Tahir, M.K.; Warholm, M.; Jorner
 Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985
 A>Title: Identification of three classes of cytosolic glutathione transferase common to
 A:Reference number: A24735; MUID:86042654; PMID:3864155
 A:Accession: C37520
 A:Molecule type: protein
 A:Residues: 1-17 <MAN>
 A:Superfamily: glutathione transferase
 C:Keywords: transferase

Query Match
 Best Local Similarity 30.6%; Score 19; DB 2; Length 17;
 50.0%; Pred. No. 4.4e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 FLPVN 9
 : |||
 Db 7 YFPVVD 12

RESULT 24

S70612
 alpha-macroglobulin proteinase inhibitor, tetrameric - bloodfluke planorb (fragment)

C:Species: Biomphalaria glabrata (bloodfluke planorb)
 C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
 C:Accession: S70612
 R:Bender, R.C.; Bayne, C.J.
 Biochem. J. 316, 893-900, 1996
 A>Title: Purification and characterization of a tetrameric alpha-macroglobulin proteinase
 A:Reference number: S70612; MUID:96265058; PMID:8670168
 A:Accession: S70612
 A:Molecule type: protein
 A:Residues: 1-18 <BEN>
 A:Cross-references: UNIPROT:Q9TWEO
 C:Complex: homotetramer
 C:Function:
 A:Description: inhibits proteinases possessing different catalytic mechanisms by steric

Query Match
 Best Local Similarity 30.6%; Score 19; DB 2; Length 18;
 36.4%; Pred. No. 4.6e+03;
 Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 FFLPVVN 12
 : |||
 Db 3 YFISAPNVV 13

RESULT 25
 JQ2030

hypothetical 1.9K protein - Oryzia pseudotsugata multicapsid nuclear polyhedrosis virus
 N:Alternate names: ORF2 mini gene protein
 C:Species: Oryzia pseudotsugata multicapsid nuclear polyhedrosis virus, OPMNPV
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
 C:Accession: JQ2030
 R:Russell, R.L.O.; Rohmann, G.F.
 J. Gen. Virol. 74, 1191-1195, 1993
 A>Title: Nucleotide sequence of the ubiquitin-39K gene region from the Oryzia pseudotsug
 A:Reference number: PQ0633; MUID:93286576; PMID:8389803
 A:Accession: JQ2030
 A:Molecule type: DNA
 A:Residues: 1-17 <RUS>
 A:Cross-references: DDBJ:D13375; NID:g222217; PDB:BA02640.1; PDB:dl003144; PDB:g222222

Query Match
 Best Local Similarity 29.8%; Score 18.5; DB 2; Length 17;
 85.7%; Pred. No. 5.3e+03;
 Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 5 LPVNVN 11
 : |||
 Db 3 LP-VNVN 8

RESULT 26

LFECFS

phesT operon leader peptide - Escherichia coli (strain K-12)

N:Alternate names: phenylalanyl-tRNA synthetase operon leader peptide
 C:Species: Escherichia coli

C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C:Accession: S11551; I53984; G64930; S06908
 R:Payat, G.; Mayaux, J.F.; Secerdot, C.; Fromant, M.; Springer, M.; Grunberg-Manago, M.;
 J. Mol. Biol. 171, 239-261, 1983
 A>Title: Escherichia coli phenylalanyl-tRNA synthetase operon region. Evidence for an at
 A:Reference number: A30391; MUID:84090239; PMID:6317865
 A:Accession: S11551

A:Molecule type: DNA
 A:Residues: 1-14 <RAY>
 A:Cross-references: UNIPROT:P06985; EMBL:V00291; NID:g43065; PDB:CAA23563.1; PDB:g43069
 R:Mayaux, J.
 Gene 30, 137-146, 1984
 A>Title: IS4 transposition in the attenuator region of the Escherichia coli phesT opero
 A:Reference number: I53984; MUID:85077605; PMID:6096210
 A:Accession: I53984
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-14 <RES>

A:Cross-references: GB:M13251; NID:g147182; PDB:AAA24333.1; PDB:g147185
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A>Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: G64930
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-14 <BLAT>
 A:Cross-references: GB:AE000266; GB:U00096; NID:g1787997; PDB:AACT4785.1; PDB:g1788008;
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: phem
 A:Map position: 37 min
 C:Function:
 A:Description: probably involved in attenuation regulation of phenylalanyl-tRNA synthetase
 C:Superfamily: phesT leader peptide

Query Match
 Best Local Similarity 29.0%; Score 18; DB 1; Length 14;
 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FFF 4
 : |||
 Db 8 FFF 10

RESULT 27

pheST operon leader peptide - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
F90931
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: F90931
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasegawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90931
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <NAV>
A:Cross-references: UNIPROT:P06985; GB:BA000007; PIDD:BA035845.1; PID:g13361889; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: EC82422
C:Superfamily: pheST leader peptide

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFF 4
|||
Db 8 PFF 10

RESULT 28

B85780
pheST operon leader peptide - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: B85780
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Linn, A.; Dimlant, E.; Potamouotis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: B85780
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <STO>
A:Cross-references: UNIPROT:P06985; GB:AE005174; NID:g12515726; PIDD:AA056702.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: phem
C:Superfamily: pheST leader peptide

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFF 4
|||
Db 8 PFF 10

RESULT 29

A60737
pollen allergen Lol p IV - perennial ryegrass (fragments)
C:Species: Lolium perenne (perennial ryegrass)
C:Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 17-Mar-1999
C:Accession: A60737
R:Jaggi, K.S.; Ekramoddoullah, A.K.M.; Kish, F.T.
Int. Arch. Allergy Appl. Immunol. 89, 342-348, 1999
A:Title: Allergenic fragments of ryegrass (Lolium perenne) pollen allergen Lol p IV.
A:Reference number: A60737; MUID:90007726; PMID:2793222
A:Accession: A60737
A:Status: preliminary

A:Molecule type: protein
A:Residues: 1-14 <JAG>
A:Keywords: pollen

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 33.3%; Pred. No. 5.4e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 PFLPVNVYL 11
|:::
Db 1 FLSPVVGLT 9

RESULT 30

AG0705
phenylalanyl-tRNA synthetase operon leader peptide [imported] - Salmonella enterica subsp.
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typh
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AG0705
R:Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Comercon, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AG0705
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <PAR>
A:Cross-references: GB:AL513382; PIDD:CA020216.1; PID:g16502854; GSPDB:GN00176
C:Genetics:
A:Gene: STY1774

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFF 4
|||
Db 8 PFF 10

RESULT 31

AF0296
phenylalanyl-tRNA synthetase operon leader peptide [imported] - Yersinia pestis (strain
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF0296
R:Parhill, J.; Wren, B.W.; Thomson, N.R.; Tiltall, R.W.; Holden, M.T.G.; Prentice, M.B.
demo-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0296
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <YUR>
A:Cross-references: UNIPROT:Q8ZDM9; GB:AL590842; PIDD:CA091234.1; PID:g15980423; GSPDB:G
C:Genetics:
A:Gene: phem

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFF 4
|||
Db 8 PFF 10

RESULT 32

LFRCF

phe operon leader peptide - Escherichia coli (strain K-12)
N.Alternate names: attenuator peptide

C.Species: Escherichia coli
C.Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C.Accession: A03593; B36494; A65038

R.Zurawski, G.; Brown, K.; Killingley, D.; Yanofsky, C.
Proc. Natl. Acad. Sci. U.S.A. 75, 4271-4275, 1978

A.Title: Nucleotide sequence of the leader region of the phenylalanine operon of Escherichia coli
A.Reference number: A03593; PMID:79033820; PMID:360214

A.Accession: A03593
A.Molecule type: DNA

A.Residues: 1-15 <ZUR>
A.Cross-references: UNIPROT:P03057; GB:V00314; GB:J01658; NID:G42378; PIDN:CAA23600.1; F

R.Gavini, N.; Davidson, B.E.
J. Biol. Chem. 265, 21532-21535, 1990

A.Title: pheA mutants of Escherichia coli have a defective pheA attenuator.
A.Reference number: A36494; PMID:91072346; PMID:2254312

A.Accession: B36494
A.Molecule type: DNA

A.Residues: 1-15 <GAV>
A.Cross-references: GB:M58024; GB:J05694; NID:G147178; PIDN:AAA62783.1; PID:G147180

R.Baltner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A.Title: The complete genome sequence of Escherichia coli K-12.
A.Reference number: A64720; PMID:97426617; PMID:9278503

A.Accession: A65038
A.Status: preliminary; nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA
A.Residues: 1-15 <BLAT>

A.Cross-references: GB:A8000346; GB:U00096; NID:G2367141; PIDN:AC75647.1; PID:G1788950;
A.Experimental source: strain K-12, substrain MG1655

C.Genetics:
A.Gene: pheU, pheA

A.Map position: 56 min
C.Superfamily: pheA leader peptide

Query Match 29.0%; Score 18; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.8e+03; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4
|||
Db 6 FFF 8

RESULT 33

27K protein A 3.4/5 - rice (fragment)

C.Species: Oryza sativa (rice)
C.Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 24-Feb-1995

C.Accession: PS0185
R.Kamo, M.; Tsugita, A.

submitted to JIPID, June 1991
A.Reference number: PS0184

A.Accession: PS0185
A.Molecule type: protein

A.Residues: 1-15 <KAM>

Query Match 29.0%; Score 18; DB 2; Length 15;

Best Local Similarity 50.0%; Pred. No. 5.8e+03; Indels 0; Gaps 0;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 VVNVLP 12
:|:|
Db 5 IVDVAP 10

RESULT 34

S71306 heat shock protein 90 - rat (fragment)

C.Species: Rattus norvegicus (Norway rat)

C.Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C.Accession: S71306

R.Concannon, M.; Sweda, L.I.; Levine, R.L.; Stadman, E.R.; Friguet, B.
Arch. Biochem. Biophys. 331, 232-240, 1996

A.Title: Age-related decline of rat liver multicatalytic proteinase activity and protect
A.Reference number: S71306; PMID:9629287; PMID:8660703

A.Accession: S71306
A.Molecule type: protein

A.Residues: 1-15 <CON>
A.Experimental source: liver

A.Keywords: heat shock; phosphoprotein; stress-induced protein

Query Match 29.0%; Score 18; DB 2; Length 15;

Best Local Similarity 50.0%; Pred. No. 5.8e+03; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 PVNVLP 11
:|:|
Db 9 PIVERTL 14

RESULT 35

hypothetical protein EC3461 [imported] - Escherichia coli (strain O157:H7, substrain RI
C.Species: Escherichia coli

C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C.Accession: E91061

R.Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gatawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hatori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001
A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc

A.Reference number: A96629; PMID:21156231; PMID:11258796
A.Accession: E91061

A.Status: preliminary
A.Molecule type: DNA

A.Residues: 1-15 <HAY>
A.Cross-references: UNIPROT:O8X2E0; UNIPROT:O8FEZ7; GB:BA000007; PIDN:BAB36884.1; PID:91

A.Experimental source: strain O157:H7, substrain RIMD 0509952
C.Genetics:
A.Gene: EC3461

Query Match 29.0%; Score 18; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.8e+03; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4
|||
Db 6 FFF 8

RESULT 36

chemoattractant protein - earthworm (Lumbricus terrestris) (fragment)

C.Species: Lumbricus terrestris (common earthworm)
C.Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004

C.Accession: A36279
R.Jiang, X.C.; Inouchi, J.; Wang, D.; Halpern, M.

J. Biol. Chem. 265, 8736-8744, 1990
A.Title: Purification and characterization of a chemoattractant from electric shock-indu

snakes.
A.Reference number: A36279; PMID:9025680; PMID:2160465

A.Accession: A36279
A.Status: preliminary

A.Molecule type: protein
A.Residues: 1-15 <JIA>

A.Cross-references: UNIPROT:O44335

Query Match 29.0%; Score 18; DB 2; Length 15;

Best Local Similarity 60.0%; Pred. No. 5.8e+03; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FFFLP 6

Db 8 FTYLVP 12

RESULT 37

S11290
matrix protein M1 - influenza A virus (strain A/FPV/Rosstock/34 [H7N1]) (fragment)
C:Species: Influenza A virus
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: S11290
R:Robertson, J.S.
Nucleic Acids Res. 6, 3745-3757, 1979
A:Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influenza A:Reference number: S11286; MUID:80034428; PMID:493121
C:Accession: S11290
A:Molecule type: genomic RNA
A:Residues: 1-16 <ROB>
A:Cross-references: UNIPROT:Q84098; EMBL:J02112
C:Genetics:
A:Map position: segment 7
C:Superfamily: influenza virus matrix protein M1

Query Match 29.0%; Score 18; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVNVLP 12
Db 11 VLSVVP 16

RESULT 38

S68730
bleomycin-binding protein - Streptomyces verticillius (fragment)
C:Species: Streptomyces verticillius
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: S68730
R:Sugiyama, M.; Kumagai, T.; Matsuo, H.; Bhuiyan, M.Z.A.; Ueda, K.; Mochizuki, H.; Nakam
PEBS Lett. 362, 80-84, 1995
A:Title: Overproduction of the bleomycin-binding proteins from bleomycin-producing Strept
al characterisation.
A:Reference number: S68730; MUID:95212588; PMID:7535252
A:Accession: S68730
A:Molecule type: protein
A:Residues: 1-16 <SUG>
A:Cross-references: UNIPROT:Q7M0J7
A:Experimental source: ATCC 15003
C:Keywords: antibiotic resistance

Query Match 29.0%; Score 18; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 6.1e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 FLPPVNVLP 11
Db 4 FLGAVPVL 11

RESULT 39

E23734
insulin-like growth factor-binding protein 3 - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: E23734
R:Shimada, S.; Gao, L.; Shimomura, M.; Ling, N.
Mol. Endocrinol. 5, 938-948, 1991
A:Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-6
A:Reference number: A23734; MUID:92049376; PMID:1719383
A:Accession: E23734
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <SHI>

Query Match 29.0%; Score 18; DB 2; Length 17;
Best Local Similarity 57.1%; Pred. No. 6.5e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 PVPVNVLP 12
Db 9 PVRXEP 15

RESULT 40

A32220
T-cell receptor delta chain precursor V region (DN7.3-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 30-May-1997
C:Accession: A32220
R:Korman, A.J.; Maruyama, J.; Raulof, D.H.
Proc. Natl. Acad. Sci. U.S.A. 86, 267-271, 1989
A:Title: Rearrangement by inversion of a T-cell receptor delta variable region gene loca
A:Reference number: A32220; MUID:89098895; PMID:2789518
A:Accession: A32220
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-18 <KOR>
A:Cross-references: GB:M23095
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 29.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPF 4
Db 9 PPF 11

Search completed: June 7, 2005, 23:20:39
Job time : 13.1273 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 52.8 Seconds
(without alignments)
116.382 Million cell updates/sec

Title: US-10-691-157-4
Perfect score: 62
Sequence: 1 LFFFLPVNVLP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	48.4	14	Q7SBM9	Q7SBM9 neurospora
2	27	43.5	13	Q7R8X6	Q7R8X6 plasmodium
3	26	41.9	12	RANS_RANCA	P82820 rana catesb
4	26	41.9	13	TEML_RANPI	P82848 rana pipien
5	26	41.9	15	Q7RPE9	Q7RPE9 plasmodium
6	26	41.9	17	Q8HKE6	Q8HKE6 thipicephal
7	26	41.9	17	Q9ERZ2	Q9ERZ2 mus musculi
8	25	40.3	13	CRBL_VESMA	P17232 vespa manda
9	25	40.3	15	Q9TNO1	Q9TNO1 mus sp. bet
10	24	38.7	17	Q7IUQ2	Q7IUQ2 homo sapien
11	24	38.7	18	Q7TQB5	Q7TQB5 mus musculi
12	24	38.7	12	Q91BM7	Q91BM7 autocographa
13	23	37.1	12	GRAR_RANRU	P40754 rana rugosa
14	23	37.1	13	CRBL_VESLE	P17235 vespaula lew
15	23	37.1	13	CRBL_VESXA	P17234 vespa xanth
16	23	37.1	13	TEIA_RANBO	P84116 rana boylii
17	23	37.1	17	Q8HKE6	Q8HKE6 thipicephal
18	23	37.1	18	Q8NED1	Q8NED1 homo sapien
19	23	37.1	18	Q8NED1	Q8NED1 plasmodium
20	22	35.5	13	BLAC_STRGR	P81173 streptomyce
21	22	35.5	15	Q367Z7	Q367Z7 homo sapien
22	22	35.5	15	Q464S6	Q464S6 clostridium
23	22	35.5	15	Q71IM5	Q71IM5 lactobacilli
24	22	35.5	16	Q6QVE1	Q6QVE1 phaseoculis v
25	22	35.5	17	UP36_UPEMJ	P82443 uperoleia v
26	22	35.5	17	Q9SKO7	Q9SKO7 sus scrofa
27	22	35.5	17	Q8OT36	Q8OT36 mus musculi
28	21.5	34.7	14	TEMC_RANLU	P82832 rana luteiv
29	21	33.9	9	Q9PBE5	Q9PBE5 kluyveromyc
30	21	33.9	11	Q9TQSO	Q9TQSO bos taurus
31	21	33.9	13	CRBL_VESAN	P17233 vespa anali

32	21	33.9	13	1	CRBL_VESCR	P01518 vespa crabr
33	21	33.9	13	1	CRBL_VESTR	P17231 vespa tropi
34	21	33.9	13	1	HPB9_RANES	P32416 rana esculie
35	21	33.9	13	1	TEMA_RANTE	P56917 rana tempor
36	21	33.9	13	1	TEMF_RANTE	P56921 rana tempor
37	21	33.9	14	1	CRBL_VESOR	P17336 vespa orien
38	21	33.9	15	2	Q9QVD7	Q9QVD7 rattus sp.
39	21	33.9	17	2	Q9URC6	Q9URC6 saccharomyc
40	21	33.9	17	2	Q95F78	Q95F78 homo sapien
41	21	33.9	17	2	Q95F78	Q95F78 hiziakia fus
42	21	33.9	18	2	Q19969	Q19969 gossypium a
43	21	33.9	18	2	Q19979	Q19979 gossypium t
44	20	32.3	8	2	Q40530	Q40530 nicotiana d
45	20	32.3	9	2	Q7M2N7	Q7M2N7 bos indicus
46	20	32.3	10	2	Q7Z212	Q7Z212 salvelinus
47	20	32.3	12	2	Q7RW16	Q7RW16 neurospora
48	20	32.3	13	2	HPAL_RANES	P32415 rana esculie
49	20	32.3	13	2	Q6LBE3	Q6LBE3 vibrio harv
50	20	32.3	14	2	Q8M099	Q8M099 lockus natu
51	20	32.3	14	2	P82340	P82340 pisum sativ
52	20	32.3	15	1	TEBI_BOTUA	P84026 bochrops ja
53	20	32.3	15	2	Q6JCR8	Q6JCR8 bemisia arg
54	20	32.3	15	2	Q68425	Q68425 buchmera ap
55	20	32.3	15	2	Q8XP44	Q8XP44 salmoneila
56	20	32.3	15	2	Q7CPZ9	Q7CPZ9 salmoneila
57	20	32.3	16	2	Q9UWK4	Q9UWK4 methanobact
58	20	32.3	17	2	Q06800	Q06800 saccharomyc
59	20	32.3	17	2	Q712V6	Q712V6 homo sapien
60	20	32.3	17	2	Q6URW9	Q6URW9 spiranthes
61	20	32.3	18	1	ALAL_CYPDPO	P82153 cydia pomon
62	20	32.3	18	2	Q7R809	Q7R809 plasmodium
63	20	32.3	18	2	Q7R9Y4	Q7R9Y4 plasmodium
64	20	32.3	18	2	Q8M0A0	Q8M0A0 lockus leuc
65	20	32.3	18	2	Q700A1	Q700A1 cicier ariet
66	19	30.6	5	1	PAP2_PAPMA	P81864 padachirus
67	19	30.6	8	2	P83532	P83532 lactobacilli
68	19	30.6	9	2	Q9GD36	Q9GD36 juncus efflu
69	19	30.6	10	2	Q7RS14	Q7RS14 plasmodium
70	19	30.6	10	2	Q67B09	Q67B09 bacterioph
71	19	30.6	11	2	Q9A1Z7	Q9A1Z7 carsonella
72	19	30.6	12	2	Q9G196	Q9G196 petunia hyb
73	19	30.6	12	2	Q37071	Q37071 sargassum p
74	19	30.6	13	1	TEIE_RANCL	P82884 rana clamit
75	19	30.6	13	1	TEMD_RANTE	P56919 rana tempor
76	19	30.6	13	2	Q14462	Q14462 homo sapien
77	19	30.6	13	2	Q16007	Q16007 homo sapien
78	19	30.6	13	2	Q6TKD3	Q6TKD3 praecitrull
79	19	30.6	13	2	Q6TKD4	Q6TKD4 sechium edu
80	19	30.6	13	2	Q6TKD5	Q6TKD5 sticyos angu
81	19	30.6	13	2	Q6TKD6	Q6TKD6 trichosanthe
82	19	30.6	13	2	Q6TKD7	Q6TKD7 luffa grave
83	19	30.6	13	2	Q6TKD8	Q6TKD8 luffa echin
84	19	30.6	13	2	Q6TKD9	Q6TKD9 cucurbita p
85	19	30.6	13	2	Q6TKD0	Q6TKD0 benincasa h
86	19	30.6	13	2	Q6TKX1	Q6TKX1 marah orege
87	19	30.6	13	2	Q6TKX2	Q6TKX2 cyclanthera
88	19	30.6	13	2	Q6TKX3	Q6TKX3 echinocysti
89	19	30.6	13	2	Q6TKX4	Q6TKX4 luffa quing
90	19	30.6	13	2	Q6TKX5	Q6TKX5 lagenaria l
91	19	30.6	13	2	Q6TKX6	Q6TKX6 citrullus l
92	19	30.6	13	2	Q6TKX7	Q6TKX7 citrullus c
93	19	30.6	13	2	Q6TKX8	Q6TKX8 acanthosicy
94	19	30.6	13	2	Q6TKX9	Q6TKX9 bryonia dio
95	19	30.6	13	2	Q6TKF0	Q6TKF0 coccolina pa
96	19	30.6	13	2	Q6TKF1	Q6TKF1 diplocyclos
97	19	30.6	13	2	Q6TKF2	Q6TKF2 ecballium e
98	19	30.6	13	2	Q9QVK6	Q9QVK6 rattus sp.
99	19	30.6	13	2	Q9PXB5	Q9PXB5 duck hepatic
100	19	30.6	14	1	UC15_MAIZE	P80621 zea mays (m

ALIGNMENTS

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RESULT 1
Q7SBM9 PRELIMINARY; PRT; 14 AA.
ID 07SBM9
AC 07SBM9
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE Predicted protein.
GN Name=NCU05740.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCB1_TaxID=5141;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Seltrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Korbe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gierre S.,
RA Kamai M., Kamysseis M., Mucelli E., Biele C., Rudd S., Frishman D.,
RA Kiyotova S., Raasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Omani S.A.,
RA Desouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Nativig D.O., Alex L.A., Mannhaupt G., Eboole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX0100165; EAA33802.1; -
SQ SEQUENCE 14 AA; 1563 MW; 4B270FF67ACB7CB7 CRC64;

Query Match
Best Local Similarity 48.4%; Score 30; DB 2; Length 14;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFFLPVNVNVL 11
| | | | |
| | | | |
Db 3 LLLPLSLVAL 13

RESULT 2
Q7RBX6 PRELIMINARY; PRT; 13 AA.
ID 07RBX6
AC 07RBX6;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY07094;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCB1_TaxID=73229;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=17XNL;
RA PubMed=1236885; DOI=10.1038/nature01099;
RA Carlton J.M., Anguioni S.V., Suh B.B., Kooji T.W., Petrea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selenig J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Freiser P.R., Bergman L.W., Vaideya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,

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RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002528; EAA19451.1; -
KW Hypothetical protein.
SQ SEQUENCE 13 AA; 1611 MW; DFB71AF6048E29C9 CRC64;

Query Match
Best Local Similarity 43.5%; Score 27; DB 2; Length 13;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PFFLPVNVN 10
| | | | |
| | | | |
Db 5 PFFLSMISL 13

RESULT 3
RAN5_RANCA STANDARD; PRT; 12 AA.
ID RAN5_RANCA
AC P82820;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ranatuerin 5.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCB1_TaxID=8400;
RN [1]
RC SEQUENCE.
RC TISSUE=skin secretion;
RX PubMed=9784389;
RA Goraya U., Knopp F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
RT American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592(1998).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Antibiotic; Direct protein sequencing.
SQ SEQUENCE 12 AA; 1335 MW; C8531D12A92735BD CRC64;

Query Match
Best Local Similarity 41.9%; Score 26; DB 1; Length 12;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPPVNVNVL 11
| | | | |
| | | | |
Db 1 FLPIASL 8

RESULT 4
TEM1_RANPI STANDARD; PRT; 13 AA.
ID TEM1_RANPI
AC P82848;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Temporin-1P.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCB1_TaxID=8404;
RN [1]
RC SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=skin secretion;
RX MEDLINE=20117700; PubMed=10651828;
RA Goraya U., Wang Y., Li Z., O'Flaherty M., Knopp F.C., Platz J.E.,
RA Conlon J.M.;
RT "Peptides with antimicrobial activity from four different families

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RT Isolated from the skins of the North American frogs *Rana luteiventris*,
 Rana berlandieri and *Rana pipiens*."
 RL Eur. J. Biochem. 267:894-900(2000)."
 CC -1- FUNCTION: Antibacterial activity against Gram-positive bacterium
 S. aureus.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- MASS SPECTROMETRY: MW=1368; METHOD=Electrospray; RANGE=1-13;
 CC NOTE=Ref.1.
 CC -1- SIMILARITY: Belongs to the frog skin active peptide (TSAP) family.
 CC Brevinin subfamily.
 CC Annotation: Amphibian defense peptide; Antibiotic;
 KM Direct protein sequencing.
 KW MOD RES 13 13 Leucine amide.
 FT SEQUENCE 13 AA; 1370 MW; 3EP3402B9DF92338 CRC64;
 SQ

Query Match 41.9%; Score 26; DB 1; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LFFPVNVL 11
 Db 1 LFFPVNKL 8

RESULT 5

07RPE9 PRELIMINARY; PRT; 15 AA.
 AC 07RPE9;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN Name=PY01510;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_Taxid=73339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RX PubMed=1236865; DOI=10.1038/nature01099;
 RA Carlton J.M., Anguioni S.V., Suh B.B., Kooij T.W., Pettea M.,
 Silva J.C., Ermolaeva M.D., Allen J.E., Sengut J.D., Koo H.L.,
 Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallow J., van Aken S.E., Riedmiller S.B., Feldlyum T.V.,
 Cho J.K., Quackenbush J., Sedegah M., Shoib A., Cummings L.M.,
 Florens L., Yates F.R., III, Raine J.D., Sindén R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 van Lin L.H., Jansz C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data
 CC EMBL: AABL0100400; EAA20851.1; --
 DR EMBL Hypothetical protein.
 KW NON TER 15 15
 FT SEQUENCE 15 AA; 1927 MW; DE1B84632CB57860 CRC64;
 SQ

Query Match 41.9%; Score 26; DB 2; Length 15;
 Best Local Similarity 55.6%; Pred. No. 1.8e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LFFFLPVVN 9
 Db 5 LFFFLPVNKT 13

RESULT 6

08HK86

ID 08HK86 PRELIMINARY; PRT; 17 AA.
 AC 08HK86;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN Name=ND1;
 OS Rhinipcephalus pulchellus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Rhinipcephalus.
 OX NCBI_Taxid=72859;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22660786; PubMed=12775521; DOI=10.1080/106351503093325;
 RA Murrell A., Campbell N.J.H., Barker S.C.;
 RT "The value of idiosyncratic markers and changes to conserved tRNA
 RT sequences from the mitochondrial genome of hard ticks (Acari: Ixodida:
 RT Ixodidae) for phylogenetic inference.";
 RL Syst. Biol. 52:296-310(2003).
 DR EMBL: AY059228; AAL79425.1; --
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1 1
 SQ SEQUENCE 17 AA; 2121 MW; 15A93BB8C1743136 CRC64;
 SQ

Query Match 41.9%; Score 26; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 2e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FFFLPVNVL 11
 Db 2 FFFFLSMINPI 11

RESULT 7

09ER22 PRELIMINARY; PRT; 17 AA.
 AC 09ER22;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Protein tyrosine phosphatase RPTP-GM1 (Fragment).
 GN Name=Pytpg;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Wright M.B., Foerzler D., Pech M.;
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF265561; AAG22700.1; --
 FT NON TER 17 17
 SQ SEQUENCE 17 AA; 2001 MW; 834A1F2920F07DBF CRC64;
 SQ

Query Match 41.9%; Score 26; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFL 5
 Db 4 LFFFL 8

RESULT 8

CRBL_VESMA
 ID CRBL_VESMA STANDARD; PRT; 13 AA.
 AC P17232;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Vespid chemotactic peptide M (VESP-M).
 OS Vespa mandarina (Hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 NCBI_TaxID=7446;

RA Yashura T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
 RA Fujino M.;
 RL (in) Munekata E. (eds.);
 RL Peptide chemistry 1983, pp.185-190. Protein Research Foundation, Osaka
 (1984).
 CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
 of neutrophils.
 KM Amination; Chemotaxis; Direct protein sequencing;
 KM Mast cell degranulation.
 FT MOD_RES 13 13 Leucine amide.
 SQ SEQUENCE 13 AA; 1384 MW; 265040289DF92338 CRC64;

Query Match 40.3%; Score 25; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2.3e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 FLPPVVNV 11
 ID 1 FLPIIGKL 8

RESULT 9
 Q9TNO1 PRELIMINARY; PRT; 15 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Beta 2M- class I-binding PEPTIDE=MAJOR histocompatibility complex H-
 DE 2KB-specific molecule POORLY associated with beta 2-microglobulin
 DE (Fragment).

OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94240094; PubMed=8183884;
 RA Joyce S., Kuzushima K., Kepcs G., Angeletti R.H., Nathanson S.G.;
 RT "Characterization of an incompletely assembled major
 RT histocompatibility class I molecule (H-2B) associated with unusually
 RT long peptides: implications for antigen processing and presentation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149(1994).

FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1754 MW; 2CEACDA0F180DC7 CRC64;

Query Match 40.3%; Score 25; DB 2; Length 15;
 Best Local Similarity 71.4%; Pred. No. 2.7e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 LPPVVNV 11
 ID 7 LPPVVKVM 13

RESULT 10
 Q71UO2 PRELIMINARY; PRT; 17 AA.

AC 071UO2;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Advanced glycosylation end product-specific receptor (Fragment).

GN Name=RAGE;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Blazkova M., Kankova K.;
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF065212; AAD15889.1;
 DR GO; GO:0004872; F:receptor activity; IEA.

FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1906 MW; 5E9B9ED01E183530 CRC64;

Query Match 38.7%; Score 24; DB 2; Length 17;
 Best Local Similarity 57.1%; Pred. No. 4.5e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FLPPVVNV 10
 ID 2 FLPPVGI 8

RESULT 11
 Q7TOB5 PRELIMINARY; PRT; 18 AA.

DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Programmed cell death 1 ligand 2 (Fragment).
 DE Name=Pcdcl192;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=22791977; PubMed=12909129; DOI=10.1016/S0161-5890(03)00085-3;
 RA Goraki K.S., Shin T., Crafton E., Otsubo M., Rattis F.M., Huang X.,
 RA Kelleher E., Francisco U., Pardoll D., Iwashima H.;
 RT "A set of genes selectively expressed in mature dendritic cells:
 RT utility of related cis-acting sequences for lentiviral gene
 RT transfer.";
 RL Mol. Immunol. 40:35-47(2003).

DR EMBL; AY225192; AA034707.1; --
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1999 MW; A9B68E78F78F517 CRC64;

Query Match 38.7%; Score 24; DB 2; Length 18;
 Best Local Similarity 30.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 LPPFLPPVVNV 10
 ID 1 MLLLPILNLT 10

RESULT 12
 Q91BM7 PRELIMINARY; PRT; 18 AA.

AC 091BM7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE P10 peptide (Fragment).
 OS Autographa californica nuclear polyhedrosis virus (AcNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OX Nucleopolyhedrovirus.
 NCBI_TaxID=46015;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=90085829; PubMed=2688302;
 RA Kuzio J., Jacques R., Faulkner P.;
 RT "Identification of p74, a gene essential for virulence of baculovirus
 RT occlusion bodies.";
 RL Virology 173:759-763(1989).
 DR EMBL; M31301; AAA46728.2; -.
 FT NON TER
 SQ SEQUENCE 18 AA; 1923 MW; FFA5B122C2BFD17A CRC64;

Query Match 38.7%; Score 24; DB 2; Length 18;
 Best Local Similarity 62.5%; Pred. No. 4.7e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LPVNVLP 12
 | | | | |
 Db 9 LVVNVNP 16

RESULT 13
 GRAR_RANRU STANDARD; PRT; 12 AA.
 AC P40754;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Granuliberin-R.
 OS Rana rugosa (wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=78062810; PubMed=589733;
 RA Nakajima T., Yasuhara T.;
 RT "A new mast cell degranulating peptide, granuliberin-R, in the frog
 RT (Rana rugosa) skin."
 RL Chem. Pharm. Bull. 25:2464-2465(1977).
 RN [2]
 RP SYNTHESIS.
 RX MEDLINE=78189201; PubMed=657408;
 RA Nakajima T., Yasuhara T., Hirai Y., Kitada C., Fujino M., Takeyama M.,
 RA Koyama K., Yajima H.;
 RT "Synthesis of the dodecapeptide amide corresponding to the entire
 RT amino acid sequence of granuliberin-R, a new frog skin peptide from
 RT Rana rugosa."
 RL Chem. Pharm. Bull. 26:1222-1230(1978).
 CC -1- FUNCTION: Mast cell degranulating peptide.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 KW Amidation; Amphibian defense peptide; Direct protein sequencing;
 KW Mast cell degranulation.
 FT MOD RES 12 Serine amide.
 FT MOD RES 12
 SQ SEQUENCE 12 AA; 1424 MW; 2B974EB9CA1B5047 CRC64;

Query Match 37.1%; Score 23; DB 1; Length 12;
 Best Local Similarity 66.7%; Pred. No. 4.8e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFFLPV 7
 | | | | |
 Db 1 PFFLPV 6

RESULT 14
 CRBL_VESLE STANDARD; PRT; 13 AA.
 AC P17235;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Vespid chemotactic peptide L (VESCP-L).

OS Vesputia lewisii (yellow jacket) (wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vesputia.
 OX NCBI_TaxID=7452;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
 RL (in) Izumiya N. (eds.);
 RL Peptide Chemistry 1984, pp.177-182. Protein Research Foundation, Osaka
 RL (1985).
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
 CC of neutrophils.
 KW Amidation; Chemotaxis; Direct protein sequencing;
 KW Mast cell degranulation.
 FT MOD RES 13 Leucine amide.
 FT MOD RES 13
 SQ SEQUENCE 13 AA; 1384 MW; C850402B8819233D CRC64;

Query Match 37.1%; Score 23; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 PFPVV 8
 | | | | |
 Db 1 PFPVV 5

RESULT 15
 CRBL_VESXA STANDARD; PRT; 13 AA.
 AC P17234;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Vespid chemotactic peptide X (VESCP-X).
 OS Vespa xanthoptera (Japanese hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7448;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
 RL (in) Izumiya N. (eds.);
 RL Peptide Chemistry 1984, pp.177-182. Protein Research Foundation, Osaka
 RL (1985).
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
 CC of neutrophils.
 KW Amidation; Chemotaxis; Direct protein sequencing;
 KW Mast cell degranulation.
 FT MOD RES 13 Leucine amide.
 FT MOD RES 13
 SQ SEQUENCE 13 AA; 1368 MW; C85040365DF9233D CRC64;

Query Match 37.1%; Score 23; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 PFPVV 8
 | | | | |
 Db 1 PFPVV 5

RESULT 16
 TEIA_RANBO STANDARD; PRT; 13 AA.
 AC P84116;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Temporalin-18Ya.
 OS Rana boylii (foochill yellow-legged frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OK NCBI_Taxid=160499;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA PubMed=14531844;
 RA Conlon J.M., Sonnevend A., Patel M., Davidson C., Nielsen P.F.,
 RA Pal T., Rollins-Smith L.A.;
 RT "Isolation of peptides of the brevinn-1 family with potent
 RT candidicidal activity from the skin secretions of the frog Rana
 RT boylii.";
 RL J. Pept. Res. 62:207-213(2003).
 CC -1- FUNCTION: Antibacterial activity against Gram-positive bacterium
 CC S.aureus.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- MASS SPECTROMETRY: MW=1381.9; METHOD=MALDI; RANGE=1-13;
 CC NOTE=Ref.1.
 CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
 CC Brevinn subfamily.
 KW Amidation; Amphibian defense peptide; Antibiotic;
 KW Direct protein sequencing.
 FT MOD_RES 13 13 Leucine amide.
 FT UNSURE 13 13 L or I.
 FT UNSURE 13 13
 SQ SEQUENCE 13 AA; 1384 MW; C850402B9DECC3D CRC64;

Query Match 37.1%; Score 23; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 FFLPV 8
 DB 1 FFLPI 5

RESULT 17
 ID 08HKF6 PRELIMINARY; PRT; 17 AA.
 AC 08HKF6;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 OS Name=ND1;
 OS Rhinoceros everts.
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodidae; Ixodidae; Rhinoceros everts.
 OC NCBI_Taxid=60190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22660786; PubMed=12775521; DOI=10.1080/10635150309325;
 RA Murrell A., Campbell N.J.H., Barker S.C.;
 RT "The value of idiosyncratic markers and changes to conserved tRNA
 RT sequences from the mitochondrial genome of hard ticks (Acari: Ixodidae;
 RT Ixodidae) for phylogenetic inference.";
 RL Syst. Biol. 52:296-310(2003).
 DR EMBL; AY059219; AAL79415.1; -;
 DR GO; GO:0005739; C:mitochondrion; IRA.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 2071 MW; 15AFD0CC174322 CRC64;

Query Match 37.1%; Score 23; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 6.6e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 FFLPVVNL 11
 DB 2 FFLSVNNT 11

RESULT 18
 ID 08NED1 PRELIMINARY; PRT; 18 AA.
 AC 08NED1;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OK NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC032027; AA032027.1; -;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 18 AA; 2050 MW; B71A655B65FD253F CRC64;

Query Match 37.1%; Score 23; DB 2; Length 18;
 Best Local Similarity 80.0%; Pred. No. 7e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 FFLPV 6
 DB 1 FFLPV 5

RESULT 19
 ID 07RAU4 PRELIMINARY; PRT; 18 AA.
 AC 07RAU4;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=PY06405;
 OS Plasmodium yoelii yoelii.
 OS Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 OK NCBI_Taxid=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RX PubMed=1236865; DOI=10.1038/nature01099;
 RA Carlton J.M., Anguilo S.V., Suh B.B., Koo J.T.W., Pertea M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallow S.J., van Aken S.E., Riedmiller S.B., Feldblum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shalish A., Cummings L.M.,
 RA Florens L., Yates F.R., III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Jansz C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAL01002164; EAA18620.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 18 AA; 2023 MW; FABC67565CD73D1E CRC64;

Query Match 37.1%; Score 23; DB 2; Length 18;
 Best Local Similarity 36.4%; Pred. No. 7e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 FFLPVVNL 11
 DB 1 FFLPVVNL 11

Db 6 LPFPPVITIL 16

RESULT 20

BLAC_STRGR STANDARD; PRT; 13 AA.

AC P81173;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Beta-lactamase (EC 3.5.2.6) (Fragment).

OS Streptomyces griseus.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycetaceae; Streptomycetaceae; Streptomycetes.

OC NCBI_TaxId=1911;

RN [1]

RP SEQUENCE.

RC STRAIN=NRRL B-2682;

RX MEDLINE=98386507; PubMed=9720038;

RA Deak E., Szabo I., Kalmanczelyi A., Gal Z., Barabas G., Panyige A.;

RT "Membrane-bound and extracellular beta-lactamase production with

RL Microbiology 144:2169-2177(1998).

CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-

CC -1- SUBCELLULAR LOCATION: Secreted and membrane-bound.

CC -1- SIMILARITY: Belongs to the class-A beta-lactamase family.

DR InterPro; IPR000871; Beta_lactamase_A.

DR PROSITE; PS00146; BETA_LACTAMASE_A; PARTIAL.

KW Antibiotic resistance; Direct protein sequencing; Hydrolase; Membrane.

FT NON TER 13

SQ SEQUENCE 13 AA; 1236 MW; 14C5129118D54760 CRC64;

Query Match 35.5%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 LPVVNV 10
|:|:|
Db 6 LPVVNV 11

RESULT 21

Q36727 PRELIMINARY; PRT; 15 AA.

AC Q36727;

DT 01-NOV-1996 (TRENBLREL. 01, Created)

DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)

DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)

DE ND2 protein (Fragment).

GN Name=ND2;

OS Homo sapiens (Human).

OC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94380052; PubMed=8093052;

RA Koegl S., Eggenberger R., Mehrezn P., Graeber M.B.;

RT "No association of mutations at nucleotide 5460 of mitochondrial NADH

RL Biochem. Biophys. Res. Commun. 203:745-749(1994).

DR EMBL; S73804; A001413.1; -

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON TER 1

SQ SEQUENCE 15 AA; 1923 MW; D58870F163B6060 CRC64;

Query Match 35.5%; Score 22; DB 2; Length 15;
Best Local Similarity 37.5%; Pred. No. 8.8e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 LPFPLPV 8
|:|:|:|
Db 6 LPFPLRL 13

RESULT 22

Q46456 PRELIMINARY; PRT; 15 AA.

AC Q46456;

DT 01-NOV-1996 (TRENBLREL. 01, Created)

DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)

DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)

DE Tetanus toxin (Fragment).

OS Clostridium tetani.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OC NCBI_TaxId=1513;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=87053814; PubMed=3536478;

RA Eisel U., Jarasch W., Goretzki K., Henechen A., Engels J., Weller U.,

RT "Tetanus toxin: primary structure, expression in E. coli, and homology

RL with botulinum toxins.";

RL EMBL; X04436; CAA28032.1; -

DR EMBL; X04436; CAA28032.1; -

FT NON TER 1

SQ SEQUENCE 15 AA; 1706 MW; 08110F73DCCD7EC5 CRC64;

Query Match 35.5%; Score 22; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 8.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 PVPVNL 11
|:|:|
Db 7 PVPVNL 12

RESULT 23

Q711M5 PRELIMINARY; PRT; 15 AA.

AC Q711M5;

DT 05-JUL-2004 (TRENBLREL. 27, Created)

DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)

DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)

DE Glycosyltransferase family 2 protein (Fragment).

OC Lactobacillus delbrueckii (subsp. lactis).

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;

OC Lactobacillus.

OC NCBI_TaxId=29397;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=ATCC 4797;

RA Langenheilm J.F., Ulrich R.L.;

RT Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF496244; AAQ06912.1; -

DR GO; GO:0016740; F:transferase activity; IEA.

KW Transferase.

FT NON TER 15

SQ SEQUENCE 15 AA; 1701 MW; CB7B95B8DFAEC9B CRC64;

Query Match 35.5%; Score 22; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 8.8e+03;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 5 LPVVNV 11
|:|:|:|
Db 5 LPVSVII 11

RESULT 24

Q6QVE1 PRELIMINARY; PRT; 16 AA.

ID Q6QVE1

AC Q6QVE1;
 DT 05-JUN-2004 (TREMBlrel. 27, Created)
 DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)
 DE Ribonuclease H (Fragment).
 CN Name=RNase H;
 OS Phaseolus vulgaris (Kidney bean) (French bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eusteroideae; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
 OC NCBI_TaxID=3885;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15060605; DOI=10.1139/g03-102;
 RA Gallardo L.M., Galtan E., Baccam P., Tohme J.;
 RT "Isolation and characterization of RNase-LTR sequences of Ty1-copia
 retrotransposons in common bean (Phaseolus vulgaris L.)."
 RL Genome 47:84-95(2004).
 DR EMBL; AY524258; AAS18555.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 16 AA; 1935 MW; 3E60812E8ED26A23 CRC64;

Query Match 35.5%; Score 22; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFPL 5
 ||||
 Db 13 PFPL 16

RESULT 25
 UP36 UPEMJ STANDARD; PRT; 17 AA.
 AC P82043;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Uperin 3.6.
 OS Uperoleia mjobergii (Australian toadlet).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OC NCBI_TaxID=104954;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "New antibiotic uperin peptides from the dorsal glands of the
 Australian toadlet Uperoleia mjobergii.";
 RL Aust. J. Chem. 49:1135-1131(1996).
 CC -1- FUNCTION: Shows antibacterial activity against B.cereus, L.lactis,
 CC L.limonu, M.lureus, S.aureus, S.epidermis and S.ubertis.
 CC -1- SUBCELLULAR LOCATION: secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -1- MASS SPECTROMETRY: MW=1826; METHOD=FA; RANGE=1-17; NOTE=Ref.1.
 KW Amittation; Amphibian defense peptide; Antibiotic;
 KW direct protein sequencing.
 FT MOD_RES 17 17 Proline amide.
 SQ SEQUENCE 17 AA; 1778 MW; 784DBB46263CA3D CRC64;

Query Match 35.5%; Score 22; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.9e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVNVL 11
 |||||
 Db 9 VVNVL 13

RESULT 26
 Q95KQ7 PRELIMINARY; PRT; 17 AA.

AC Q95KQ7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE B-cell CLL/Lymphoma 9 (Fragment).
 CN Name=BCL9;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22042654; PubMed=12047235;
 RA Knoll A., Dvorak J., Konner G.A., Cepica S.;
 RT "Linkage and cytogenetic mapping of the BCL9 gene to porcine
 chromosome 4.";
 RL Anim. Genet. 33:162-163(2002).
 DR EMBL; AJ146470; CAC94923.1; -.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1825 MW; 90F402DC8C5CF231 CRC64;

Query Match 35.5%; Score 22; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 9.9e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 LPVVNVLP 12
 |||||
 Db 10 LPVVNVLP 17

RESULT 27
 Q80T36 PRELIMINARY; PRT; 17 AA.
 AC Q80T36;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE G protein-coupled receptor type 16, brain-specific angiotensin II receptor 1
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100;
 RA Vassilatis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E.,
 RA Morfitt M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,
 RA Bergmann J.E., Galtanar G.A.;
 RT "The G protein-coupled receptor repertoire of human and mouse.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908(2003).
 DR EMBL; AY55613; AAO85125.1; -.
 DR GO; GO:0004872; P:receptor activity; IEA.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 2133 MW; A20F02808DBA5BFB CRC64;

Query Match 35.5%; Score 22; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFPL 5
 |||||
 Db 3 PFPL 6

RESULT 28
 TEMC_RANLU STANDARD; PRT; 14 AA.
 AC P82832;
 DT 29-MAR-2004 (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DB Temporal-11c.
 OS Rana luteiventris (Spotted frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 RN NCB1_TaxID=58176;
 [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20117700; PubMed=10651828;
 RA Gozaya J., Wang Y., Li Z., O'Flaherty M., Knopp F.C., Platz J.E.,
 RA Conlon J.M.;
 RT "Peptides with antimicrobial activity from four different families
 isolated from the skins of the North American frogs Rana luteiventris,
 Rana berlandieri and Rana dipiens.";
 RL Eur. J. Biochem. 267:894-900(2000).
 CC -1- FUNCTION: Antibacterial activity against Gram-positive bacterium
 S.aureus. Weak activity against Gram-negative bacterium E.coli and
 C.albicans.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- MASS SPECTROMETRY: MW=1603.1; METHOD=Electrospray; RANGE=1-14;
 CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
 CC Brevitin subfamily.
 KW Amidation; Amphibian defense peptide; Antibiotic;
 KW Direct protein sequencing; Fungicide.
 FT MOD_RES 14 Leucine amide.
 FT MOD_RES 14
 SQ SEQUENCE 14 AA; 1604 MW; 0B540E1B7FCA8924 CRC64;

Query Match 34.7%; Score 21.5; DB 1; Length 14;
 Best Local Similarity 44.4%; Pred. No. 1e+04; 0; Indels 1; Gaps 1;
 Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 4 FLVPV-VNVL 11
 |||:|:|:
 DB 1 FLPIILNLI 9

RESULT 29
 Q9P8B5 PRELIMINARY; PRT; 9 AA.
 AC Q9P8B5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE His4 protein (Fragment).
 GN Name=His4;
 OS Kluyveromyces lacticis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCB1_TaxID=28985;
 [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL-Y1140;
 RX MEDLINE=99448382; PubMed=10518937; DOI=10.1016/S0014-5793(99)01105-9;
 RA Lamas-Maceliras M., Bepetanza Cerdan E., Freire-Picos M.A.;
 RT "Kluyveromyces lacticis His4 transcriptional regulation: similarities
 and differences to Saccharomyces cerevisiae His4 gene.";
 RL FEBS Lett. 458:72-76(1999).
 DR EMBL; AJ238494; CAB87125.1; -.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.6e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 LPVVNV 10
 |||||:
 DB 2 LPVVV 7

RESULT 30
 Q9TOS0 PRELIMINARY; PRT; 11 AA.
 AC Q9TOS0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE C-kit (Fragment).
 GN Name=kit;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCB1_TaxID=9913;
 [1]
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=20154958; PubMed=10690368;
 RA Olsen H.G., Vage D.I., Lien S., Klungland H.;
 RT "A polymorphism in the bovine c-kit gene.";
 RL Anim. Genet. 31:71-71(2000).
 DR EMBL; AJ243424; CAB60775.1; -.
 DR EMBL; AJ243060; CAB60774.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 9.8e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVVNV 10
 |||||:
 DB 4 VPVSV 9

RESULT 31
 CRBL_VESAN STANDARD; PRT; 13 AA.
 ID CRBL_VESAN
 AC P17233;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Vespid chemotactic peptide A (VESP-A).
 OS Vespa analis (Hornet).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCB1_TaxID=7449;
 [1]
 RN RP SEQUENCE.
 RC TISSUE=Venom;
 RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
 RA Fujino M.;
 RL (In) Munekata B. (eds.);
 RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation, Osaka
 (1984).
 CC -1- FUNCTION: Maat cell degranulating peptide. Induces the chemotaxis
 of neutrophils.
 CC Amidation; Chemotaxis; Direct protein sequencing;
 KW Maat cell degranulation.
 FT MOD_RES 13
 FT MOD_RES 13 Leucine amide.
 SQ SEQUENCE 13 AA; 1386 MW; C8554365DF9233D CRC64;

Query Match 33.9%; Score 21; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLVPV 8
 |||||:
 DB 1 FLVPMI 5

RESULT 32
 ID CRBL_VESCR STANDARD; PRT; 13 AA.
 AC P01518;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Crabrolin.
 OS Vespa crabro (European hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
 NCBI_TaxID=7445;
 OK NCBI_TaxID=7445;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=84289390; PubMed=6206053;
 RA Argiolas A., Pisano J.J.;
 RT "Isolation and characterization of two new peptides, mastoparan C and crabrolin, from the venom of the European hornet, *Vespa crabro*.";
 RL J. Biol. Chem. 259:10106-10111(1984).
 RN [2]
 RP SYNTHESIS, AND ANTIMICROBIAL ACTIVITY.
 RX MEDLINE=97419326; PubMed=9273892;
 RA Krishnakumari V., Nagaraj R.;
 RT "Antimicrobial and hemolytic activities of crabrolin, a 13-residue peptide from the venom of the European hornet, *Vespa crabro*, and its analogs.";
 RL J. Pept. Res. 50:88-93(1997).
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis of neutrophils. Has antimicrobial and hemolytic activity.
 DR PIR; A01781; ZVHP1.
 KW Amidation; Antibiotic; Chemotaxis; Direct protein sequencing;
 KM Mast cell degranulation.
 FT MOD_RES 13 AA; 1497 MW; 51SEF8FCEH8D2407 CRC64;
 SQ SEQUENCE

Query Match 33.9%; Score 21; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPPV 8
 |||:
 Db 1 FLPLI 5

RESULT 33
 ID CRBL_VESTR STANDARD; PRT; 13 AA.
 AC P17231;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Vespid Chemotactic Peptide T (VESP-T).
 OS Vespa tropica (Hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
 NCBI_TaxID=7450;
 OK NCBI_TaxID=7450;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Yasuhara T., Nakajima T., Erspamer V.;
 RL (In) Sakakibara S. (eds.);
 RL Peptide Chemistry 1982, pp.213-218, Protein Research Foundation, Osaka (1983).
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis of neutrophils.
 KW Amidation; Chemotaxis; Direct protein sequencing;
 KM Mast cell degranulation.
 FT MOD_RES 13 AA; 1354 MW; 22014036SDFE5338 CRC64;
 SQ SEQUENCE

Query Match 33.9%; Score 21; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPPV 8
 |||:
 Db 1 FLPLI 5

RESULT 34
 ID HPB9_RANES STANDARD; PRT; 13 AA.
 AC P32416;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hemolytic protein B9 (Fragment).
 OS Rana esculenta (Edible frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 NCBI_TaxID=8401;
 OK NCBI_TaxID=8401;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90198965; PubMed=2317508; DOI=10.1016/0304-4165(90)90140-R;
 RA Stimaco M., de Blase D., Severini C., Alta M., Erspamer G.F.,
 RA Barra D., Bossa F.;
 RT "Purification and characterization of bioactive peptides from skin extracts of *Rana esculenta*.";
 RL Biochim. Biophys. Acta 1033:318-323(1990).
 CC -1- FUNCTION: Shows hemolytic activity.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S09019; S09019.
 KW Amidation; Amphibian defense peptide; Direct protein sequencing;
 KM Hemolysis.
 FT MOD_RES 13 AA; 1402 MW; C6B41A765DF9287D CRC64;
 FT NON_TER 13
 SQ SEQUENCE

Query Match 33.9%; Score 21; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPPV 8
 |||:
 Db 1 FLPLI 5

RESULT 35
 ID TEMA_RANTE STANDARD; PRT; 13 AA.
 AC P56917;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Temporin A.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 NCBI_TaxID=8407;
 OK NCBI_TaxID=8407;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Stimaco M., Mignogna G., Canofenti S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT "Temporins, antimicrobial peptides from the European red frog *Rana temporaria*.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -1- FUNCTION: Has antibacterial activity against Gram-positive bacteria.
 CC -1- SUBCELLULAR LOCATION: Secreted.

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CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevin subfamily.
KW Amidation: Amphibian defense peptide; Antibiotic;
KW Direct protein sequencing.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1398 MW; 2653612B9DECD408 CRC64;

Query Match
Best Local Similarity 33.9%; Score 21; DB 1; Length 13;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPVV 8
   |||:
   1 FLPVI 5
DB

RESULT 36
TEMP_RANTE STANDARD; PRT; 13 AA.
ID TEMP_RANTE
AC P56921;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tempoxin F.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OK NCBI_TaxID=8407;
RN (1)
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Tempoxins", antimicrobial peptides from the European red frog Rana
RT temporaria."
CC -1- FUNCTION: Has antibacterial activity against Gram-negative and
CC Gram-positive bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevin subfamily.
KW Amidation: Amphibian defense peptide; Antibiotic;
KW Direct protein sequencing.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;

Query Match
Best Local Similarity 33.9%; Score 21; DB 1; Length 13;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPVV 8
   |||:
   1 FLPVI 5
DB

RESULT 37
CRBL_VESOR STANDARD; PRT; 14 AA.
ID CRBL_VESOR
AC P17236;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Histamine releasing peptide II (HR-II).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OK NCBI_TaxID=7447;
RN (1)
RP SEQUENCE.

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RC TISSUE=Venom;
RA Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA Roznov B.V., Gubchik I.S.;
RT "Structure and properties of histamine releasing peptides from the
RT venom of Vespa orientalis hornet."
RL Bioorg. Khim. 7:1467-1477(1981).
CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
DR PIR: JN0390; JN0390.
KW Amidation; Chemotaxis; Direct protein sequencing;
KW Mast cell degranulation.
FT MOD_RES 14
SQ SEQUENCE 14 AA; 1524 MW; 22015B46CEDFD38 CRC64;

Query Match
Best Local Similarity 33.9%; Score 21; DB 1; Length 14;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPVV 8
   |||:
   1 FLPVI 5
DB

RESULT 38
O9QVD7 PRELIMINARY; PRT; 15 AA.
ID O9QVD7
AC O9QVD7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Inositol 1,4,5-trisphosphate binding protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OK NCBI_TaxID=10118;
RN (1)
RP SEQUENCE.
RX MEDLINE=92202192; PubMed=1313009;
RA Kanamatsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
RA Iwanaga S., Hirata M.;
RT "Putative inositol 1,4,5-trisphosphate binding proteins in rat brain
RT cytosol."
RL J. Biol. Chem. 267:6518-6525(1992).
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 15 AA; 1726 MW; 1F161D1E2ADF88BD CRC64;

Query Match
Best Local Similarity 33.9%; Score 21; DB 2; Length 15;
Matches 1; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 LFFPLPVNV 10
   :||:
   1 IYFMAIIDI 10
DB

RESULT 39
O9URC6 PRELIMINARY; PRT; 17 AA.
ID O9URC6
AC O9URC6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Lipid-binding protein (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OK NCBI_TaxID=4932;
RN (1)
RP SEQUENCE.
RX MEDLINE=91353077; PubMed=1882548;
RX Creutz C.E., Snyder S.L., Kamouris N.G.;
RT "Calcium-dependent secretory vesicle-binding and lipid-binding

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RT proteins of Saccharomyces cerevisiae.";

RL Yeast 7:229-244(1991).

DR GO; GO:0005853; C:eukaryotic translation elongation factor 1. . .; IEA.

DR GO; GO:0003746; P:translation elongation factor activity; IEA.

DR GO; GO:0006414; P:translational elongation; IEA.

DR InterPro; IPR001662; EFL_G.

DR ProDom; PD006217; EFL_G; 1.

FT NON_TER 1

SQ SEQUENCE 17 AA; 1959 MW; C2EB654328774AD2 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;

Best Local Similarity 33.3%; Pred. No. 1.5e+04;

Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 FLPVV 12

Db 4 YVPFVAP 12

RESULT 40

O95795 PRELIMINARY; PRT; 17 AA.

AC O95795; 01-MAY-1999 (TRENBLER). 10, Created)

DT 01-MAY-1999 (TRENBLER). 10, Last sequence update)

DT 01-JUN-2003 (TRENBLER). 24, Last annotation update)

DE Advanced glycosylation end product-specific receptor (Fragment).

CN Name=RAGE;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI Taxid=9606;

RN [1] _SEQUENCE FROM N.A.

RA Blazkova M., Kankova K.;

RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF065211; AAD15888.1; .

DR GO; GO:0004872; F:receptor activity; IEA.

KW Receptor.

FT NON_TER 1

FT NON_TER 17

SQ SEQUENCE 17 AA; 1727 MW; 38C7EB8959B00D72 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;

Best Local Similarity 80.0%; Pred. No. 1.5e+04;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 FLPVV 8

Db 12 FLPAV 16

Search completed: June 7, 2005, 23:18:57
Job time : 55.8 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 7, 2005, 22:52:07 ; Search time 80.7273 Seconds
(without alignments)
71.864 Million cell updates/sec

Title: US-10-691-157-5
Perfect score: 81
Sequence: 1 DLEMPVLPEPPFV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	81	100.0	15	4 AAB72504	Aab72504 Colostrien
2	81	100.0	15	4 AAB59332	Aab59332 Ewe colos
3	81	100.0	15	4 AAB72250	Aab72250 Colostrien
4	81	100.0	15	4 AAB72536	Aab72536 Colostrien
5	81	100.0	15	5 AAO14581	Aao14581 Neural ce
6	81	100.0	15	5 AAM51040	Aam51040 Colostrien
7	81	100.0	15	5 AAE20232	Aae20232 Colostrien
8	81	100.0	15	5 ADN60299	Adn60299 Constitue
9	81	100.0	15	8 ADS74398	AdS74398 Ovine col
10	81	100.0	15	4 AAB59332	Aab59332 Ewe colos
11	57	70.4	10	4 AAE07187	Aae07187 Colostrien
12	51	63.0	10	4 AAE07197	Aae07197 Modified
13	39.5	48.8	15	5 AAD71712	Aad71712 Transcrip
14	39	48.1	17	7 ADF14579	Adf14579 Glutren-de
15	36	44.4	18	4 AAB72530	Aab72530 Colostrien
16	36	44.4	18	4 AAB59330	Aab59330 Ewe colos
17	36	44.4	18	4 AAB72267	Aab72267 Colostrien
18	36	44.4	18	4 AAB72552	Aab72552 Colostrien
19	36	44.4	18	5 AAO14558	Aao14558 Neural ce
20	36	44.4	18	5 AAM51056	Aam51056 Colostrien
21	36	44.4	18	5 AAE20249	Aae20249 Colostrien
22	36	44.4	18	8 ADN60316	Adn60316 Constitue
23	36	44.4	18	8 ADS74406	AdS74406 Ovine col
24	35	43.2	12	8 ADH14551	Adh14551 Barley ho
25	35	43.2	12	8 ADH14849	Adh14849 Gliadin r

26	34	42.0	14	2 AAR93469	Aar93469 GST-SRC p
27	34	42.0	15	4 AAB72507	Aab72507 Colostrien
28	34	42.0	15	4 AAB59313	Aab59313 Ewe colos
29	34	42.0	15	4 AAB72253	Aab72253 Colostrien
30	34	42.0	15	4 AAB72539	Aab72539 Colostrien
31	34	42.0	15	5 AAO14584	Aao14584 Neural ce
32	34	42.0	15	5 AAM51043	Aam51043 Colostrien
33	34	42.0	15	5 AAE20235	Aae20235 Colostrien
34	34	42.0	15	5 ABB09569	Abb09569 Human LI
35	34	42.0	15	5 ADN60302	Adn60302 Constitue
36	34	42.0	15	8 ADR31399	Adr31399 Heat ehoc
37	34	42.0	15	8 ADS74389	AdS74389 Ovine col
38	34	42.0	16	4 AAB59344	Aab59344 Ewe colos
39	34	42.0	17	6 ADH14830	Adh14830 Gliadin r
40	34	42.0	18	6 AAE34144	Aae34144 T-cell st
41	33	40.7	12	8 ADM96406	Adm96406 Immature
42	33	40.7	14	2 AAR58339	Aar58339 Hypocensi
43	33	40.7	14	7 ADF14537	Adf14537 Eptlope o
44	33	40.7	14	7 ADF14521	Adf14521 Eptlope o
45	33	40.7	14	7 ADF14850	Adf14850 T cell st
46	33	40.7	14	7 ADF14513	Adf14513 Glutren-de
47	33	40.7	14	7 ADF14529	Adf14529 Eptlope o
48	33	40.7	14	8 ADG37024	Adg37024 Bovine ca
49	33	40.7	15	8 ADJ38553	Adj38553 HSV-2 UR2
50	33	40.7	16	8 ADH14805	Adh14805 Gliadin r
51	33	40.7	17	8 ADH14823	Adh14823 Gliadin r
52	33	40.7	17	8 ADH14828	Adh14828 Gliadin r
53	33	40.7	17	8 ADH14826	Adh14826 Gliadin r
54	32	39.5	13	8 ADQ15567	Adq15567 Targeting
55	32	39.5	15	2 AAW85209	Aaw85209 Helper T-
56	32	39.5	15	2 AAW85195	Aaw85195 Helper T-
57	32	39.5	15	2 AAW85329	Aaw85329 Helper T-
58	32	39.5	15	4 ABP24651	Abp24651 HIV DR su
59	32	39.5	15	4 ABP24658	Abp24658 HIV DR su
60	32	39.5	15	8 ADH14851	Adh14851 Gliadin r
61	32	39.5	16	2 AAR29099	Aar29099 Chymotryp
62	32	39.5	16	8 ADH14810	Adh14810 Gliadin r
63	32	39.5	16	8 ADR31998	Adr31998 Heat shoc
64	31.5	38.9	18	6 ADB12816	AdB12816 Antihyper
65	31	38.3	10	2 AAR93548	Aar93548 Random.10
66	31	38.3	10	4 AAB75678	Aab75678 HLA class
67	31	38.3	10	6 ABR47334	AbR47334 Staphyloc
68	31	38.3	12	6 ABR47208	AbR47208 Staphyloc
69	31	38.3	12	6 ABR75157	AbR75157 Elemental
70	31	38.3	12	7 ADB67069	AdB67069 GaAs bind
71	31	38.3	12	7 AAO24131	Aao24131 Chaperoni
72	31	38.3	12	7 ADG91636	Adg91636 Phage sin
73	31	38.3	12	8 ADL99339	AdL99339 Nanobstruc
74	31	38.3	12	8 ADO07136	Ado07136 GaAs seml
75	31	38.3	13	3 AAD07345	Aad07345 M13 colip
76	31	38.3	13	3 AAY57715	Aay57715 Human cju
77	31	38.3	17	8 ADH14703	Adh14703 Gliadin r
78	31	38.3	18	3 AAY57716	Aay57716 Human cju
79	30	37.0	9	6 ABR25398	AbR25398 Human can
80	30	37.0	9	6 ABR24394	AbR24394 Human can
81	30	37.0	9	6 ABR24628	AbR24628 Human can
82	30	37.0	9	6 ABR25632	AbR25632 Human can
83	30	37.0	9	6 ABR24838	AbR24838 Human can
84	30	37.0	9	6 ABR25012	AbR25012 Human can
85	30	37.0	10	6 ADH14530	Adh14530 Gliadin r
86	30	37.0	10	6 ABR24490	AbR24490 Human can
87	30	37.0	10	6 ABR24879	AbR24879 Human can
88	30	37.0	10	6 ABR25765	AbR25765 Human can
89	30	37.0	10	6 ABR25070	AbR25070 Human can
90	30	37.0	10	6 ABR24761	AbR24761 Human can
91	30	37.0	11	7 ADE15739	AdE15739 E. coli t
92	30	37.0	11	8 ADP19622	AdP19622 Antigenic
93	30	37.0	12	7 ADE15738	AdE15738 E. coli t
94	30	37.0	13	4 AAY71992	Aay71992 Autotaxin
95	30	37.0	13	7 ADE15737	AdE15737 E. coli t
96	30	37.0	13	7 ADM74834	AdM74834 Potentia
97	30	37.0	13	8 ADH14550	Adh14550 Barley ho
98	30	37.0	13	8 ADH14819	Adh14819 Gliadin r

99 30 37.0 14 7 ADE15736
100 30 37.0 14 7 ADP14522

Adel5736 E. coli t
Adf14522 Epitope o

ALIGNMENTS

RESULT 1
AAB72504
ID AAB72504 standard; peptide; 15 AA.

XX AAB72504;

XX 09-MAY-2001 (first entry)

XX Colostrinin peptide #5.

XX Dermatalogical; oxidative stress regulator; colostrinin.

XX Unidentified.

XX WO200112650-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US022665.

XX 17-AUG-1999; 99US-0149310P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

PT Modulating oxidative stress level in a cell, involves contacting the cell
PT with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations.

PS Claim 6; Page 25; 48pp; English.

CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidizing species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLPEPPFPV 15
|||
1 DLEMPVLPEPPFPV 15

DB 1 DLEMPVLPEPPFPV 15

AC AAB59322;

XX 21-MAR-2001 (first entry)

XX Ewe colostrinin peptide fragment B-7.

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

OS Ovis sp.
XX WO200075173-A2.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-GB002128.

XX 02-JUN-1999; 99GB-00012852.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-071058/08.

PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.

PS Claim 7; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLPEPPFPV 15
|||
1 DLEMPVLPEPPFPV 15

DB 1 DLEMPVLPEPPFPV 15

AC AAB72250;

XX 14-MAY-2001 (first entry)

XX Colostrinin derived cytokine inducing peptide SEQ ID 5.

KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.

XX Synthetic.

XX WO20011937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US022818.

XX 17-AUG-1999; 99US-0149311P.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2001-202804/20.
XX Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator.
XX
XX Claim 1; Page 34; 50pp; English.
XX
XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The peptides
CC have immune response modulatory activity, and are capable of inducing
CC cytokines. Colostrinin and its derived peptides are useful for inducing
CC cytokine production, for modulating an immunological response and for
CC inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLEMPVLPEPPPPV 15
DB 1 DLEMPVLPEPPPPV 15
RESULT 4
AAB72536
ID AAB72536 standard; peptide; 15 AA.
XX
XX AAB72536;
XX
XX 09-MAY-2001 (first entry)
XX
XX Colostrinin peptide #5.
XX
XX Colostrinin peptide #5.
XX
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
XX colostrum.
XX
XX Unidentified.
XX
XX WO200112651-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US022774.
XX
XX 17-AUG-1999; 99US-0149633P.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Boldogh I;
XX
XX WPI; 2001-226545/23.
XX
XX Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating damaged
PT neural cells in a patient.
XX
XX Claim 6; Page 21; 35pp; English.
XX
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLEMPVLPEPPPPV 15
DB 1 DLEMPVLPEPPPPV 15
RESULT 5
AA014581
ID AA014581 standard; peptide; 15 AA.
XX
XX AA014581;
XX
XX 27-MAY-2002 (first entry)
XX
XX
XX Neural cell regulatory colostrinin peptide 5.
XX
XX
XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
XX neural cell formation; proline-rich polypeptide aggregate; colostrum;
XX neural cell treatment.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FT Modified-site 15 /note="Optional C-terminal amide"
FT
XX
XX WO200213851-A1.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US022777.
XX
XX 17-AUG-2000; 2000WO-US022777.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Boldogh I, Stanton JG, Hughes TK;
XX
XX WPI; 2002-269152/31.
XX
XX Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX
XX Claim 7; Page 21; 37pp; English.
XX
XX The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLEMPVLPEPPPPV 15
DB 1 DLEMPVLPEPPPPV 15
RESULT 6
AAM51040

ID AAM51040 standard; peptide; 15 AA.
XX AAM51040;
AC
XX
XX
DT 30-MAY-2002 (first entry)
XX
XX Colostriin constituent peptide.
DE
XX Colostriin; colostrum; immunomodulator; cardiovascular;
XX blood cell regulator; cytokine inducer; beta-casein; human.
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT Modified-site 15 /note="optional C-terminal amidation"
FT
XX
XX WO200213849-A1.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US022775.
XX
XX 17-AUG-2000; 2000WO-US022775.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX (REGE-) REGEN THERAPEUTICS PLC.
XX
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
XX WPI; 2002-269150/31.
XX
XX Modulation of blood cell proliferation in a patient involves use of blood
XX cell regulator selected from colostriin, its constituent peptide and/or
XX analog.
XX
XX Claim 1; Page 34; 54pp; English.
XX
XX
XX The present sequence is that of a colostriin constituent peptide that is
XX preferred for use as an immunological regulator and as a blood cell
XX regulator in claimed methods of the invention. It is classified as having
XX a beta-casein homologue precursor. Methods are claimed for: inducing a
XX cytokine in a cell by contact with an immunological regulator, where the
XX cell is present in a cell culture, a tissue, an organ or an organism, and
XX the cell is mammalian, including human; modulating an immune response in
XX a cell by contact with the immunological regulator under conditions
XX effective to induce a cytokine; modulating an immune response in a
XX patient by administering an immunological regulator under conditions
XX effective to induce a cytokine, where the immunological regulator is
XX administered topically or as part of a dietary supplement, and where the
XX immune response is specific or non specific, an interferon response or an
XX antibody response; modulating blood cell proliferation by contacting
XX blood cells with a blood cell regulator, where the blood cells are
XX present in a cell culture or an organism, are mammalian or human, and
XX where the blood cells are increased in number or differentiated; and a
XX method for modulating blood cell proliferation in a patient. A claimed
XX cytokine-inducing composition comprises a pharmaceutical carrier and an
XX active agent such as the present peptide. Cytokines induced by this
XX peptide in human leucocyte cultures include interferon-gamma, tumour
XX necrosis factor-alpha, interleukin-6 and interleukin-10
XX
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 81; DB 5; length 15;
Best Local Similarity 100.0%; Pred.No.1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7

AAE20232
ID AAE20232 standard; peptide; 15 AA.
XX AAE20232;
AC
XX
XX
DT 18-JUN-2002 (first entry)
XX
XX Colostriin constituent peptide #5.
DE
XX
XX Blood cell regulator; colostriin; constituent peptide; oxidative stress;
XX therapy; oxidative damage; skin; aging; wound healing; cell replacement;
XX tissue; organ; cosmetic procedure; repair; regeneration; preservation;
XX transplantation; implantation; dermatological; vulnary.
XX
XX Unidentified.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 15 /note="Optionally C-terminal amide"
FT
XX
XX WO200213850-A1.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US022776.
XX
XX 17-AUG-2000; 2000WO-US022776.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
XX
XX WPI; 2002-269151/31.
XX
XX Composition useful for the modulation of blood cell proliferation in a
XX patient comprises a blood cell regulator selected from colostriin, its
XX constituent peptide and/or analog.
XX
XX
XX Claim 6; Page 25; 51pp; English.
XX
XX
XX The invention relates to a composition which comprises a blood cell
XX regulator selected from colostriin, its constituent peptide and/or
XX analogue. The invention is used for modulating the oxidative stress level
XX in a cell e.g. mammalian or human cell present in a cell culture, tissue,
XX organ, or organism; or for treating oxidative damage to the skin of a
XX patient e.g. animal or human; to modulate oxidative stress during/ after
XX a premature birth or normal birth, preventing/delaying aging in a
XX patient; enhancing wound healing, and the reduction of side effects of
XX cosmetic procedures. The method changes the level of an oxidising species
XX in the cell, such as decreases or prevents increase in the level of
XX damage to a biomolecule of the patient selected from DNA, protein and/or
XX lipid, compared to the same conditions when the oxidative stress
XX regulator is not present. The modulation of oxidative stress results in
XX enhanced repair, regeneration, and replacement of cells, tissues and
XX organs (e.g. kidney, liver, pancreas, skin, and the other internal and
XX external organs), as well as enhanced preservation of such organs for
XX transplantation, implantation, or scientific research. The present
XX sequence is a colostriin constituent peptide
XX
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 81; DB 5; length 15;
Best Local Similarity 100.0%; Pred.No.1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
ADN60299
ID ADN60299 standard; peptide; 15 AA.


```

XX AC ADN60299;
XX XX
XX DT 29-JUL-2004 (first entry)
XX DE Constituent peptide of colostrinin SEQ ID NO:5.
XX XX
XX XX modulator; colostrinin; intracellular signaling molecule modulator;
XX XX 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;
XX XX DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNE inhibitor;
XX XX 4HNE-protein adduct formation reduction;
XX XX 4HNE-mediated glutathione depletion inhibition; p53 inhibition;
XX XX c-Jun NH2-terminal kinase inhibition.
XX OS Synthetic.
XX XX
XX XX WO2004037851-A2.
XX XX
XX PD 06-MAY-2004.
XX XX
XX PF 22-OCT-2003; 2003WO-US033423.
XX XX
XX PR 22-OCT-2002; 2002US-0420369P.
XX XX
XX XX (TEXA ) UNIV TEXAS SYSTEM.
XX XX (BOLD/) BOLDOGH I.
XX XX (STAN/) STANTON J G.
XX XX (GEOR/) GEORGIADES J A.
XX XX (HUGH/) HUGHES T K.
XX XX (KRUZ/) KRUZEL M.
XX XX
XX PI Bolodogh I, Stanton JG, Georgiades JA, Hughes TK, Kruznel M;
XX XX WPI; 2004-365494/34.
XX XX
XX PT Use of colostrinin for e.g. modulating an intracellular signaling
XX PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a
XX PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
XX PT a cell.
XX XX
XX PS Claim 6; SEQ ID NO 5; 46pp; English.
XX XX
XX CC The present invention describes the use of a modulator selected from
XX CC colostrinin, its constituent peptide, its active analogue, and a
XX CC combination of these, for modulating an intracellular signaling molecule
XX CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,
XX CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
XX CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
XX CC The modulator has cytostatic activity, and can be used as a 4HNE
XX CC inhibitor. The modulator is useful in the manufacture of a medicament for
XX CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated
XX CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,
XX CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.
XX CC Colostrinin, or its constituent peptide or active analogue is useful for
XX CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
XX CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
XX CC The present sequence represents a synthetic constituent peptide of
XX CC colostrinin, which can be used as a modulator in the present invention.
XX XX
XX SQ Sequence 15 AA;

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Query Match 100.0%; Score 81; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 DLEMPVLVPEPPFV 15
   |||||
Db 1 DLEMPVLVPEPPFV 15

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RESULT 9
ADST74398
ID ADST74398 standard; peptide; 15 AA.

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XX AC ADST74398;
XX XX
XX DT 16-DEC-2004 (first entry)
XX DE Ovine colostrinin peptide.
XX XX
XX XX Colostrum; colostrinin; sheep; peptide purification.
XX XX
XX OS Ovis aries.
XX XX
XX XX WO2004081038-A1.
XX XX
XX PD 23-SEP-2004.
XX XX
XX PF 10-MAR-2004; 2004WO-GB001014.
XX XX
XX PR 11-MAR-2003; 2003GB-00005552.
XX PR 08-MAR-2004; 2004GB-00005190.
XX XX
XX XX (REGG-), REGEN THERAPEUTICS PLC.
XX XX
XX PI Georgiades JA, Polanowski A, Wilusz T, Kruznel M;
XX XX WPI; 2004-67519/66.
XX XX
XX DR Recovering peptides such as colostrinin from mammalian colostrum, by
XX XX mixing colostrum with alcohol to form alcohol phase containing peptides
XX XX and precipitate, separating alcohol phase from precipitate, and
XX XX recovering alcohol phase.
XX XX
XX PS Example; SEQ ID NO 15; 41pp; English.
XX XX
XX CC The present sequence is that of a peptide that can be recovered from
XX CC ovine colostrum using the method of the invention. The invention
XX CC provides a method for the recovery of peptides (especially colostrinin)
XX CC from colostrum in substantially pure, biologically active form and in
XX CC high yield. The method involves mixing the colostrum with an alcohol to
XX CC form an alcohol phase containing the colostrinin and a precipitate
XX CC containing higher molecular weight caseins and other proteins. Best
XX CC results are obtained using methanol or ethanol of at least 80%, and
XX CC preferably up to 100%, purity. The alcohol phase is then separated from
XX CC the precipitate, and the colostrinin is separated from the alcohol,
XX CC preferably by evaporation, to form a colostrinin-rich phase, which is
XX CC recovered. A precipitation agent, such as ammonium sulfate, may be added
XX CC either to the alcohol phase or, preferably, to the colostrinin-rich phase
XX CC to induce precipitation of the colostrinin peptides. The method is
XX CC generally applicable to the separation of peptides from fluids containing
XX CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic
XX CC acids. In an example from the invention, the antigenic profile of
XX CC peptides recovered from sheep colostrum using the alcohol precipitation
XX CC methods was determined by ELISA using antibodies prepared against 9
XX CC synthetic peptides, including a peptide having the present sequence
XX CC (denoted antigen class B-8).
XX XX
XX SQ Sequence 15 AA;

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```

Query Match 100.0%; Score 81; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 DLEMPVLVPEPPFV 15
   |||||
Db 1 DLEMPVLVPEPPFV 15

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RESULT 10
AAB59352
ID AAB59352 standard; peptide; 16 AA.
XX XX
XX AC AAB59352;
XX XX
XX DT 21-MAR-2001 (first entry)

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XX DE Ewe colostrinin peptide fragment derived sequence #12.
XX PR
XX XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX XX
XX OS Ovis sp.
XX PN WO20075173-A2.
XX PD 14-DEC-2000.
XX PF 02-JUN-2000; 200WO-GB002128.
XX PR 02-JUN-1999; 99GB-00012852.
XX PA (REGG-) REGEN THERAPEUTICS PLC.
XX PI Georgiades JA;
XX DR WPI; 2001-071058/08.
XX PT Peptides having an N-terminal amino acid sequence isolated from
XX PT colostrinin for treating e.g. disorders of the central nervous system and
XX PT immune system, viral and bacterial infections, and diseases characterized
XX PT by amyloid plaques.
XX PS Claim 8; Page 27; 63pp; English.
XX CC The present invention provides the sequences of a number of peptides
XX CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
XX CC fragment of colostrum. These peptides can be used in the treatment of
XX CC central nervous system disorders such as senile dementia, Parkinson's
XX CC disease, Alzheimer's disease, psychosis and neurosis, immune system
XX CC disorders such as bacterial and viral infections, to improve the
XX CC development of a child's immune system, as a dietary supplement, and to
XX CC promote the dissolution of beta-amyloid plaques
XX CC
XX SQ Sequence 16 AA;
XX
XX Query Match 100.0%; Score 81; DB 4; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-05;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DLEMPVLVPEPPFV 15
XX Db 2 DLEMPVLVPEPPFV 16
XX
XX RESULT 11
XX ID AAE07187 standard; peptide; 10 AA.
XX AC AAE07187;
XX XX
XX DT 06-NOV-2001 (first entry)
XX XX
XX DE Colostrinin peptide 3.
XX XX
XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
XX KW central nervous system disorder; neurodegenerative disorder; weight loss;
XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
XX KW acquired immunological deficiency; neurological disorder; dementia;
XX KW antiviral.
XX OS
XX XX Unidentified.
XX OS
XX PN WO200155199-A1.
XX XX
XX PD 02-AUG-2001.
XX XX
XX PF 26-JAN-2001; 2001WO-GB000329.

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XX XX 26-JAN-2000; 2000GB-00001825.
XX PR
XX XX (REGG-) REGEN THERAPEUTICS PLC.
XX PA
XX XX Georgiades JA;
XX PI
XX DR WPI; 2001-488775/53.
XX XX
XX PT Peptide useful as an interalia in the treatment of e.g. disorders of the
XX PT immune system and the central nervous system comprises ten amino-terminal
XX PT amino acid sequence derived from peptides present in colostrinin.
XX PS Claim 1; Page 15; 40pp; English.
XX XX
XX CC The invention relates to colostrinin peptide fragments which are useful,
XX CC inter alia, in the treatment of chronic disorders of the immune system
XX CC and the central nervous system. Colostrinin peptides are used as a
XX CC medicament in the treatment of neurological disorders e.g., dementia,
XX CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
XX CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and
XX CC neurosis, in acquired immunological deficiencies, chronic bacterial and
XX CC viral infections and diseases characterised by the presence of beta-
XX CC amyloid plaques and as a dietary supplement for babies, small children,
XX CC adults and senile persons, who have been subjected to chemotherapy or
XX CC have suffered from cachexia or weight loss due to the chronic disease.
XX CC Colostrinin peptides are also used as food additives and as an auxiliary
XX CC withdrawal treatment for drug addicts, after a period of detoxification
XX CC and in persons dependent on stimulants. Colostrinin peptides are used to
XX CC prepare antibodies and to treat emotional disturbances, e.g. emotional
XX CC disturbances of psychiatric patients in a state of depression. These
XX CC colostrinin peptides improves the development of immune system in a new
XX CC born child and to correct the immunological deficiencies in a child. The
XX CC present sequence is colostrinin peptide 3 related to the invention
XX CC
XX SQ Sequence 10 AA;
XX
XX Query Match 70.4%; Score 57; DB 4; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.041;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 PVLVPEPPFV 14
XX Db 1 PVLVPEPPFV 10
XX
XX RESULT 12
XX ID AAE07197 standard; peptide; 10 AA.
XX AC AAE07197;
XX XX
XX DT 06-NOV-2001 (first entry)
XX XX
XX DE Modified colostrinin cyclic peptide #3.
XX XX
XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
XX KW central nervous system disorder; neurodegenerative disorder; weight loss;
XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
XX KW acquired immunological deficiency; neurological disorder; dementia;
XX KW antiviral; cyclic.
XX OS
XX XX Synthetic.
XX OS
XX FT Key location/Qualifiers
XX FT Modified-site 1
XX FT /note= "N-terminal acetyl; this residue forms a cyclic
XX FT linkage with Pro found at the C-terminal end"
XX XX
XX PN WO200155199-A1.
XX XX
XX PD 02-AUG-2001.

```

XX 26-JAN-2001; 2001WO-GB000329.
PF
XX
XX 26-JAN-2000; 2000GB-00001825.
PR
XX
XX (REGB-) REGEN THERAPEUTICS PLC.
PA
XX
XX Georgiades JA;
PI
XX
XX MPI; 2001-488775/53.
DR
XX
XX Peptide useful as an interalia in the treatment of e.g. disorders of the
PT immune system and the central nervous system comprises ten amino-terminal
PT amino acid sequence derived from peptides present in colostrinin.
XX
XX Example 2; Page 8; 40pp; English.
PS
XX The invention relates to colostrinin peptide fragments which are useful,
CC inter alia, in the treatment of chronic disorders of the immune system
CC and the central nervous system. Colostrinin peptides are used as a
CC medicament in the treatment of neurological disorders e.g., dementia,
CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and
CC neurosis, in acquired immunological deficiencies, chronic bacterial and
CC viral infections and diseases characterised by the presence of beta-
CC amyloid plaques and as a dietary supplement for babies, small children,
CC adults and senile persons, who have been subjected to chemotherapy or
CC have suffered from cachexia or weight loss due to the chronic disease.
CC Colostrinin peptides are also used as food additives and as an auxiliary
CC withdrawal treatment for drug addicts, after a period of detoxification
CC and in persons dependent on stimulants. Colostrinin peptides are used to
CC prepare antibodies and to treat emotional disturbances, e.g. emotional
CC disturbances of psychiatric patients in a state of depression. These
CC colostrinin peptides improves the development of immune system in a new
CC born child and to correct the immunological deficiencies in a child. The
CC present sequence is modified colostrinin cyclic peptide #3 related to the
CC invention
XX
XX Sequence 10 AA;
SQ
XX
XX Query Match 63.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 PVLPEVPPFP 13
DB 2 PVLPEVPPFP 10
XX
XX RESULT 13
AAU77172
ID AAU77172 standard; peptide; 15 AA.
XX
XX AAU77172;
AC
XX
XX 02-JUL-2002 (first entry)
DT
XX
XX Transcriptional control factor ZFM1 isomer 25.63 N-terminal peptide.
DE
XX
XX Human; transcriptional control factor ZFM1 isomer 25.63; HIV;
KW malignant tumour; haemopathy; human immunodeficiency virus; cancer;
KW immunological disease; inflammation; cytostatic; hemostatic; virucide;
KW immunomodulatory; antiinflammatory; gene therapy.
XX
XX Homo sapiens.
OS
XX
XX WO200220588-A1.
PN
XX
XX 14-MAR-2002.
PD
XX
XX 02-JUL-2001; 2001WO-CN001127.
PF
XX
XX 07-JUL-2000; 2000CN-00117050.
PR

XX
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX MPI; 2002-339796/37.
DR
XX
XX Human transcriptional control factor ZFM1 isomer 25.63 and encoding
PT polynucleotide, used in diagnosis and treatment of malignant tumors,
PT hemopathy, human immunodeficiency virus infection, immunological diseases
PT and inflammation.
XX
XX Example 5; Page 14; 38pp; Chinese.
PS
XX
XX The invention relates to the human transcriptional control factor ZFM1
CC isomer 25.63 and the polynucleotide encoding it. The sequences of the
CC invention are used in diagnosis and treatment of malignant tumours,
CC haemopathy, human immunodeficiency virus (HIV) infection, immunological
CC diseases and various inflammations. This sequence represents the human
CC transcriptional control factor ZFM1 isomer 25.63 N-terminal peptide, used
CC in ELISA
XX
XX Sequence 15 AA;
SQ
XX
XX Query Match 48.8%; Score 39.5; DB 5; Length 15;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
OY 4 MPVLEVPFPV 15
DB 1 MPIL-VERKPPV 11
XX
XX RESULT 14
ADFL4579
ID ADFL4579 standard; peptide; 17 AA.
XX
XX ADFL4579;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Gluten-derived peptide - SEQ ID 74.
DE
XX
XX plant; deamidation; tissue transglutaminase; celiac disease; CD;
KW gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; Sjogren syndrome; diabetes;
KW immunosuppressive; antirheumatic; anticholelithic; antidiabetic;
KW dermatological; antiinflammatory.
XX
XX Unidentified.
OS
XX
XX EP1332760-A1.
PN
XX
XX 06-AUG-2003.
PD
XX
XX 04-FEB-2002; 2002EP-00075456.
PF
XX
XX 04-FEB-2002; 2002EP-00075456.
PR
XX
XX (ZIER-) ACAD ZIERKHUIS LBIDEN.
PA
XX
XX MPI; 2003-647889/62.
DR
XX
XX New gluten peptides or epitopes prone to deamidation by tissue
PT transglutaminase, useful for treating celiac disease or an autoimmune
PT disease, rheumatoid arthritis, multiple sclerosis, systemic lupus
PT erythematosus, or diabetes.
XX
XX Disclosure; SEQ ID NO 74; 143pp; English.
PS
XX
XX The invention relates to a novel peptide or epitope which is prone to
CC deamidation by tissue transglutaminase (tTG) and is a causative factor of
CC celiac disease (CD, gluten intolerance) or an autoimmune disease such as

CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
 CC Sjogren syndrome or diabetes. The peptide of the invention demonstrates
 CC immunosuppressive, antirheumatic, antidiabetic, antidiabetic,
 CC dermatological and antiinflammatory activities whilst pharmaceutical
 CC compositions comprising the peptides or epitopes may be useful for the
 CC treatment of a celiac disease or an autoimmune disease such as rheumatoid
 CC arthritis, multiple sclerosis, systemic lupus erythematosus, Sjogren
 CC syndrome or diabetes. Gluten-derived peptides may be useful in the
 CC preparation of therapeutic agents capable of eliminating a subset of
 CC cells, particularly gluten-sensitive or auto-antigen sensitive T cells.
 CC The current sequence is that of the gluten-derived peptide of the
 CC invention.

CC Sequence 17 AA;

Query Match 48.1%; Score 39; DB 7; Length 17;
 Best Local Similarity 66.7%; Pred. No. 39;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 PVLPEVPEPP 13
 :||:||||
 Db 1 PVLPEVPEPP 9

RESULT 15
 AAB72520
 ID AAB72520 standard; peptide; 18 AA.

XX AAB72520;

DT 09-MAY-2001 (first entry)

XX Colostrinin peptide #21.

DE Dermato logical; oxidative stress regulator; colostrinin.

XX Unidentified.

OS WO200112650-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US022665.

XX 17-AUG-1999; 99US-0149310P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

PI WPI; 2001-218342/22.

DR Modulating oxidative stress level in a cell, involves contacting the cell
 XX with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations.

PT Claim 6; Page 26; 48pp; English.

PS The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidizing species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient

XX Sequence 18 AA;

Query Match 44.4%; Score 36; DB 4; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPP 12

Db 3 EMPPEKYPVEPP 14
 :||:||||

RESULT 16
 AAB59330
 ID AAB59330 standard; peptide; 18 AA.

XX AAB59330;

AC 21-MAR-2001 (first entry)

XX Ewe colostrinin peptide fragment C-5.

DE Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX Ovis sp.

XX WO200075173-A2.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-GB002128.

XX 02-JUN-1999; 99GB-00012852.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-071058/08.

DR Peptides having an N-terminal amino acid sequence isolated from
 XX colostrinin for treating e.g. disorders of the central nervous system and
 PT immune system, viral and bacterial infections, and diseases characterized
 PT by amyloid plaques.

XX Claim 7; Page 27; 63pp; English.

PS The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrinin. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques

XX Sequence 18 AA;

Query Match 44.4%; Score 36; DB 4; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPP 12
 :||:||||
 Db 3 EMPPEKYPVEPP 14

RESULT 17
 AAB72267
 ID AAB72267 standard; peptide; 18 AA.

XX AAB72267;

AC 14-MAY-2001 (first entry)

DT Colostrinin derived cytokine inducing peptide SEQ ID 22.

XX Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;

KW neurosis, infection.
 XX Synthetic.
 OS WO20011937-A2.
 XX
 PN 22-FEB-2001.
 XX
 PD 17-AUG-2000; 2000WO-US022818.
 XX
 PF 17-AUG-1999; 99US-0149311P.
 XX
 PR (TEXA) UNIV TEXAS SYSTEM.
 XX (REGS-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX WPI; 2001-202804/20.
 DR
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator.
 XX
 XX Claim 1; Page 34; 50pp; English.
 PS
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides
 CC have immune response modulatory activity, and are capable of inducing
 CC cytokines. Colostrinin and its derived peptides are useful for inducing
 CC cytokine production, for modulating an immunological response and for
 CC inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies
 CC
 SQ Sequence 18 AA;
 XX
 QY Query Match 44.4%; Score 36; DB 4; Length 18;
 XX Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 XX Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Db 1 DLEMPVLPVEPF 12
 3 EMPFPKYPVEPF 14
 RESULT 18
 AAB72552
 ID AAB72552 standard; peptide; 18 AA.
 XX
 AC AAB72552;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #21.
 XX
 KW Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX
 OS Unidentified.
 XX
 PN WO200112651-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US022774.
 XX
 PR 17-AUG-1999; 99US-0149633P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.

XX
 PI Boldogh I;
 XX
 DR WPI; 2001-226545/23.
 XX
 PT Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating damaged
 PT neural cells in a patient.
 XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
 XX
 SQ Sequence 18 AA;
 XX
 QY Query Match 44.4%; Score 36; DB 4; Length 18;
 XX Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 XX Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Db 1 DLEMPVLPVEPF 12
 3 EMPFPKYPVEPF 14
 RESULT 19
 AA014598
 ID AA014598 standard; peptide; 18 AA.
 XX
 AC AA014598;
 XX
 DT 27-MAY-2002 (first entry)
 XX
 DE Neural cell regulatory colostrinin peptide 21.
 XX
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 18 /note="Optional C-terminal amide"
 FT
 XX
 XX WO200213851-A1.
 XX
 PN 21-FEB-2002.
 XX
 PD 17-AUG-2000; 2000WO-US022777.
 XX
 PF 17-AUG-2000; 2000WO-US022777.
 XX
 PR 17-AUG-2000; 2000WO-US022777.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I, Stanton JG, Hughes TK;
 XX
 DR WPI; 2002-269152/31.
 XX
 PT Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 7; Page 21; 37pp; English.
 XX
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention
CC
XX
SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 5; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPEPFP 12
::| |||||
Db 3 EMPPEKPEPPEP 14

RESULT 20
AAM51056
ID AAM51056 standard; peptide; 18 AA.

AC AAM51056;
DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide (casein amino acids 121-138).

XX Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; beta-casein; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 18 /note="optional C-terminal amidation"

PN WO200213849-A1.

PD 21-FEB-2002.

PF 17-AUG-2000; 2000WO-US022775.

PR 17-AUG-2000; 2000WO-US022775.

PA (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Stanton GU, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

PT Modulation of blood cell proliferation in a patient involves use of blood
PT cell regulator selected from colostrinin, its constituent peptide and/or
PT analog.

PS Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide that is
CC preferred for use as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. It is classified as having
CC a beta-casein homologue precursor, and corresponds to casein amino acids
CC 121-138. Methods are claimed for: inducing a cytokine in a cell by
CC contact with an immunological regulator, where the cell is present in a
CC cell culture, a tissue, an organ or an organism, and the cell is
CC mammalian, including human; modulating an immune response in a cell by
CC contact with the immunological regulator under conditions effective to
CC induce a cytokine; modulating an immune response in a patient by
CC administering an immunological regulator under conditions effective to
CC topically or as part of a dietary supplement, and where the immune
CC response is specific or non specific, an interferon response or an
CC antibody response; modulating blood cell proliferation by contacting
CC blood cells with a blood cell regulator, where the blood cells are
CC present in a cell culture or an organism, are mammalian or human, and
CC where the blood cells are increased in number or differentiated; and a

CC method for modulating blood cell proliferation in a patent. A claimed
CC cytokine-inducing composition comprises a pharmaceutical carrier and an
CC active agent such as the present peptide. Cytokines induced by this
CC peptide in human leucocyte cultures include interferon-gamma, tumour
CC necrosis factor-alpha and interleukin-10
XX

SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 5; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPEPFP 12
::| |||||
Db 3 EMPPEKPEPPEP 14

RESULT 21
AAE20249
ID AAE20249 standard; peptide; 18 AA.

AC AAE20249;

DT 18-JUN-2002 (first entry)

DE Colostrinin constituent peptide #21.

XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; veterinary.

OS Unidentified.

XX Key Location/Qualifiers

FT Modified-site 18 /note="Optionally C-terminal amide"

PN WO200213850-A1.

PD 21-FEB-2002.

PF 17-AUG-2000; 2000WO-US022776.

PR 17-AUG-2000; 2000WO-US022776.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Stanton GU, Hughes TK, Boldogh I;

XX WPI; 2002-269151/31.

PT Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog.

PS Claim 6; Page 26; 51pp; English.

XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress level
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
CC organ, or organism; or for treating oxidative damage to the skin of a
CC patient e.g. animal or human; to modulate oxidative stress during/ after
CC a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and

CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide

XX
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 5; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPP 12
 :: |||||
 Db 3 EMPFPKYPVVEPP 14

RESULT 22

ID ADN60316 standard; peptide; 18 AA.

XX ADN60316;

XX 29-JUL-2004 (first entry)

DE Constituent peptide of colostrinin SEQ ID NO:22.

XX modulator; colostrinin; intracellular signaling molecule modulator;
 KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibitor;
 KW DNA damage; beta-amyloid; retinoic acid; cyclostatic; 4HNE inhibitor;
 KW 4HNE-protein adduct formation reduction;
 KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;
 KW c-Jun NH2-terminal kinase inhibition.

XX Synthetic.

XX WO2004037851-A2.

XX 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033423.

XX 22-OCT-2002; 2002US-0420369P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (BOLD/) BOLDOGH I.

XX (STAN/) STANTON J G.

XX (GEOR/) GEORGIADIS J A.

XX (HUGH/) HUGHES T K.

XX (KRUZ/) KRUZEL M.

XX Bolodogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;

XX WPI; 2004-365494/34.

XX Use of colostrinin for e.g. modulating an intracellular signaling

XX molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a

XX cell, inhibiting apoptosis in a cell, or protecting against DNA damage in

XX a cell.

XX Claim 6; SEQ ID NO 22; 46pp; English.

XX The present invention describes the use of a modulator selected from
 CC colostrinin, its constituent peptide, its active analogue, and a
 CC combination of these, for modulating an intracellular signaling molecule
 CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
 CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
 CC The modulator has cyclostatic activity, and can be used as a 4HNE
 CC inhibitor. The modulator is useful in the manufacture of a medicament for
 CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated
 CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,
 CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.
 CC Colostrinin, or its constituent peptide or active analogue is useful for
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,

CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
 CC The present sequence represents a synthetic constituent peptide of
 CC colostrinin, which can be used as a modulator in the present invention.

XX
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 8; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPP 12
 :: |||||
 Db 3 EMPFPKYPVVEPP 14

RESULT 23

ID AD574406 standard; peptide; 18 AA.

XX AD574406;

XX 16-DEC-2004 (first entry)

DE Ovine colostrinin peptide.

XX Colostrum; colostrinin; sheep; peptide purification.

XX Ovis aries.

XX WO2004081038-A1.

XX 23-SEP-2004.

XX 10-MAR-2004; 2004WO-GB001014.

XX 11-MAR-2003; 2003GB-00005552.

XX 08-MAR-2004; 2004GB-00005190.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;

XX WPI; 2004-67519/66.

XX Recovering peptides such as colostrinin from mammalian colostrum, by
 PT mixing colostrum with alcohol to form alcohol phase containing peptides
 PT and precipitate, separating alcohol phase from precipitate, and
 PT recovering alcohol phase.

XX Disclosure; SEQ ID NO 23; 41pp; English.

XX The present sequence is that of a peptide that can be recovered from
 CC ovine colostrinin using the method of the invention. The invention
 CC provides a method for the recovery of peptides (especially colostrinin)
 CC from colostrum in substantially pure, biologically active form and in
 CC high yield. The method involves mixing the colostrum with an alcohol to
 CC form an alcohol phase containing the colostrinin and a precipitate
 CC containing higher molecular weight caseins and other proteins. Best
 CC results are obtained using methanol or ethanol of at least 80%, and
 CC preferably up to 100%, purity. The alcohol phase is then separated from
 CC the precipitate, and the colostrinin is separated from the alcohol,
 CC preferably by evaporation, to form a colostrinin-rich phase, which is
 CC recovered. A precipitation agent, such as ammonium sulfate, may be added
 CC either to the alcohol phase or, preferably, to the colostrinin-rich phase
 CC to induce precipitation of the colostrinin peptides. The method is
 CC generally applicable to the separation of peptides from fluids containing
 CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic
 CC acids.

XX Sequence 18 AA;

Query Match 44.4%; Score 36; DB 8; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 DLEMPVLPEVPP 12
 :: |||||
 Db 3 EMPPEKYPVEPP 14

RESULT 24
 ADH14551
 ID ADH14551 standard; peptide; 12 AA.
 AC ADH14551;
 DT 11-MAR-2004 (first entry)
 DE Barley hordein related gliadin peptide SEQ ID NO:41.
 KM coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 KM vaccine.
 OS Synthetic.
 PN WO2003104273-A2.
 PD 18-DEC-2003.
 PF 05-JUN-2003; 2003WO-GB002450.
 PR 05-JUN-2002; 2002GB-00012885.
 PA (ISIS-) ISIS INNOVATION LTD.
 PI Anderson RP, Hill AVS, Jewell DP;
 PI Anderson RP, Hill AVS, Jewell DP;
 DR WPI; 2004-043640/04.
 XX Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.
 XX
 PS Claim 1; SEQ ID NO 41; 177pp; English.
 XX
 CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.
 CC
 SQ Sequence 12 AA;

Query Match 43.2%; Score 35; DB 8; Length 12;
 Best Local Similarity 55.6%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 PVLPEVPP 13
 | : | : |||
 Db 1 PLOPOQPP 9

RESULT 25
 ADH14849
 ID ADH14849 standard; peptide; 12 AA.
 AC ADH14849;
 XX

DT 11-MAR-2004 (first entry)
 XX
 DE Gliadin related epitope peptide.
 XX
 KM coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 KM vaccine.
 OS Synthetic.
 PN WO2003104273-A2.
 PD 18-DEC-2003.
 PF 05-JUN-2003; 2003WO-GB002450.
 PR 05-JUN-2002; 2002GB-00012885.
 PA (ISIS-) ISIS INNOVATION LTD.
 PI Anderson RP, Hill AVS, Jewell DP;
 PI Anderson RP, Hill AVS, Jewell DP;
 DR WPI; 2004-043640/04.
 XX
 PT Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.
 XX
 PS Example 13; Page 96; 177pp; English.
 XX
 CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.
 CC
 SQ Sequence 12 AA;

Query Match 43.2%; Score 35; DB 8; Length 12;
 Best Local Similarity 55.6%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 PVLPEVPP 13
 | : | : |||
 Db 1 PLOPOQPP 9

RESULT 26
 AAR93469
 ID AAR93469 standard; peptide; 14 AA.
 AC AAR93469;
 DT 09-MAY-1996 (first entry)
 DE GST-SRC protein tyrosine kinase derived peptide #3.
 XX
 KM SH3 ligand; SH3 binding agent; biased phage library;
 KM recognition sequence; src SH3 domain; Paget's disease; restenosis;
 KM rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47;
 KM p67; complex; chronic myelogenous leukaemia; cancer.
 OS Synthetic.
 XX
 PN WO9524419-A1.
 XX

PD 14-SEP-1995.
XX
XX 13-MAR-1995; 95WO-US003208.
XX
PR 11-MAR-1994; 94US-00209835.
XX
PR 06-JAN-1995; 95US-00369832.
XX
XX (ARIA-) ARIAD PHARM INC.
XX
PI Rickles RJ, Brugge JS, Bortfield MC, Zoller MJ;
XX WPI; 1995-328231/42.
XX
DR WPI; 1995-328231/42.
XX
PT Identification of peptide(s) binding specifically to SH3 domains - for
XX use in inhibiting interactions mediated by SH3 domains in treatment of
XX e.g. osteoporosis and cancer.
XX
PS Disclosure; Fig 5; 74pp; English.
XX
XX The sequences given in AAR93457-71 represent peptides which are SH3
XX ligands/SH3 binding agents. They represent a biased phage library which
XX comprises five random amino acids flanking the decapeptide -RSRRPVPVP or
XX derivatives of this, which was identified as a recognition sequence for
XX the Src SH3 domain. These sequences were identified using the method of
XX the invention. The method comprises contacting the SH3 domain with a
XX mixture of peptides under conditions permitting a ligand to bind to an
XX SH3 domain to form a complex. Any unbound peptides are removed and the
XX complexed peptide ligands are dissociated from the complexes. The
XX selected peptides are enriched by re-contacting them with the SH3 domain
XX and then candidates which bind to the SH3 domain are detected. The
XX isolated SH3 binding peptides may be used in the diagnosis, prevention
XX and treatment of conditions or diseases resulting from cellular processes
XX mediated by an SH3-based interaction. Such diseases include Paget's
XX disease. Other conditions treatable with these peptides include
XX osteoporosis, rheumatoid arthritis, gout and other problems in which an SH3
XX of neutrophil oxidase p47 and p67 complex is implicated, etc
XX
SQ Sequence 14 AA;

Query Match 42.0%; Score 34; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 LEMPVPVPVP 13
Db 3 LPPPLPARRPP 14

RESULT 27
AAB72507
ID AAB72507 standard; peptide; 15 AA.
XX
AC AAB72507;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostriatin peptide #8.
XX
KW Dermatological; oxidative stress regulator; colostriatin.
XX
OS Unidentified.
XX
PN WO200112650-A2.
XX
XX 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US022665.
XX
PR 17-AUG-1999; 99US-0149310P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;

XX
DR WPI; 2001-218342/22.
XX
XX
PT Modulating oxidative stress level in a cell, involves contacting the cell
XX with an oxidative stress regulator selected from colostriatin, its
XX constituent peptide, analog or their combinations.
XX
XX Claim 6; Page 25; 48pp; English.
XX
CC The present invention relates to a method for modulating the oxidative
XX stress level in a cell or a patient, comprising contacting the cell with,
XX or administering to the patient, an oxidative stress regulator selected
XX from colostriatin, or its constituent peptide (e.g. the present peptide),
XX to change the level of an oxidising species in the cell. The method can
XX be used to treat oxidative damage to skin, by decreasing or preventing an
XX increase in the level of damage to a biomolecule of the patient
XX
SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 4; Length 15;
Best Local Similarity 70.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLVPVPVP 14
Db 5 PVLKVPVPVP 14

RESULT 28
AAB59313
ID AAB59313 standard; peptide; 15 AA.
XX
AC AAB59313;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostriatin peptide fragment A-4.
XX
KW Sheep; colostriatin; proline rich polypeptide; colostrium; immune disorder;
XX central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
OS Ovis sp.
XX
PN WO200075173-A2.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-GB002128.
XX
PR 02-JUN-1999; 99GB-00012852.
XX
PA (REGG-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
DR WPI; 2001-071058/08.
XX
XX Peptides having an N-terminal amino acid sequence isolated from
XX colostriatin for treating e.g. disorders of the central nervous system and
XX immune system, viral and bacterial infections, and diseases characterized
XX by amyloid plaques.
XX
PS Claim 7; Page 27; 63pp; English.
XX
XX The present invention provides the sequences of a number of peptides
XX found in ewe's colostriatin. Colostriatin is the proline-rich polypeptide
XX fragment of colostrum. These peptides can be used in the treatment of
XX central nervous system disorders such as senile dementia, Parkinson's
XX disease, Alzheimer's disease, psychosis and neurosis, immune system
XX disorders such as bacterial and viral infections, to improve the
XX development of a child's immune system, as a dietary supplement, and to
XX promote the dissolution of beta-amyloid plaques

SQ Sequence 15 AA:

Query Match 42.0%; Score 34; DB 4; Length 15;
 Best Local Similarity 70.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 PVLPEPPPF 14
 | | | | |
 DB 5 PRLKVEVFPF 14

RESULT 29

AAB72253
 ID AAB72253 standard; peptide; 15 AA.

AC AAB72253;

DT 14-MAY-2001 (first entry)

DE Colostriin derived cytokine inducing peptide SEQ ID 8.

XX Colostriin; immune response; cytokine; blood cell proliferation;
 XX central nervous system disorder; neurological disorder; mental disorder;
 XX dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 XX neurosis; infection.

OS Synthetic.

PN WO200111937-A2.

XX 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022818.

PR 17-AUG-1999; 99US-0149311P.

XX (TEXA) UNIV TEXAS SYSTEM.
 XX (REG-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostriin as an immunological
 PT regulator.

PS Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from colostriin,
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides
 CC have immune response modulatory activity, and are capable of inducing
 CC cytokines. Colostriin and its derived peptides are useful for inducing
 CC cytokine production, for modulating an immunological response and for
 CC inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies

SQ Sequence 15 AA:

Query Match 42.0%; Score 34; DB 4; Length 15;
 Best Local Similarity 70.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 PVLPEPPPF 14
 | | | | |
 DB 5 PRLKVEVFPF 14

RESULT 30

AAB72539
 ID AAB72539 standard; peptide; 15 AA.

AC AAB72539;

DT 09-MAY-2001 (first entry)

DE Colostriin peptide #8.

XX Neuroprotective; neural cell differentiation regulator; colostriin;
 XX colostrum.

OS Unidentified.

PN WO200112651-A2.

XX 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022774.

PR 17-AUG-1999; 99US-0149633P.

XX (TEXA) UNIV TEXAS SYSTEM.

PI Boldogh I;

XX WPI; 2001-226545/23.

XX Use of colostriin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating damaged
 PT neural cells in a patient.

PS Claim 6; Page 21; 35pp; English.

XX The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostriin and
 CC colostriin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostriin is a polypeptide complex found in colostrum

SQ Sequence 15 AA:

Query Match 42.0%; Score 34; DB 4; Length 15;
 Best Local Similarity 70.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 PVLPEPPPF 14
 | | | | |
 DB 5 PRLKVEVFPF 14

RESULT 31

AAO14584
 ID AAO14584 standard; peptide; 15 AA.

AC AAO14584;

DT 27-MAY-2002 (first entry)

DE Neural cell regulatory colostriin peptide 8:

XX Neural cell differentiation; neural cell regulator; colostriin peptide;
 XX neural cell formation; proline-rich polypeptide aggregate; colostrum;
 XX neural cell treatment.

OS Unidentified.

FH Key Location/Qualifiers

FT Modified-site 15 /note="Optional C-terminal amide"
 XX XX

XX WO200213851-A1.

PD 21-FEB-2002.
XX 17-AUG-2000; 2000WO-US022777.
XX 17-AUG-2000; 2000WO-US022777.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Boldogh I, Stanton JG, Hughes TK;
XX WPI, 2002-269152/31.
XX Promoting cell differentiation in a patient involves use of blood cell
XX regulator selected from colostrinin, its constituent peptide and/or
XX analog.
XX Claim 7, Page 21, 37pp; English.
XX The invention comprises a method for promoting cell differentiation (e.g.
XX neutral cell differentiation). The method involves contacting cells with a
XX neutral cell regulator (i.e. a colostrinin peptide) in order to change the
XX cells in morphology to form neural cells. Colostrinin is a proline-rich
XX polypeptide aggregate that is present in colostrum. The method of the
XX invention is useful for promoting the differentiation of cells and for
XX treating damaged neural cells in a patient. The present amino acid
XX sequence represents a specifically claimed colostrinin peptide used in
XX the method of the invention
SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 5; Length 15;
Best Local Similarity 70.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLVPEPPF 14
| | | | |
Db 5 PVLKVEVPF 14

RESULT 32

AAW51043
ID AAW51043 standard; peptide; 15 AA.

AC AAW51043;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide.

KW Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; human.

OS Homo sapiens.

Key Location/Qualifiers
FT Modified-site 15 /note="optional C-terminal amidation"

PN WO200213849-A1.

PD 21-FEB-2002.

PF 17-AUG-2000; 2000WO-US022775.

PR 17-AUG-2000; 2000WO-US022775.

PA (TEXA) UNIV TEXAS SYSTEM.

PI (REGG-) REGEN THERAPEUTICS PLC.

Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
WPI, 2002-269150/31.

PT Modulation of blood cell proliferation in a patient involves use of blood
PT cell regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX Claim 1, Page 34, 54pp; English.
XX The present sequence is that of a colostrinin constituent peptide that is
XX preferred for use as an immunological regulator and as a blood cell
XX regulator in claimed methods of the invention. Methods are claimed for:
XX inducing a cytokine in a cell by contact with an immunological regulator,
XX where the cell is present in a cell culture, a tissue, an organ or an
XX organism, and the cell is mammalian, including human; modulating an
XX immune response in a cell by contact with the immunological regulator
XX under conditions effective to induce a cytokine; modulating an immune
XX response in a patient by administering an immunological regulator under
XX conditions effective to induce a cytokine, where the immunological
XX regulator is administered topically or as part of a dietary supplement,
XX and where the immune response is specific or non specific, an interferon
XX response or an antibody response; modulating blood cell proliferation by
XX contacting blood cells with a blood cell regulator, where the blood cells
XX are present in a cell culture or an organism, are mammalian or human, and
XX where the blood cells are increased in number or differentiated; and a
XX method for modulating blood cell proliferation in a patient. A claimed
XX cytokine-inducing composition comprises a pharmaceutical carrier and an
XX active agent such as the present peptide. Cytokines induced by this
XX peptide in human leucocyte cultures include interferon-gamma, tumour
XX necrosis factor-alpha, interleukin-6 and interleukin-10
SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 5; Length 15;
Best Local Similarity 70.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLVPEPPF 14
| | | | |
Db 5 PVLKVEVPF 14

RESULT 33

AAE20235
ID AAE20235 standard; peptide; 15 AA.

AC AAE20235;

DT 18-JUN-2002 (first entry)

DE Colostrinin constituent peptide #8.

KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnery.

OS Unidentified.

Key Location/Qualifiers
FT Modified-site 15 /note="Optionally C-terminal amide"

PN WO200213850-A1.

PD 21-FEB-2002.

PF 17-AUG-2000; 2000WO-US022776.

PR 17-AUG-2000; 2000WO-US022776.

PA (TEXA) UNIV TEXAS SYSTEM.

Stanton GJ, Hughes TK, Boldogh I;
WPI, 2002-269151/31.

XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog.
PS Claim 6; Page 25; 51pp; English.
XX
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress level
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
CC organ, or organism; or for treating oxidative damage to the skin of a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide
SQ Sequence 15 AA;
Query Match 42.0%; Score 34; DB 5; Length 15;
Best Local Similarity 70.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 5 PVLVPEPPF 14
DB 5 PVLVPEPPF 14
RESULT 34
ABB09569
ID ABB09569 standard; peptide; 15 AA.
XX
XX ABB09569;
AC
XX
XX 06-SEP-2002 (first entry)
DT
XX
XX Human I1 factor ORF2 associated protein 10.45 N-terminal peptide.
DE
XX
XX Human; I1 factor ORF2 associated protein 10.45; open reading frame;
KW I1 element ORF2-like protein homologue; recombinant production; tumour;
KW cancer; protein metabolism disorder; cytostatic; gene therapy;
KW N-terminal peptide; enzyme linked immunosorbent assay; ELISA.
XX
XX Homo sapiens.
OS
XX
XX CN1338469-A.
PN
XX
XX 06-MAR-2002.
PD
XX
XX 21-AUG-2000; 2000CN-00119641.
PF
XX
XX 21-AUG-2000; 2000CN-00119641.
PR
XX
XX 21-AUG-2000; 2000CN-00119641.
PA
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PI
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-384269/42.
DR
XX
XX New polypeptide-human I1 factor ORF2 associated protein 10.45 for
PT treating diseases such as a tumor, or a protein metabolism disorder.
PT
XX
XX Example 6; Page 21 (Disclosure); 33pp; Chinese.
XX

CC The invention relates to human I1 factor ORF2 associated protein 10.45
CC (ABB09568) and nucleic acids encoding it (ABL55410). The protein has a
CC molecular weight of 10.45 kD and has 65% identity and 77% homology over a
CC 95 amino acid stretch with a human I1 element ORF2-like protein given in
CC Genbank accession number AF003535. The invention also relates to a method
CC for the recombinant production of the protein, an antagonist of the
CC protein, and the use of the protein, gene and antagonist in therapeutic
CC applications. I1 factor ORF2 associated protein 10.45 can be used in the
CC treatment of a variety of diseases such as tumours and disorders of
CC protein metabolism. The present sequence represents the 15 N-terminal
CC amino acid of human I1 factor ORF2 associated protein 10.45 used in
CC ELISA (enzyme linked immunosorbent assay) in an exemplification of the
CC invention
SQ Sequence 15 AA;
Query Match 42.0%; Score 34; DB 5; Length 15;
Best Local Similarity 45.5%; Pred. No. 2e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 2 LEMPVLVPEPPF 12
DB 5 LEKPIVPLQKF 15
RESULT 35
ADN60302
ID ADN60302 standard; peptide; 15 AA.
XX
XX ADN60302;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX Constituent peptide of colostrinin SEQ ID NO:8.
DE
XX
XX modulator; colostrinin; intracellular signaling molecule modulator;
KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;
KW DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNE inhibitor;
KW 4HNE-protein adduct formation reduction;
KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;
KW c-Jun NH2-terminal kinase inhibition.
XX
XX Synthetic.
OS
XX
XX WO2004037851-A2.
PN
XX
XX 06-MAY-2004.
PD
XX
XX 22-OCT-2003; 2003WO-US033423.
PF
XX
XX 22-OCT-2002; 2002US-0420369P.
PR
XX
XX (TEXA) UNTV TEXAS SYSTEM.
PA (BOLD/) BOLDGCH I.
PA (STAN/) STANTON J G.
PA (GEOR/) GEORGIADIS J A.
PA (HUGH/) HUGHES T K.
PA (KRUZ/) KRUZEL M.
XX
XX Boldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;
PI
XX
XX WPI; 2004-365494/34.
DR
XX
XX Use of colostrinin for e.g. modulating an intracellular signaling
PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a
PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
PT a cell.
PT
XX
XX Claim 6; SEQ ID NO 8; 46pp; English.
PS
XX
XX The present invention describes the use of a modulator selected from
CC colostrinin, its constituent peptide, its active analogue, and a
CC combination of these, for modulating an intracellular signaling molecule
CC

CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
 CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
 CC The modulator has cytostatic activity, and can be used as a 4HNE
 CC inhibitor. The modulator is useful in the manufacture of a medicament for
 CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated
 CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,
 CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.
 CC Colostrium, or its constituent peptide or active analogue is useful for
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
 CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
 CC The present sequence represents a synthetic constituent peptide of
 CC colostrinin, which can be used as a modulator in the present invention.
 CC
 XX
 SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 8; Length 15;
 Best Local Similarity 70.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLVPEPPPE 14
 :|||
 Db 5 PVLKVEVPP 14

RESULT 36

ADRS1999
 ID ADR31999 standard; peptide; 15 AA.

AC ADR31999;

DT 02-DEC-2004 (first entry)

DE Heat shock protein 20-derived peptide SEQ ID NO:313;

KM heat shock protein 20; HSP20; scar; wound healing; vulnery;

XX gene therapy.

OS Synthetic.

PN WO2004075914-A1.

PD 10-SEP-2004.

PF 20-FEB-2004; 2004WO-US004999.

PR 21-FEB-2003; 2003US-0448954P.

PR 17-OCT-2003; 2003US-0512211P.

PR 16-DEC-2003; 2003US-0530306P.

PA (UNVAR-) UNIV ARIZONA STATE.

PI Brophy C, Panitch A, Parmiter C, Furnish E, Komalavilas P;

DR WPI; 2004-653328/63.

XX Reducing scar formation and/or promoting wound healing comprises

PT administering to an individual an amount of heat shock protein 20-derived

PT polypeptides.

PS Disclosure; SEQ ID NO 313; 113pp; English.

CC The invention relates to a novel method for reducing scar formation or
 CC promoting wound healing, comprising administering to an individual an
 CC amount to reduce scar formation or promote wound healing of a polypeptide
 CC comprising a sequence of formula X1-A(X2)APLP-X3. Within the formula X1 =
 CC 0-14 amino acids of the sequence of heat shock protein 20 (HSP20) between
 CC residues 1 and 14 of a sequence having 160 amino acids fully defined in
 CC the specification (ADR31985); X2 = Ser, Thr, Tyr, Asp, Glu,
 CC hydroxylysine, hydroxyproline, phosphoserine analogues and
 CC phosphotyrosine analogues; and X3 = 0-140 amino acids of hsp20 between
 CC residues 21 and 160 of ADR31985; or 0, 1, 2 or 3 amino acids of a
 CC sequence of genus Z1-Z2-Z3, where Z1 is Gly or Asp, Z2 is Leu or Lys, and

CC '23 is Ser, Thr or Lys. A polypeptide of the invention has vulnery
 CC activity, and may have a use in gene therapy. The method is useful for
 CC reducing initial scar formation and/or for promoting wound healing. The
 CC present sequence represents a HSP20-derived peptide of the invention.
 CC
 XX
 SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 8; Length 15;
 Best Local Similarity 60.0%; Pred. No. 2e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LEMPVLPVP 11
 :|||
 Db 1 MEIPVPVMP 10

RESULT 37

ADRS74389
 ID AD574389 standard; peptide; 15 AA.

AC AD574389;

DT 16-DEC-2004 (first entry)

DE Ovine colostrinin peptide.

KM Colostrum; colostrinin; sheep; peptide purification.

OS Ovis aries.

PN WO2004081038-A1.

PD 23-SEP-2004.

PF 10-MAR-2004; 2004WO-GB001014.

PR 11-MAR-2003; 2003GB-00005552.

PR 08-MAR-2004; 2004GB-00005190.

PA (REGS-) REGEN THERAPEUTICS PLC.

PI Georgiades JA, Polanowski A, Wilusz T, Kruszal MJ;

DR WPI; 2004-677519/66.

XX Recovering peptides such as colostrinin from mammalian colostrum, by

PT mixing colostrum with alcohol to form alcohol phase containing peptides

PT and precipitate, separating alcohol phase from precipitate, and

PT recovering alcohol phase.

PS Disclosure; SEQ ID NO 4; 41pp; English.

CC The present sequence is that of a peptide that can be recovered from
 CC ovine colostrinin using the method of the invention. The invention
 CC provides a method for the recovery of peptides (especially colostrinin)
 CC from colostrum in substantially pure, biologically active form and in
 CC high yield. The method involves mixing the colostrum with an alcohol to
 CC form an alcohol phase containing the colostrinin and a precipitate
 CC containing higher molecular weight caseins and other proteins. Best
 CC results are obtained using methanol or ethanol of at least 80%, and
 CC preferably up to 100%, purity. The alcohol phase is then separated from
 CC the precipitate, and the colostrinin is separated from the alcohol,
 CC preferably by evaporation, to form a colostrinin-rich phase, which is
 CC recovered. A precipitation agent, such as ammonium sulfate, may be added
 CC either to the alcohol phase or, preferably, to the colostrinin-rich phase
 CC to induce precipitation of the colostrinin peptides. The method is
 CC generally applicable to the separation of peptides from fluids containing
 CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic
 CC acids.

Query Match 42.0%; Score 34; DB 8; Length 15;

PR 12-APR-2001; 2001EP-00201377.
 PR 16-NOV-2001; 2001EP-00204383.

XX
 PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.

XX PI Drifhout JW, Koning P, Mcadam SN, Solld LM;
 XX DR WPI; 2003-093000/08.

XX
 PT Novel isolated or recombinant human leukocyte antigen-DQ restricted T-
 PT cell receptor for treating food-related immune enteropathy, such as celiac
 PT sprue, tropical sprue, giardiasis and food allergies of childhood.

XX PS Disclosure; Fig 2; 64pp; English.

XX
 CC The present invention relates to novel isolated or recombinant human
 CC leukocyte antigen (HLA)-DQ restricted T-cell receptor or its functional
 CC equivalent and/or fragment, capable of recognising a prolamine-derived
 CC peptide. The invention relates to recombinant or synthetic prolamine
 CC derived peptides involved in food-related immune enteropathy. The
 CC pharmaceutical composition is useful to treat food-related immune
 CC enteropathies such as celiac sprue, tropical sprue, giardiasis or food
 CC allergies of childhood. It is useful to induce tolerance, treat gluten-
 CC sensitivity and to eliminate gluten-sensitive T-cells. Sequences of the
 CC invention are useful to decrease the amount of toxic prolamine-derived
 CC peptides in food or food components and to select and/or breed a cereal.
 CC The cereal is useful for inclusion in a diet for a gluten sensitive
 CC individual. Blocking substances are useful to decrease the binding of HLA
 CC -DQ restricted T-cell receptor to a prolamine-derived peptide involved in
 CC food-related immune enteropathy for depletion of T-cells bearing the HLA-
 CC DQ restricted T-cell receptor. The present sequence is T-cell stimulatory
 CC gluten peptide. This sequence is used in the invention

XX SQ Sequence 18 AA;

Query Match 42.0%; Score 34; DB 6; Length 18;
 Best Local Similarity 45.5%; Pred. No. 2.4e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMPVLPVPERP 13
 : | | : | |
 DB 4 QQPYLQLQPPF 14

Search completed: June 7, 2005, 23:10:50
 Job time : 83.7273 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:57:32 ; Search time 20.4545 Seconds
(without alignments)
54.743 Million cell updates/sec

Title: US-10-691-157-5
Perfect score: 81
Sequence: 1 DLEMPVLVPBPFFV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 183464

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUTS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	4	US-09-641-803-5
2	36	44.4	18	4	US-09-641-803-22
3	34	42.0	15	4	US-09-641-803-8
4	32	39.5	15	4	US-09-009-953-97
5	32	39.5	15	4	US-09-009-953-111
6	32	39.5	15	1	US-07-702-771-5
7	32	39.5	16	1	US-08-438-883-5
8	32	39.5	16	1	US-08-741-599-5
9	31	38.3	8	1	US-08-360-239B-2
10	31	38.3	12	4	US-09-914-259-179
11	30	37.0	15	2	US-08-687-956A-8
12	30	37.0	15	3	US-08-743-168B-15
13	30	37.0	15	3	US-09-807-278-5
14	30	37.0	15	5	PTC-US96-10435-15
15	30	37.0	15	5	US-08-602-999A-451
16	30	37.0	16	4	US-09-500-124-451
17	29	35.8	13	1	US-08-205-938A-21
18	29	35.8	13	5	PTC-US95-02626-21
19	29	35.8	14	3	US-08-630-916A-56
20	29	35.8	15	2	US-08-687-956A-7
21	29	35.8	16	3	US-08-602-999A-202
22	29	35.8	16	3	US-08-602-999A-406
23	29	35.8	16	4	US-09-500-124-202
24	29	35.8	16	4	US-09-500-124-406
25	29	35.8	17	3	US-08-987-743-11
26	29	35.8	18	1	US-08-205-938A-22
27	29	35.8	18	5	PTC-US95-02626-22

28	34.6	10	4	US-09-239-043D-2314	Sequence 2314, Ap
29	34.6	15	3	US-08-684-187-1	Sequence 1, Appl
30	34.6	15	4	US-09-009-953-120	Sequence 120, App
31	34.6	16	2	US-08-844-312-9	Sequence 9, Appl
32	34.6	17	3	US-08-602-999A-360	Sequence 360, App
33	34.6	17	4	US-09-500-124-360	Sequence 360, App
34	34.6	18	3	US-08-630-916A-103	Sequence 103, App
35	34.6	18	3	US-08-602-999A-317	Sequence 317, App
36	34.6	18	3	US-08-630-916A-159	Sequence 159, App
37	34.6	18	4	US-09-500-124-317	Sequence 317, App
38	34.6	18	4	US-09-879-957-159	Sequence 159, App
39	33.3	6	2	US-08-672-805-6	Sequence 6, Appl
40	33.3	8	3	US-08-828-712-12	Sequence 12, Appl
41	33.3	8	3	US-08-993-165-25	Sequence 25, Appl
42	33.3	8	3	US-08-993-165-28	Sequence 28, Appl
43	33.3	8	3	US-08-993-165-30	Sequence 30, Appl
44	33.3	8	4	US-09-063-276-12	Sequence 12, Appl
45	33.3	8	4	US-09-540-448-25	Sequence 25, Appl
46	33.3	8	4	US-09-540-448-28	Sequence 28, Appl
47	33.3	8	4	US-09-496-761-1	Sequence 1, Appl
48	33.3	8	4	US-09-496-761-6	Sequence 6, Appl
49	33.3	8	4	US-09-324-782-12	Sequence 12, Appl
50	33.3	8	4	US-09-668-143-12	Sequence 12, Appl
51	33.3	8	4	US-09-668-143-13	Sequence 13, Appl
52	33.3	8	4	US-09-668-143-14	Sequence 14, Appl
53	33.3	8	4	US-08-929-847-26	Sequence 26, Appl
54	33.3	8	4	US-08-929-847-29	Sequence 29, Appl
55	33.3	8	4	US-09-813-484-26	Sequence 26, Appl
56	33.3	8	4	US-09-813-484-29	Sequence 29, Appl
57	33.3	8	4	US-10-046-801-25	Sequence 25, Appl
58	33.3	8	4	US-10-046-801-28	Sequence 28, Appl
59	33.3	8	4	US-10-266-463A-46	Sequence 46, Appl
60	33.3	9	3	US-08-828-712-13	Sequence 13, Appl
61	33.3	9	3	US-08-828-712-14	Sequence 14, Appl
62	33.3	9	3	US-09-063-276-13	Sequence 13, Appl
63	33.3	9	3	US-09-063-276-14	Sequence 14, Appl
64	33.3	9	4	US-09-324-782-13	Sequence 13, Appl
65	33.3	9	4	US-09-324-782-14	Sequence 14, Appl
66	33.3	9	4	US-09-668-143-13	Sequence 13, Appl
67	33.3	9	4	US-09-668-143-14	Sequence 14, Appl
68	33.3	9	4	US-08-913-612A-47	Sequence 47, Appl
69	33.3	9	4	US-10-266-463A-47	Sequence 47, Appl
70	33.3	10	1	US-08-214-650-40	Sequence 40, Appl
71	33.3	10	4	US-09-051-380-16	Sequence 16, Appl
72	33.3	10	4	US-09-239-043D-2313	Sequence 2313, Ap
73	33.3	14	3	US-09-208-966-11	Sequence 11, Appl
74	33.3	14	3	US-09-775-052A-11	Sequence 11, Appl
75	33.3	14	6	5164482-18	Patent No. 5164482
76	33.3	15	1	US-08-230-047-27	Sequence 27, Appl
77	33.3	15	3	US-08-602-999A-467	Sequence 467, App
78	33.3	15	4	US-09-500-124-467	Sequence 467, App
79	33.3	15	4	US-08-448-446-251	Sequence 251, App
80	33.3	15	4	US-09-647-372B-74	Sequence 74, Appl
81	33.3	16	2	US-08-844-312-10	Sequence 10, Appl
82	33.3	16	3	US-08-602-999A-200	Sequence 200, App
83	33.3	16	3	US-08-602-999A-220	Sequence 220, App
84	33.3	16	4	US-09-500-124-200	Sequence 200, App
85	33.3	16	4	US-09-500-124-220	Sequence 220, App
86	33.3	17	4	US-08-469-260A-251	Sequence 251, App
87	33.3	17	4	US-08-488-446-251	Sequence 251, App
88	33.3	17	4	US-08-467-344A-251	Sequence 251, App
89	33.3	17	4	US-08-426-098B-272	Sequence 272, App
90	33.3	17	4	US-08-424-550B-251	Sequence 251, App
91	33.3	18	2	US-08-374-650C-80	Sequence 80, Appl
92	32.7	15	4	US-09-205-256-379	Sequence 379, Appl
93	32.7	15	4	US-08-179-984-3	Sequence 3, Appl
94	32.1	6	2	US-08-540-118-5	Sequence 5, Appl
95	32.1	6	2	US-08-747-137-167	Sequence 167, Appl
96	32.1	6	4	US-09-185-818-5	Sequence 5, Appl
97	32.1	7	3	US-09-365-581A-2	Sequence 2, Appl
98	32.1	7	4	US-09-626-821A-2	Sequence 2, Appl
99	32.1	8	1	US-08-360-239B-1	Sequence 1, Appl
100	32.1	8	3	US-08-993-165-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-09-641-803-5
; Sequence 5, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-5

Query Match

Best Local Similarity 100.0%; Score 81; DB 4; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPYLPVEPPFV 15
| | | | | | | | | | | | | | | | |

DB 1 DLEMPYLPVEPPFV 15

RESULT 2

US-09-641-803-22
; Sequence 22, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-22

Query Match

Best Local Similarity 44.4%; Score 36; DB 4; Length 18;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPYLPVEPPF 12
: : | | | | |

DB 3 EMPFPCYVPEPPF 14

RESULT 3

US-09-641-803-8
; Sequence 8, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-8

Query Match

Best Local Similarity 42.0%; Score 34; DB 4; Length 15;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLXVPEPPF 14
| | | | |

DB 5 PVLXVPEPPF 14

RESULT 4

US-09-009-953-97
; Sequence 97, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; REACTIVE DR Restricted Epitopes
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,953
; FILING DATE: 21-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,713
; FILING DATE: 23-JAN-1997
; APPLICATION NUMBER: US 60/037,432
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-011520US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-09-009-953-97

Query Match 39.5%; Score 32; DB 4; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LEMPVLPEVPP 13
DB 2 LNFPIPIETVP 13

RESULT 5
US-09-009-953-111
Sequence 111, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
REACTIVE DR RESTRICTED EPITOPES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
TELEFAX: 415-576-0300
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-09-009-953-111

Query Match 39.5%; Score 32; DB 4; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LEMPVLPEVPP 13
DB 4 LNFPIPIETVP 15

RESULT 6
US-07-702-771-5
Sequence 5, Application US/07702771
Patent No. 5610276
GENERAL INFORMATION:
APPLICANT: Wong, Gail L.
APPLICANT: McCormick, Frank
TITLE OF INVENTION: Cloning and Purification of p62
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation
STREET: 1400 Fifty-third Street
CITY: Emeryville
STATE: California
ZIP: 94608-2997
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/702,771
FILING DATE: 17-MAY-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory J.
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: 2594
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-420-3300
TELEFAX: 415-658-5239
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: internal
ORIGINAL SOURCE: Mbs musculus
US-07-702-771-5

Query Match 39.5%; Score 32; DB 1; Length 16;
Best Local Similarity 45.5%; Pred. No. 1e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 EMPVLPEVPP 13
DB 4 EMPVLPEVPP 14

RESULT 7
US-08-438-883-5
Sequence 5, Application US/08438883
Patent No. 5731427
GENERAL INFORMATION:
APPLICANT: Wong, G.
APPLICANT: McCormick, F.
TITLE OF INVENTION: Purification and Cloning of p62
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,883
FILING DATE: 10-MAY-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/702,771
FILING DATE: 17-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 27527/33275
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: N
FRAGMENT TYPE: internal
ORIGINAL SOURCE: Mus musculus
US-08-438-883-5

Query Match 39.5%; Score 32; DB 1; Length 16;
Best Local Similarity 45.5%; Pred. No. 1e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EMPVLPEVEPP 13
| : : : : :
Db 4 EMVLIPVKQYP 14

RESULT 8
US-08-741-599-5
Sequence 5, Application US/08741599
Patent No. 5773237
GENERAL INFORMATION:
APPLICANT: Wong, G.
TITLE OF INVENTION: Purification and Cloning of p62
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,599
FILING DATE: 01-NOV-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/702,771
FILING DATE: 17-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 0892.003/33583
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: N
FRAGMENT TYPE: internal
ORIGINAL SOURCE: Mus musculus
US-08-741-599-5

Query Match 39.5%; Score 32; DB 1; Length 16;
Best Local Similarity 45.5%; Pred. No. 1e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EMPVLPEVEPP 13
| : : : : :
Db 4 EMVLIPVKQYP 14

RESULT 9
US-08-360-239B-2
Sequence 2, Application US/08360239B
Patent No. 5801222
GENERAL INFORMATION:
APPLICANT: Pettit, George R.
TITLE OF INVENTION: Isolation and Structure of
TITLE OF INVENTION: the Human Cancer Cell Growth Inhibitory Cyclic
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Richard R. Mybeck
STREET: 8010 East Morgan Trail, #10
CITY: Scottsdale
STATE: Arizona
COUNTRY: USA
ZIP: 85258-1234
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,239B
FILING DATE: 12/20/94
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Richard R. Mybeck
REGISTRATION NUMBER: 17,886
REFERENCE/DOCKET NUMBER: 4997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (602)-483-1285
TELEFAX: (602)-483-7452
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
TYPE: amino acid
TOPOLOGY: cyclic
MOLECULE TYPE:
DESCRIPTION: Cyclooctapeptide
DESCRIPTION: phakellistatin 11
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: circular
ORIGINAL SOURCE:
ORGANISM: Phakellia sp.
DEVELOPMENTAL STAGE: whole organism
FEATURE:

NAME/KEY: phakellistatin 11
NAME/KEY: amino acid analysis, high resolution
NAME/KEY: nuclear magnetic resonance and mass
NAME/KEY: spectral MS/MS techniques
OTHER INFORMATION: Phakellistatin is a
OTHER INFORMATION: cell growth inhibitory peptide with
OTHER INFORMATION: activity in murine lymphocytic leukemia
OTHER INFORMATION: cell line of 0.20 mg/ml.
US-08-360-239B-2

Query Match 38.3%; Score 31; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 BPPFP 15
DB 2 QPPFP 7

RESULT 10
US-09-914-259-179
Sequence 179, Application US/09914259
Patent No. 6495336
GENERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 179
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Identified from M13 bacteriophage peptide display library.
US-09-914-259-179

Query Match 38.3%; Score 31; DB 4; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LPVPP 13
DB 5 LPVTPP 11

RESULT 11
US-08-687-956A-8
Sequence 8, Application US/08687956A
Patent No. 5861157
GENERAL INFORMATION:
APPLICANT: BURNIE, JAMES P
APPLICANT: MATTHEWS, RUTH C
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: PILLSBURY, MADISON & SUTRO, LLP
STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
FLOOR
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,956A
FILING DATE: 29-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9401689.6
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 50885/222892
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/861-3000
TELEFAX: 202/822-0944
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Streptococcus sobrinus
STRAIN: Streptococcus sobrinus MUCOB 263
US-08-687-956A-8

Query Match 37.0%; Score 30; DB 2; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVPP 11
DB 4 DONIDKPPVP 14

RESULT 12
US-08-743-168B-15
Sequence 15, Application US/08743168B
Patent No. 6271015
GENERAL INFORMATION:
APPLICANT: Gilula, No. 6271015ton B
APPLICANT: Cravatt, Benjamin F
APPLICANT: Ierner, Richard A
TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSER: The Scripps Research Institute
STREET: 10550 No. 6271015th Torrey Pines Road
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,168B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/489,535
FILING DATE: 12-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 485.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 15;
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-743-168B-15

Query Match 37.0%; Score 30; DB 3; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 5 PVLVPEPPF 14
|:|:|:|:
DB 5 PTVP--PPPF 12

RESULT 13
US-09-807-278-5
Sequence 5, Application US/09807278
Patent No. 6753310
GENERAL INFORMATION:
APPLICANT: Otsuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: NEOVASCULAR-SPECIFIC PEPTIDES
FILE REFERENCE: Q64027
CURRENT APPLICATION NUMBER: US/09/807,278
CURRENT FILING DATE: 2001-04-11
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: JP 1998-295198
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 15
TYPE: PRT
ORGANISM: phage library
US-09-807-278-5

Query Match 37.0%; Score 30; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLVPEPPF 13
|:|:|:|:
DB 5 PALPVLFP 13

RESULT 14
PCT-US96-10435-15
Sequence 15, Application PC/TUS9610435
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: CIS-9, 10-OCTADECENOMITASE
NUMBER OF SEQUENCES: 32
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10435
FILING DATE: 12-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/489,535
FILING DATE: 12-JUN-1995
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal

PCT-US96-10435-15

Query Match 37.0%; Score 30; DB 5; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 5 PVLVPEPPF 14
|:|:|:|:
DB 5 PTVP--PPPF 12

RESULT 15
US-08-602-999A-451
Sequence 451, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOLKES, Dana M.
APPLICANT: RIDER, James B.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18, 872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 451:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-451

Query Match 37.0%; Score 30; DB 3; Length 16;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLVPEPP 11
|:|:|:|:
DB 6 PLPPIKP 12

RESULT 16
US-09-500-124-451
Sequence 451, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.

APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edwards
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 451:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-451

Query Match 37.0%; Score 30; DB 4; Length 16;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLPEP 11
DB 6 PVLPEP 12

RESULT 17
US-08-205-938A-21
Sequence 21, Application US/08205938A
Patent No. 5466671
GENERAL INFORMATION:
APPLICANT: TEMPEST, PAUL
APPLICANT: CASTELS, PETER
TITLE OF INVENTION: APIDACIN-TYPE PEPTIDE ANTIBIOTICS WITH
TITLE OF INVENTION: IMPROVED ACTIVITIES AND/OR DIFFERENT
TITLE OF INVENTION: ANTIBACTERIAL SPECTRUM
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,938A
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45061
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-205-938A-21

Query Match 35.8%; Score 29; DB 1; Length 13;
Best Local Similarity 36.4%; Pred. No. 2.3e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMPVLPVEP 13
DB 1 QVPIRQSP 11

RESULT 18
PCT-US95-02626-21
Sequence 21, Application PC/TUS9502626
GENERAL INFORMATION:
APPLICANT: SLOAN-KEYTERING INSTITUTE FOR CANCER RESEARCH
APPLICANT: TEMPEST, PAUL
APPLICANT: CASTELS, PETER
TITLE OF INVENTION: APIDACIN-TYPE PEPTIDE ANTIBIOTICS WITH IMPROVED
TITLE OF INVENTION: ACTIVITIES AND/OR DIFFERENT ANTIBACTERIAL SPECTRUM
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02626
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,938
FILING DATE: 02-MAR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45061-A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US95-02626-21

Query Match 35.8%; Score 29; DB 5; Length 13;
Best Local Similarity 36.4%; Pred. No. 2.3e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMPVLVPEPP 13
DB 1 QVLRPSQPRP 11

RESULT 19

US-08-630-916A-56
Sequence 56, Application US/08630916A
Patent No. 6011137
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: Kay, Brian K.
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING MW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8664/9741
INFORMATION FOR SEQ. ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-916A-56

Query Match 35.8%; Score 29; DB 3; Length 14;
Best Local Similarity 45.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 EMPVLVPEPP 13
DB 1 EYPPYPPPPYP 11

RESULT 20

US-08-687-956A-7
Sequence 7, Application US/08687956A
Patent No. 5861157
GENERAL INFORMATION:
APPLICANT: BURKE, JAMES P
APPLICANT: MATTHEWS, RUTH C
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI

NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: PILLSBURY, MADISON & SUTRO, LLP
STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
STREET: FLOOR
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,956A
FILING DATE: 29-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9401689.6
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 50885/222892
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/861-3000
TELEFAX: 202/822-0944
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORGANISM: Streptococcus sobrinus
STRAIN: Streptococcus sobrinus MUCOB 263
US-08-687-956A-7

Query Match 35.8%; Score 29; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EMPVLVPEP 11
DB 6 ELVDLPVEP 14

RESULT 21

US-08-602-999A-202
Sequence 202, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 202:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-202

Query Match
Best Local Similarity 35.8%; Score 29; DB 3; Length 16;
Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLEMPVLP 8
| | | | |
DB 3 DERPVLVP 10

RESULT 22
US-08-602-999A-406
Sequence 406, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OULLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
NUMBER OF SEQUENCES: 467
TITLE OF INVENTION: ISOLATING AND USING SAME
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 406:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-406

Query Match
Best Local Similarity 35.8%; Score 29; DB 3; Length 16;
Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEMPVLP 8
| | | | |
DB 4 LKMPVLP 10

RESULT 23
US-09-500-124-202
Sequence 202, Application US/09500124
Patent No. 643920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OULLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
NUMBER OF SEQUENCES: 467
TITLE OF INVENTION: ISOLATING AND USING SAME
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 202:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-202

Query Match
Best Local Similarity 35.8%; Score 29; DB 4; Length 16;
Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLEMPVLP 8
| | | | |

Db 3 DERPVLP 10

RESULT 24

US-09-500-124-406
Sequence 406, Application US/09500124
Patent No. 6432920

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAN, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION/DOCKET NUMBER: 18,872
REFERENCE/DOCKET INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 406:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-406

Query Match 35.8%; Score 29; DB 4; Length 16;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEMPVLP 8
Db 4 LKLPVLP 10

RESULT 25

US-08-987-743-11
Sequence 11, Application US/08987743
Patent No. 6123938

GENERAL INFORMATION:
APPLICANT: Stern, Robert
APPLICANT: Gaska, Anthony
APPLICANT: Frost, Gregory I.
APPLICANT: Wong, Tim M.
TITLE OF INVENTION: Purification and Microsequencing of
TITLE OF INVENTION: Hyaluronidase Isozymes

FILE REFERENCE: 9076/088CIP2
CURRENT APPLICATION NUMBER: US/08/987,743
CURRENT FILING DATE: 1997-12-09
EARLIER APPLICATION NUMBER: 08/733,360
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11
LENGTH: 17
TYPE: PRT
ORGANISM: H. sapiens
US-08-987-743-11

Query Match 35.8%; Score 29; DB 3; Length 17;
Best Local Similarity 54.5%; Pred. No. 3.1e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PVLPEPPPPV 15
Db 4 PLLPNXPFTTV 14

RESULT 26

US-08-205-938A-22
Sequence 22, Application US/08205938A
Patent No. 546671

GENERAL INFORMATION:
APPLICANT: TEMPEST, PAUL
APPLICANT: CASTELLS, PETER
TITLE OF INVENTION: APIDACIN-TYPE PEPTIDE ANTIBIOTICS WITH
TITLE OF INVENTION: IMPROVED ACTIVITIES AND/OR DIFFERENT
TITLE OF INVENTION: ANTIBACTERIAL SPECTRUM
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,938A
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45061
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-205-938A-22

Query Match 35.8%; Score 29; DB 1; Length 18;
Best Local Similarity 36.4%; Pred. No. 3.3e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMPVLPVEPP 13
Db 6 QVPIRPSQPRP 16

RESULT 27
PCT-US95-02626-22
Sequence 22, Application PC/TUS9502626
GENERAL INFORMATION:
APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH
APPLICANT: TEMPEST, PAUL
APPLICANT: CASTEELS, PETER
TITLE OF INVENTION: APIRACIN-TYPE PEPTIDE ANTIBIOTICS WITH IMPROVED
TITLE OF INVENTION: ACTIVITIES AND/OR DIFFERENT ANTIBACTERIAL SPECTRUM
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02626
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,938
FILING DATE: 02-MAR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45061-A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid.
TOPOLOGY: linear
MOLBSCU TYPE: peptide
PCT-US95-02626-22

Query Match 35.8%; Score 29; DB 5; Length 18;
Best Local Similarity 36.4%; Pred. No. 3.3e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMPVLPEPPFP 13
DB 6 QVPFRSOPRP 16

RESULT 28
US-09-239-043D-2314
Sequence 2314, Application US/09239043D
Patent No. 6689363
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Vitello, Maria A.
APPLICANT: Livingston, Brian D.
APPLICANT: Kubo, Esteban
APPLICANT: Cells, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Cheanut, Robert
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0060007
CURRENT APPLICATION NUMBER: US/09/239,043D

CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/978,291
PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: US 08/820,360
PRIOR FILING DATE: 1997-03-12
PRIOR APPLICATION NUMBER: US 60/013,363
PRIOR FILING DATE: 1996-03-13
PRIOR APPLICATION NUMBER: US 08/461,603
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
PRIOR APPLICATION NUMBER: US 08/344,824
PRIOR FILING DATE: 1994-11-23
PRIOR APPLICATION NUMBER: US 08/278,634
PRIOR FILING DATE: 1994-07-21
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR FILING DATE: 1994-02-16
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 2579
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2314
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HBV analog peptide
US-09-239-043D-2314

Query Match 34.6%; Score 28; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 LPVPEPPFV 15
DB 2 LPVDPPFSV 10

RESULT 29
US-08-684-187-1
Sequence 1, Application US/08684187A
Patent No. 6020171
GENERAL INFORMATION:
APPLICANT: SAITO, ATSUSHI
APPLICANT: SHINAGAWA, HIDEO
APPLICANT: NAKATA, ATSUGO
TITLE OF INVENTION: METHOD OF PREPARING PLASMID HAVING BOTH EXPRESSING
TITLE OF INVENTION: ABILITY OF RETROVIRAL GENE AND PROCESSING ABILITY AFTER
TITLE OF INVENTION: TRANSLATION, AND RESULTANT PLASMID AND EXPRESSION
FILE REFERENCE: 96-0747/1c(lmc)/553
CURRENT APPLICATION NUMBER: US/08/684,187A
CURRENT FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: N-TERMINAL
US-08-684-187-1

Query Match 34.6%; Score 28; DB 3; Length 15;
Best Local Similarity 44.4%; Pred. No. 3.8e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLPEPPFP 13
DB 1 PVLPEPPFP 13

Db 1 PISPIETVP 9

RESULT 30

US-09-009-953-120
Sequence 120, Application US/09009953
Patent No. 6413517

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS Windows Version 2.0

SOFTWARE: FASTSEQ for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/009,953

FILING DATE: 21-Jan-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,713

FILING DATE: 23-Jan-1997

APPLICATION NUMBER: US 60/037,432

FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-01152005

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 120:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 120:

US-09-009-953-120

Query Match 34.6%; Score 28; DB 4; Length 15;

Best Local Similarity 44.4%; Pred. No. 3.8e+02;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLVPEVPP 13

Db 3 PISPIETVP 11

RESULT 31

US-08-844-312-9
Sequence 9, Application US/08844312
Patent No. 5948639

GENERAL INFORMATION:

APPLICANT: Carlos J. Gimeno and Dean A. Falb

TITLE OF INVENTION: NO. 5948639el TGF- β (SYMBOL 98 \{ "symbol" \}) Pathway Genes

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESSES:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/844,312

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Silveri, Jean M.

REGISTRATION NUMBER: 39, 030

REFERENCE/DOCKET NUMBER: MN1-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-844-312-9

Query Match 34.6%; Score 28; DB 2; Length 16;

Best Local Similarity 38.5%; Pred. No. 4.1e+02;

Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DLEPVLPEVPP 13

Db 4 ELESPPAPYSRYP 16

RESULT 32

US-08-602-999A-360
Sequence 360, Application US/08602999A
Patent No. 6184205

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.

APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.

APPLICANT: QUILIAM, Lawrence A.

APPLICANT: DER, Channing J.

APPLICANT: FOWLES, Dana M.

APPLICANT: RIDER, James E.

TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

TITLE OF INVENTION: ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/602,999A

FILING DATE: 16-FEB-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mastro, S. Leslie

REGISTRATION NUMBER: 18, 872

REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 360:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-360

Query Match 34.6%; Score 28; DB 3; Length 17;
Best Local Similarity 45.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLVPEPPPPF 14
DB 4 LPPEPPPPPLPF 14

RESULT 33
US-09-500-124-360
Sequence 360, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWIKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 360:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-360

Query Match 34.6%; Score 28; DB 4; Length 17;

Best Local Similarity 45.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLVPEPPPPF 14
DB 4 LPPEPPPPPLPF 14

RESULT 34
US-08-630-916A-103
Sequence 103, Application US/08630916A
Patent No. 6011137
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: KAY, Brian K.
APPLICANT: FOWIKES, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 866-8864/9741
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-916A-103

Query Match 34.6%; Score 28; DB 3; Length 18;
Best Local Similarity 30.8%; Pred. No. 4.6e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 EMPVLVPEPPPPV 15
DB 6 QLPVPPKPPPLL 18

RESULT 35
US-08-602-999A-317
Sequence 317, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWIKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 317:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-317

Query Match 34.6%; Score 28; DB 3; Length 18;
Best Local Similarity 30.8%; Pred. No. 4.6e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EMPVLPEPPFPV 15
Db 6 QLPVPKPRPL 18

RESULT 36
US-08-630-915A-159
Sequence 159, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-159

Query Match 34.6%; Score 28; DB 3; Length 18;
Best Local Similarity 30.8%; Pred. No. 4.6e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EMPVLPEPPFPV 15
Db 6 QLPVPKPRPL 18

RESULT 37
US-09-500-124-317
Sequence 317, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 317:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: unknown

MOLECULE TYPE: peptide
US-09-500-124-317

Query Match 34.6%; Score 28; DB 4; Length 18;
Best Local Similarity 30.8%; Pred. No. 4.6e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EMPVLPVEPPPV 15
Db 6 QLPVPVPPKRPRL 18

RESULT 38

US-09-879-957-159
Sequence 159, Application US/09879957
Patent No. 6709821

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. 6709821h
KAY, Brian K.
FOWLES, Dana M.
MCCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME

NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:

ADDRESSEE: Penile & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-174

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 159:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 159:

Query Match 34.6%; Score 28; DB 4; Length 18;
Best Local Similarity 30.8%; Pred. No. 4.6e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EMPVLPVEPPPV 15
Db 6 QLPVPVPPKRPRL 18

RESULT 39

US-08-672-805-6
Sequence 6, Application US/08672805
Patent No. 5831003

GENERAL INFORMATION:

APPLICANT: Baumbach, George A.,
Buetner, Joseph A.,
APPLICANT: Dadd, Christopher A.,
APPLICANT: Hammond, David J.

TITLE OF INVENTION: Peptides which bind to Prothrombin and
Thrombin

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bayer Corporation

STREET: 800 Dwight Way

STREET: P. O. Box 1966

CITY: Berkeley

STATE: California

COUNTRY: USA

ZIP: 94701-1986

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb Storage

COMPUTER: IBM

OPERATING SYSTEM: DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,805

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Gbilia, James A.

REGISTRATION NUMBER: 25772

REFERENCE/DOCKET NUMBER: MSB-7236

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 705-7910

TELEFAX: (510) 705-7904

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 6

TYPE: amino acid

STRANDEDNESS: single strand

TOPOLOGY: linear

MOLECULE TYPE:

DESCRIPTION: peptide

US-08-672-805-6

Query Match 33.3%; Score 27; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PPPPV 15
Db 1 PPPV 5

RESULT 40

US-08-828-712-12
Sequence 12, Application US/08828712
Patent No. 6015884

GENERAL INFORMATION:

APPLICANT: Schneck, Jonathan P.

APPLICANT: O'Herrin, Sean

TITLE OF INVENTION: Soluble Divalent and Multivalent
Heterodimeric Analogs of Proteins

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.

STREET: 1001 G Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,712
FILING DATE: 28-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.73713
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 508-9100
TELEFAX: (202) 508-9299
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide p2Ca
US-08-828-712-12

Query Match 33.3%; Score 27; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 VEPFPF 14
: ||||
Db 1 LSPFPF 6

Search completed: June 7, 2005, 23:23:15
Job time : 21.4545 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 23:00:52 ; Search time 67.5 Seconds

(Without alignments)
85.185 Million cell updates/sec

Title: US-10-691-157-5

Perfect score: 81
Sequence: 1 DLEMPVLVPEPPFPV 15Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 309695

Minimum DB seq length: 0
Maximum DB seq length: 18Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

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22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	81	100.0	15	US-10-691-157-5	Sequence 5, Appli
3	81	100.0	15	US-10-691-330-5	Sequence 5, Appli
4	57	100.0	10	US-10-182-110-3	Sequence 3, Appli
5	36	44.4	18	US-10-281-652-22	Sequence 22, Appli
6	36	44.4	18	US-10-691-157-22	Sequence 22, Appli
7	36	44.4	18	US-10-691-330-22	Sequence 22, Appli
8	34	42.0	15	US-10-281-652-8	Sequence 8, Appli
9	34	42.0	15	US-10-691-157-8	Sequence 8, Appli
10	34	42.0	15	US-10-691-330-8	Sequence 8, Appli
11	34	42.0	18	US-10-474-955-67	Sequence 67, Appli

12	32	39.5	13	US-10-706-391-63	Sequence 63, Appli
13	32	39.5	15	US-10-103-395-97	Sequence 97, Appli
14	32	39.5	15	US-10-103-395-111	Sequence 111, Appli
15	31	38.3	12	US-10-158-596A-10	Sequence 10, Appli
16	31	38.3	12	US-10-157-775B-10	Sequence 10, Appli
17	31	38.3	12	US-10-254-446A-10	Sequence 10, Appli
18	31	38.3	12	US-10-155-883B-10	Sequence 10, Appli
19	31	38.3	12	US-10-080-608A-179	Sequence 179, Appli
20	31	38.3	12	US-10-370-665-88	Sequence 88, Appli
21	30	37.0	15	US-10-788-992-15	Sequence 15, Appli
22	30	37.0	16	US-10-161-791-451	Sequence 451, Appli
23	30	37.0	17	US-10-211-088-97	Sequence 97, Appli
24	30	37.0	18	US-10-225-567A-1382	Sequence 1382, Appli
25	29	35.8	6	US-10-433-709-6	Sequence 6, Appli
26	29	35.8	9	US-10-353-929-171	Sequence 171, Appli
27	29	35.8	14	US-10-185-050-56	Sequence 56, Appli
28	29	35.8	16	US-10-161-791-202	Sequence 202, Appli
29	29	35.8	16	US-10-161-791-406	Sequence 406, Appli
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31	28	34.6	10	US-09-572-404B-218	Sequence 218, Appli
32	28	34.6	10	US-09-572-404B-220	Sequence 220, Appli
33	28	34.6	10	US-09-572-404B-222	Sequence 222, Appli
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35	28	34.6	10	US-10-200-708-538	Sequence 538, Appli
36	28	34.6	10	US-10-654-601-2314	Sequence 2314, Appli
37	28	34.6	11	US-10-398-104-174	Sequence 174, Appli
38	28	34.6	12	US-10-226-007-1252	Sequence 1252, Appli
39	28	34.6	13	US-10-226-007-1253	Sequence 1253, Appli
40	28	34.6	13	US-10-226-007-1261	Sequence 1261, Appli
41	28	34.6	13	US-10-467-209-21	Sequence 21, Appli
42	28	34.6	13	US-10-468-370-75	Sequence 75, Appli
43	28	34.6	13	US-10-468-496-66	Sequence 66, Appli
44	28	34.6	13	US-10-468-486-1465	Sequence 1465, Appli
45	28	34.6	13	US-10-468-486-1466	Sequence 1466, Appli
46	28	34.6	14	US-10-226-007-1254	Sequence 1254, Appli
47	28	34.6	14	US-10-226-007-1262	Sequence 1262, Appli
48	28	34.6	14	US-10-226-007-1269	Sequence 1269, Appli
49	28	34.6	14	US-10-474-955-1	Sequence 1, Appli
50	28	34.6	14	US-10-794-514A-250	Sequence 250, Appli
51	28	34.6	14	US-10-794-514A-261	Sequence 261, Appli
52	28	34.6	14	US-10-794-514A-282	Sequence 282, Appli
53	28	34.6	14	US-10-794-514A-530	Sequence 530, Appli
54	28	34.6	15	US-10-103-395-120	Sequence 120, Appli
55	28	34.6	15	US-10-226-007-1255	Sequence 1255, Appli
56	28	34.6	15	US-10-226-007-1263	Sequence 1263, Appli
57	28	34.6	15	US-10-226-007-1270	Sequence 1270, Appli
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59	28	34.6	15	US-10-475-853-11	Sequence 11, Appli
60	28	34.6	15	US-10-226-007-1256	Sequence 1256, Appli
61	28	34.6	16	US-10-226-007-1264	Sequence 1264, Appli
62	28	34.6	16	US-10-226-007-1271	Sequence 1271, Appli
63	28	34.6	16	US-10-226-007-1277	Sequence 1277, Appli
64	28	34.6	16	US-10-226-007-1282	Sequence 1282, Appli
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72	28	34.6	17	US-10-788-400-26	Sequence 26, Appli
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74	28	34.6	18	US-10-185-050-103	Sequence 103, Appli
75	28	34.6	18	US-10-226-007-1258	Sequence 1258, Appli
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81	28	34.6	18	US-10-226-007-1291	Sequence 1291, Appli
82	28	34.6	18	US-10-161-791-317	Sequence 317, Appli
83	28	34.6	18	US-10-029-386-33029	Sequence 33029, Appli
84	28	34.6	18	US-10-807-856-159	Sequence 159, Appli

85 27.5 34.0 10 10 US-09-895-298-138 Sequence 138, App
86 27.5 34.0 10 16 US-10-885-039-138 Sequence 138, App
87 27 33.3 8 9 US-09-813-484-26 Sequence 26, Appl
88 27 33.3 8 9 US-09-813-484-26 Sequence 29, Appl
89 27 33.3 8 9 US-09-954-166-12 Sequence 12, Appl
90 27 33.3 8 9 US-09-761-534A-3 Sequence 3, Appl
91 27 33.3 8 9 US-09-434-965-2 Sequence 2, Appl
92 27 33.3 8 14 US-10-145-396-2 Sequence 25, Appl
93 27 33.3 8 14 US-10-046-801-25 Sequence 28, Appl
94 27 33.3 8 14 US-10-266-463A-46 Sequence 46, Appl
95 27 33.3 8 15 US-10-394-980-338 Sequence 338, Appl
96 27 33.3 8 16 US-10-785-472-2 Sequence 2, Appl
97 27 33.3 8 17 US-10-885-523-3 Sequence 3, Appl
98 27 33.3 9 17 US-08-344-824-97 Sequence 97, Appl
99 27 33.3 9 9 US-09-954-166-13 Sequence 13, Appl
100 27 33.3 9 9

ALIGNMENTS

RESULT 1
US-10-281-652-5
; Sequence 5, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265 00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-5
Query Match 100.0%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLEMPVLVPPPPFV 15
Db 1 DLEMPVLVPPPPFV 15
RESULT 2
US-10-691-157-5
; Sequence 5, Application US/10691157
; Publication No. US2004026681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUZEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265 00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-157-5

Query Match 100.0%; Score 81; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLVPPPPFV 15
Db 1 DLEMPVLVPPPPFV 15
RESULT 3
US-10-691-330-5
; Sequence 5, Application US/10691330
; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, G. John
; APPLICANT: Boldogh, Istvan
; APPLICANT: Georgiades, Jerzy A.
; APPLICANT: Hughes, Thomas K., Jr.
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265 00390101
; CURRENT APPLICATION NUMBER: US/10/691,330
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-330-5
Query Match 100.0%; Score 81; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLEMPVLVPPPPFV 15
Db 1 DLEMPVLVPPPPFV 15
RESULT 4
US-10-182-110-3
; Sequence 3, Application US/10182110
; Publication No. US20040171553A1
; GENERAL INFORMATION:
; APPLICANT: Regen Therapeutics plc
; APPLICANT: Georgiades, Jerzy A
; TITLE OF INVENTION: Peptide Fragments of Colostrinin And Their Use
; FILE REFERENCE: AAT-14173
; CURRENT APPLICATION NUMBER: US/10/182,110

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/ CURRENT FILING DATE: 2003-04-21
/ PRIOR APPLICATION NUMBER: GB0001825.9
/ PRIOR FILING DATE: 2000-01-26
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 10
/ TYPE: PRF
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Truncated version of a peptide found in colostrinin
US-10-182-110-3

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Best Local Similarity 70.4%; Score 57; DB 16; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLPEVPEPP 14
DB 1 PVLPEVPEPP 10

RESULT 5
US-10-281-652-22
/ Sequence 22, Application US/10281652
/ Publication No. US20030091606A1
/ GENERAL INFORMATION:
/ APPLICANT: STANTON, G. John
/ APPLICANT: HUGHES, Thomas K.
/ APPLICANT: BOLDG, Istvan
/ TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
/ FILE REFERENCE: 265, 00220101
/ CURRENT APPLICATION NUMBER: US/10/281,652
/ CURRENT FILING DATE: 2002-10-28
/ PRIOR APPLICATION NUMBER: US/09/641,803
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: 60/149,310
/ PRIOR FILING DATE: 1999-08-17
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 18
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-22

Query Match
Best Local Similarity 44.4%; Score 36; DB 14; Length 18;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPF 12
DB 3 EMPFPKYPVEPF 14

RESULT 6
US-10-691-157-22
/ Sequence 22, Application US/10691157
/ Publication No. US2004026661A1
/ GENERAL INFORMATION:
/ APPLICANT: BOLDG, Istvan
/ APPLICANT: STANTON, G. John
/ APPLICANT: GEORGIADIS, Jerzy
/ APPLICANT: HUGHES, Thomas
/ APPLICANT: KRUEL, Marian
/ TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
/ FILE REFERENCE: 265, 00440101
/ CURRENT APPLICATION NUMBER: US/10/691,157
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/ CURRENT FILING DATE: 2003-10-22
/ PRIOR APPLICATION NUMBER: 10/281,652
/ PRIOR FILING DATE: 2002-10-28
/ PRIOR APPLICATION NUMBER: 09/641,803
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: 60/149,310
/ PRIOR FILING DATE: 1999-08-17
/ PRIOR APPLICATION NUMBER: 60/420,369
/ PRIOR FILING DATE: 2002-10-22
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 22
/ LENGTH: 18
/ TYPE: PRF
/ ORGANISM: artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic Peptides
US-10-691-157-22

Query Match
Best Local Similarity 44.4%; Score 36; DB 16; Length 18;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPF 12
DB 3 EMPFPKYPVEPF 14

RESULT 7
US-10-691-330-22
/ Sequence 22, Application US/10691330
/ Publication No. US20050042300A1
/ GENERAL INFORMATION:
/ APPLICANT: Boldogh, Istvan
/ APPLICANT: Stanton, G. John
/ APPLICANT: Georgiades, Jerzy A.
/ APPLICANT: Hughes, Thomas K., Jr.
/ APPLICANT: Krusel, Marian
/ TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
/ FILE REFERENCE: 265, 00390101
/ CURRENT APPLICATION NUMBER: US/10/691,330
/ CURRENT FILING DATE: 2003-10-22
/ PRIOR APPLICATION NUMBER: US 60/420,369
/ PRIOR FILING DATE: 2002-10-22
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 22
/ LENGTH: 18
/ TYPE: PRF
/ ORGANISM: artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic Peptides
US-10-691-330-22

Query Match
Best Local Similarity 44.4%; Score 36; DB 17; Length 18;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPF 12
DB 3 EMPFPKYPVEPF 14

RESULT 8
US-10-281-652-8
/ Sequence 8, Application US/10281652
/ Publication No. US20030091606A1
/ GENERAL INFORMATION:
/ APPLICANT: STANTON, G. John
/ APPLICANT: HUGHES, Thomas K.
/ APPLICANT: BOLDG, Istvan
/ TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
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;; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
;; FILE REFERENCE: 265.00220101
;; CURRENT APPLICATION NUMBER: US/10/281,652
;; CURRENT FILING DATE: 2002-10-28
;; PRIOR APPLICATION NUMBER: US/09/641,803
;; PRIOR FILING DATE: 2000-08-17
;; PRIOR APPLICATION NUMBER: 60/149,310
;; PRIOR FILING DATE: 1999-08-17
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 8
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
;; US-10-281-652-8

Query Match 42.0%; Score 34; DB 14; Length 15;
Best Local Similarity 70.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLPEVPFPF 14
| | | | |
Db 5 PKLKEVEFPF 14

RESULT 9
US-10-691-157-8
;; Sequence 8, Application US/10691157
;; Publication No. US2004026681A1
;; GENERAL INFORMATION:
;; APPLICANT: BOLDGOCH, Istvan
;; APPLICANT: STANTON, G. John
;; APPLICANT: GEORGIADIS, Jerzy
;; APPLICANT: HUGHES, Thomas
;; APPLICANT: KRUZEL, Marian
;; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
;; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
;; FILE REFERENCE: 265.0040101
;; CURRENT APPLICATION NUMBER: US/10/691,157
;; CURRENT FILING DATE: 2003-10-22
;; PRIOR APPLICATION NUMBER: 10/281,652
;; PRIOR FILING DATE: 2002-10-28
;; PRIOR APPLICATION NUMBER: 09/641,803
;; PRIOR FILING DATE: 2000-08-17
;; PRIOR APPLICATION NUMBER: 60/149,310
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/420,369
;; PRIOR FILING DATE: 2002-10-22
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 8
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: artificial
;; FEATURE:
;; OTHER INFORMATION: Synthetic Peptides
;; US-10-691-157-8

Query Match 42.0%; Score 34; DB 16; Length 15;
Best Local Similarity 70.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLPEVPFPF 14
| | | | |
Db 5 PKLKEVEFPF 14

RESULT 10
US-10-691-330-8
;; Sequence 8, Application US/10691330

;; Publication No. US20050042300A1
;; GENERAL INFORMATION:
;; APPLICANT: Boldgoch, Istvan
;; APPLICANT: Stanton, G. John
;; APPLICANT: Georgiades, Jerzy A.
;; APPLICANT: Hughes, Thomas K., Jr.
;; APPLICANT: Kruzel, Marian
;; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
;; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
;; FILE REFERENCE: 265.00390101
;; CURRENT APPLICATION NUMBER: US/10/691,330
;; CURRENT FILING DATE: 2003-10-22
;; PRIOR APPLICATION NUMBER: US 60/420,369
;; PRIOR FILING DATE: 2002-10-22
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 8
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: artificial
;; FEATURE:
;; OTHER INFORMATION: Synthetic Peptides
;; US-10-691-330-8

Query Match 42.0%; Score 34; DB 17; Length 15;
Best Local Similarity 70.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLPEVPFPF 14
| | | | |
Db 5 PKLKEVEFPF 14

RESULT 11
US-10-474-955-67
;; Sequence 67, Application US/10474955
;; Publication No. US20040241161A1
;; GENERAL INFORMATION:
;; APPLICANT: Drifhout, Jan W.
;; APPLICANT: Koning, Frits
;; APPLICANT: McAdam, Stephan N.
;; APPLICANT: Ludwig, Solli'd Magne
;; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
;; TITLE OF INVENTION: DQ BINDING PROLAMINE-DERIVED PEPTIDES
;; FILE REFERENCE: 2799/71244-PCT-US
;; CURRENT APPLICATION NUMBER: US/10/474,955
;; CURRENT FILING DATE: 2003-10-13
;; NUMBER OF SEQ ID NOS: 137
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 67
;; LENGTH: 18
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Peptide sequence in pool 57
;; NAME/KEY: MISC FEATURE
;; LOCATION: (7)-(8)
;; OTHER INFORMATION: "Y" on position 7 is P/S
;; US-10-474-955-67

Query Match 42.0%; Score 34; DB 16; Length 18;
Best Local Similarity 45.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMPVLPEVPFPF 13
| | | | |
Db 4 QQPYLQLQPPF 14

RESULT 12
US-10-706-391-63
;; Sequence 63, Application US/10706391

```
Publication No. US20040137482A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: WASHINGTON DENTAL SERVICE
APPLICANT: Eckert, Randal
APPLICANT: Qi, Fengxia
APPLICANT: Shi, Wenyuan
APPLICANT: Anderson, Maxwell H.
FILE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
FILE REFERENCE: 2101363-991600
CURRENT APPLICATION NUMBER: US/10/706,391
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 10/077,624
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 09/910,358
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.1
SEQ ID NO 63
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Design peptide
US-10-706-391-63
```

```
Query Match      39.5%; Score 32; DB 16; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 MPVLPVEPP 11
        |||||
DB      4 LPVLPVLP 11
```

```
RESULT 13
US-10-103-395-97
Sequence 97, Application US/10103395
Publication No. US20020160019A1
GENERAL INFORMATION:
APPLICANT: EPIMUNE, Inc.
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
FILE REFERENCE: 39963-20016.01
CURRENT APPLICATION NUMBER: US/10/103,395
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: US 09/009,953
PRIOR FILING DATE: 1998-01-21
PRIOR APPLICATION NUMBER: PCT/US98/01373
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: US 60/036,713
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 60/037,432
PRIOR FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 274
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-103-395-97
```

```
Query Match      39.5%; Score 32; DB 13; Length 15;
Best Local Similarity 41.7%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 LEMPVLVEPPFP 13
        ||:|:|
```

```
DB      2 LNPFSPIETVP 13
```

```
RESULT 14
US-10-103-395-111
Sequence 111, Application US/10103395
Publication No. US20020160019A1
GENERAL INFORMATION:
APPLICANT: EPIMUNE, Inc.
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
FILE REFERENCE: 39963-20016.01
CURRENT APPLICATION NUMBER: US/10/103,395
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: US 09/009,953
PRIOR FILING DATE: 1998-01-21
PRIOR APPLICATION NUMBER: PCT/US98/01373
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: US 60/036,713
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 60/037,432
PRIOR FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 274
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 111
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-103-395-111
```

```
Query Match      39.5%; Score 32; DB 13; Length 15;
Best Local Similarity 41.7%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 LEMPVLVEPPFP 13
        ||:|:|
DB      4 LNPFSPIETVP 15
```

```
RESULT 15
US-10-158-596A-10
Sequence 10, Application US/10158596A
Publication No. US20030068900A1
GENERAL INFORMATION:
APPLICANT: Belcher, Angela
APPLICANT: Flynn, Christine
TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLE NUCLEATION, SHAPE AND CRYSTAL
FILE REFERENCE: 119927-1052
CURRENT APPLICATION NUMBER: US/10/158,596A
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/296,013
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 12
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: peptide retrieved from phage biopanning
US-10-158-596A-10
```

```
Query Match      38.3%; Score 31; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 LPVTPPP 13
        ||:|:|
DB      5 LPVTPPP 11
```

```
RESULT 16
US-10-157-775B-10
; Sequence 10, Application US/10157775B
; Publication No. US20030073104A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M.
; APPLICANT: Lee, Seung-Muk
; TITLE OF INVENTION: NANOSCALING ORDERING OF HYBRID MATERIALS USING GENETICALLY ENGINE
; FILE REFERENCE: MESOSCALE VIRUS
; FILE REFERENCE: 11927-1051
; CURRENT APPLICATION NUMBER: US/10/157,775B
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/326,583
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide recognition sequence retrieved from phage biopanning
US-10-157-775B-10

Query Match
Best Local Similarity 38.3%; Score 31; DB 14; Length 12;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LPVPPFP 13
Db 5 LPMTFPF 11

RESULT 17
US-10-254-446A-10
; Sequence 10, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M.
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Escher
; APPLICANT: Lee, Seung-Muk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 11927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopat
US-10-254-446A-10

Query Match
Best Local Similarity 38.3%; Score 31; DB 14; Length 12;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LPVPPFP 13
Db 5 LPMTFPF 11

RESULT 18
US-10-155-883B-10
; Sequence 10, Application US/10155883B
; Publication No. US20030148380A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Belcher, Angela M.
; TITLE OF INVENTION: MOLECULAR RECOGNITION OF MATERIALS
; FILE REFERENCE: 11927-1049
; CURRENT APPLICATION NUMBER: US/10/155,883B
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/296,013
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide binding sequence retrieved from phage biopanning
US-10-155-883B-10

Query Match
Best Local Similarity 38.3%; Score 31; DB 14; Length 12;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LPVPPFP 13
Db 5 LPMTFPF 11

RESULT 19
US-10-080-608A-179
; Sequence 179, Application US/10080608A
; Publication No. US2003018956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Identified from M13 bacteriophage peptide display library.
US-10-080-608A-179

Query Match
Best Local Similarity 38.3%; Score 31; DB 14; Length 12;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LPVPPFP 13
Db 5 LPMTFPF 11

RESULT 20
US-10-370-685-88
; Sequence 88, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF-P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 88
```

LENGTH: 12
TYPE: PRT
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: binds to GAs

Query Match 38.3%; Score 31; DB 15; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LPVPP 13
|:|:|
DB 5 LPVPP 11

RESULT 21
US-10-788-992-15
Sequence 15, Application US/10788992
Publication No. US20040265958A1
GENERAL INFORMATION:

APPLICANT: Gilula, Norton B
Cravatt, Benjamin F
Lerner, Richard A

TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSER: The Scripps Research Institute
STREET: 10550 North Torrey Pines Road
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/788,992
FILING DATE: 26-Feb-2004
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/743,168
FILING DATE: 01-May-1998
APPLICATION NUMBER: US 08/489,535
FILING DATE: 12-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 485.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-10-788-992-15
Query Match 37.0%; Score 30; DB 16; Length 15;
Best Local Similarity 60.0%; Pred. No. 8.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 5 PVLPPPP 14
|:|:|:|
DB 5 PTVPPPP 12

RESULT 22
US-10-161-791-451
Sequence 451, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OULLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLES, Dana M.

TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996

ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 451:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-10-161-791-451
Query Match 37.0%; Score 30; DB 14; Length 16;
Best Local Similarity 57.1%; Pred. No. 9.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLPP 11
|:|:|:|
DB 6 PVLPP 12

RESULT 23
US-10-211-088-97
Sequence 97, Application US/10211088
Publication No. US20030104479A1
GENERAL INFORMATION:

APPLICANT: Bright, Gary R.
APPLICANT: Premkumar, D. David
APPLICANT: Chen, Yih-Tai

TITLE OF INVENTION: No. US20030104479A1 Fusion Proteins and Assays For Molecular B
FILE REFERENCE: 01-1022-US
CURRENT APPLICATION NUMBER: US/10/211,088
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/309,395
PRIOR FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 60/341,589
PRIOR FILING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 366
SOFTWARE: Patentin version 3.1
SEQ ID NO 97
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Binding domain
US-10-211-088-97

Query Match 37.0%; Score 30; DB 14; Length 17;
Best Local Similarity 62.5%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVLP 8
Db 7 DLELPLSP 14

RESULT 24
US-10-225-567A-1382
Sequence 1382, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 1382
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-1382

Query Match 37.0%; Score 30; DB 14; Length 18;
Best Local Similarity 41.7%; Pred. No. 1.1e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPF 12
Db 6 NLAKPTLPKTF 17

RESULT 25
US-10-433-709-6
Sequence 6, Application US/10433709
Publication No. US20050085422A1
GENERAL INFORMATION:
APPLICANT: Regen Therapeutics plc
APPLICANT: Georgiadis, Jerry A.
TITLE OF INVENTION: Peptides Derived from Colostretinun
FILE REFERENCE: NAT-14866
CURRENT APPLICATION NUMBER: US/10/433,709
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: GE0029777.0
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 6
TYPE: PRT
ORGANISM: Ovis aries
US-10-433-709-6

Query Match 35.8%; Score 29; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEPP 12
Db 1 PVEPP 5

RESULT 26
US-10-353-929-171
Sequence 171, Application US/10353929
Publication No. US20030175288A1
GENERAL INFORMATION:
APPLICANT: ITOH, Kyogo
TITLE OF INVENTION: Tumor antigen
FILE REFERENCE: GP01-1024
CURRENT APPLICATION NUMBER: US/10/353,929
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: JP P2000-231814
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 171
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Designed peptide based on the amino acid sequence of SEQ ID NO:5
US-10-353-929-171

Query Match 35.8%; Score 29; DB 14; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.5e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVEPP 13
Db 2 IPQPP 8

RESULT 27
US-10-185-050-56
Sequence 56, Application US/10185050
Publication No. US20030077577A1
GENERAL INFORMATION:
APPLICANT: Pirozqi, Gregorio
Kay, Brian K.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 233
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 28-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE

REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-185-050-56

Query Match 35.8%; Score 29; DB 14; Length 14;
Best Local Similarity 45.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 EMPVLPVEPP 13
| | | | |
| | | | |
Db 1 EYPPYPPPPYP 11

RESULT 28
US-10-161-791-202
; Sequence 202, Application US/10161791
; Publication No. US2003018683A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 202:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

US-10-161-791-202

Query Match 35.8%; Score 29; DB 14; Length 16;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLEMPVLP 8
| | | | |
| | | | |
Db 3 DPERPVLP 10

RESULT 29
US-10-161-791-406
; Sequence 406, Application US/10161791
; Publication No. US2003018683A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 406:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

US-10-161-791-406

Query Match 35.8%; Score 29; DB 14; Length 16;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEMPVLP 8
| | | | |
| | | | |
Db 4 LKLPVLP 10

RESULT 30
US-10-398-104-34
; Sequence 34, Application US/10398104

```
Publication No. US20040047880A1
GENERAL INFORMATION:
APPLICANT: De Bolle, Xavier Thomas
APPLICANT: Lelesson, Jean-Jacques
APPLICANT: Lobet, Yves
APPLICANT: Mertens, Pascal Yvon
APPLICANT: Poolman, Jan
APPLICANT: Voet, Pierre
TITLE OF INVENTION: COMPONENT FOR VACCINE
FILE REFERENCE: B45242
CURRENT APPLICATION NUMBER: US/10/398,104
CURRENT FILING DATE: 2003-01-04
PRIOR APPLICATION NUMBER: PCT/EP01/11409
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: GB 0024200.8
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 352
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-34

Query Match          34.6%; Score 28; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.5e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 PVEPPF 13
Db      3 PYDPPF 8

RESULT 31
US-09-572-404B-218
Sequence 218, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 218
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in Unknown at 11-20 and may interact with Sequen
US-09-572-404B-218

Query Match          34.6%; Score 28; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 MPVLPVEP 11
Db      2 LPVTPGEP 9

RESULT 32
US-09-572-404B-220
Sequence 220, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
```

```
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 220
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in Unknown at 10-19 and may interact with Sequen
US-09-572-404B-220

Query Match          34.6%; Score 28; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 MPVLPVEP 11
Db      2 LPVTPGEP 9

RESULT 33
US-09-572-404B-222
Sequence 222, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 222
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in Unknown at 14-23 and may interact with Sequen
US-09-572-404B-222

Query Match          34.6%; Score 28; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 MPVLPVEP 11
Db      2 LPVTPGEP 9

RESULT 34
US-10-200-708-513
Sequence 513, Application US/10200708
Publication No. US20030180314A1
GENERAL INFORMATION:
APPLICANT: Degroot, Anne S.
TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
FILE REFERENCE: 17999-001
CURRENT APPLICATION NUMBER: US/10/200,708
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/351,036
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 60/092,346
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/115,145
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: 60/130,677
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 513
```

```

; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-513

Query Match          34.6%; Score 28; DB 14; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLPEPPFP 13
   | : | : |
Db 2 PISPIETVP 10

RESULT 35
US-10-200-708-538
; Sequence 538, Application US/10200708
; Publication No. US200301080314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 538
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-538

Query Match          34.6%; Score 28; DB 14; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLPEPPFP 13
   | : | : |
Db 2 PISPIETVP 10

RESULT 36
US-10-654-601-2314
; Sequence 2314, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Kubo, Ralphan
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.006007
; CURRENT APPLICATION NUMBER: US/10/654,601
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
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; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2314
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV analog peptide
US-10-654-601-2314

Query Match          34.6%; Score 28; DB 17; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 LPVPEPPFV 15
   ||| : |||
Db 2 LPVDPPFV 10

RESULT 37
US-10-398-104-174
; Sequence 174, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Voel, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-174

Query Match          34.6%; Score 28; DB 15; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PVEPPFP 13
   | : | : |
Db 4 PYDPPF 9
```

```
RESULT 38
US-10-226-007-1252
; Sequence 1252, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1252
; LENGTH: 12
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1252

Query Match          34.6%; Score 28; DB 14; Length 12;
Best Local Similarity 41.7%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 DLEMPVLPVEPF 12
      ||:| | | |
Db      1 DLDTPPTDPPPY 12

RESULT 39
US-10-226-007-1253
; Sequence 1253, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1253
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1253

Query Match          34.6%; Score 28; DB 14; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 DLEMPVLPVEPF 12
      ||:| | | |
Db      1 DLDTPPTDPPPY 12

RESULT 40
US-10-226-007-1261
; Sequence 1261, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
```

```
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1261
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1261

Query Match          34.6%; Score 28; DB 14; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 DLEMPVLPVEPF 12
      ||:| | | |
Db      2 DLDTPPTDPPPY 13
```

Search completed: June 7, 2005, 23:31:37
Job time : 68.5 secs

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OM protein - protein search, using SW model

Run on: June 7, 2005, 22:56:36 ; Search time 13.9091 Seconds
(without alignments)
103.763 Million cell updates/sec

Title: US-10-691-157-5

Perfect score: 81
Sequence: 1 DLEMPVLVPEPPFV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	33.3	17	2	SS9481
2	25	30.9	11	2	I33098
3	25	30.9	15	2	B39109
4	24	29.6	15	2	PA0088
5	24	29.6	15	2	PS0455
6	24	29.6	17	2	G85956
7	23	28.4	16	2	PC4371
8	23	28.4	17	2	SI7274
9	22.5	27.8	17	2	SI7274
10	22	27.2	11	2	A55149
11	22	27.2	14	2	G33160
12	22	27.2	14	2	B56884
13	22	27.2	15	2	PA0060
14	22	27.2	16	2	E58503
15	22	27.2	16	2	A23892
16	22	27.2	18	2	S56715
17	22	27.2	18	2	S29166
18	21	25.9	9	2	S66419
19	21	25.9	15	2	PS0452
20	21	25.9	15	2	S20410
21	21	25.9	16	2	A20190
22	21	25.9	17	2	E23734
23	21	25.9	17	2	A49237
24	21	25.9	18	2	A28060
25	20	24.7	18	2	I78841
26	20	24.7	6	2	A61049
27	20	24.7	9	2	S66635
28	20	24.7	10	2	B59272
29	20	24.7	11	2	PA0028
30	20	24.7	11	2	PN0042

30	20	24.7	13	2	B47415	mannose-1-phosphat
31	20	24.7	13	2	S21152	tryptophyl11n-rela
32	20	24.7	14	2	H64008	hypothetical prote
33	20	24.7	15	2	PA0024	protein QA300050 -
34	20	24.7	16	1	A49761	locucapryrokinin -
35	20	24.7	16	2	A60551	leucocyte elastase
36	20	24.7	18	2	A42576	steroid receptor c
37	20	24.7	18	2	I52614	u-plasminogen acti
38	20	24.7	18	2	A28027	protein P2 - curle
39	20	24.7	18	2	A40760	basic fibroblast g
40	19	23.5	10	2	B61218	alpha-gliadin 6ha
41	19	23.5	11	2	PQ0231	beta-glucosidase (
42	19	23.5	13	2	A59387	VCAM-1 5'UTR bindi
43	19	23.5	13	2	A05174	tryptophyl11n-13 -
44	19	23.5	15	2	S29207	avenin gamma-4 - o
45	19	23.5	15	2	PA0026	protein QA300027 -
46	19	23.5	15	2	C61511	milk band B protei
47	19	23.5	15	2	A41436	alpha-macroglobuli
48	19	23.5	16	2	I40665	ILVFN leader pepti
49	19	23.5	16	2	T37075	hypothetical prote
50	19	23.5	16	2	A45454	ankyrin-binding gl
51	19	23.5	17	2	UQ2030	hypothetical 1.9K
52	19	23.5	17	2	I55612	thyroid hormone re
53	19	23.5	17	4	I51887	hypothetical BMSR1
54	19	23.5	18	2	S04229	N4-(beta-N-acetyl
55	19	23.5	18	2	PN0149	beta-Gliadine 13 -
56	19	23.5	18	2	A60915	enkephalin-degrad
57	19	23.5	18	2	A54651	insulin-like growt
58	19	23.5	18	2	I51427	hemoglobin alpha c
59	19	23.5	9	2	I51317	bHtH transcription
60	18	22.2	6	2	A60356	118K stomach cance
61	18	22.2	9	2	S26508	collagen alpha 2(V
62	18	22.2	10	2	SI8396	probable glucose-6
63	18	22.2	10	2	B33710	ornithine decarbox
64	18	22.2	11	2	A54348	N-acetylglucosamin
65	18	22.2	11	2	S21727	gamma-Interferon-1
66	18	22.2	12	2	S67528	napin - rape (frag
67	18	22.2	12	2	S70344	amine oxidase (cop
68	18	22.2	14	2	S21247	H+-transporting tw
69	18	22.2	14	2	PL0152	metal-binding prot
70	18	22.2	14	2	A60158	disaggregatase - M
71	18	22.2	15	2	PA0071	superoxide dismuta
72	18	22.2	15	2	A56963	acid phosphatase (
73	18	22.2	16	2	C45133	casein kinase II (
74	18	22.2	16	2	PA0048	protein QA100047 -
75	18	22.2	16	2	B23692	transcription fact
76	18	22.2	17	2	I49593	cystic fibrosis tr
77	18	22.2	17	2	I84733	gene CTRP protein
78	18	22.2	18	2	S29264	ovomemerythrin - d
79	18	22.2	18	2	S09722	2S albumin small c
80	18	22.2	18	2	S09723	T-cell receptor de
81	18	22.2	18	2	I46653	serine proteinase
82	18	22.2	18	2	S71592	caseinoglycin, car
83	18	22.2	18	2	A39040	ubiquitin-carrier
84	18	22.2	15	2	A54397	catch-relaxing pep
85	17.5	21.6	8	2	ECMWCR	hypothetical prote
86	17	21.0	8	2	SI6324	enamelin f - bovin
87	17	21.0	8	2	SI0783	spasmogenic toxin
88	17	21.0	8	2	A46306	coat protein beta
89	17	21.0	9	2	SI3636	locustamotopropin I
90	17	21.0	9	2	A61620	translation elonga
91	17	21.0	9	2	PC7074	angiotensin I - Ja
92	17	21.0	10	2	A60624	angiotensin precu
93	17	21.0	10	2	A90917	angiotensin precu
94	17	21.0	10	2	A90345	angiotensin precu
95	17	21.0	11	1	XAVIBH	bradykinin-potent
96	17	21.0	11	2	PC2254	Cytochrome P450 3A
97	17	21.0	11	2	S07207	Critia-angiotensin
98	17	21.0	12	2	C36201	1-aminocyclopropan
99	17	21.0	12	2	S01749	collagen alpha 1(I
100	17	21.0	12	2	B45691	probable minor cap

ALIGNMENTS

RESULT 1

SS9481
hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)
C/Species: Phaseolus vulgaris (kidney bean)
C/Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C/Accession: SS9481
R/Mojtaszek, P.; Trethowan, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A/Title: Specificity in the immobilisation of cell wall proteins in response to different
A/Reference number: SS9481; MUID:96011753; PMID:754825
A/Accession: SS9481

A/Molecule type: protein
A/Residues: 1-17 <MO>

A/Cross-references: UNIPROT:Q7M113
C/Keywords: glycoprotein; hydroxyproline
F/6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match

Best Local Similarity 33.3%; Score 27; DB 2; Length 17;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 1 DLEMPVLPEPPPEPV 15
| : | | | | |
DB 1 DMTLP--PVPPEPV 13

RESULT 2

I33098
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C/Species: Plasmodium falciparum
C/Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C/Accession: I33098
R/Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A/Reference number: A33098
A/Accession: I33098
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-11 <NIC>

Query Match

Best Local Similarity 30.9%; Score 25; DB 2; Length 11;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EMPVLPPV 9
| : | : | : | : |
DB 5 ELPLPPI 11

RESULT 3

B39109
hypothetical 1.5K protein - hepatitis C virus
N/Alternate names: hypothetical protein 2
C/Species: hepatitis C virus
C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C/Accession: B39109; JQ1585
R/Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A/Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A/Reference number: A39109; MUID:91156678; PMID:1705704
A/Accession: B39109

A/Status: not compared with conceptual translation
A/Molecule type: mRNA

A/Residues: 1-15 <HAN>

A/Cross-references: GB:M58406

R/Kumar, U.; Cheng, D.; Thomas, H.; Nonjardino, J.

J. Gen. Virol. 73, 1521-1525, 1992

A/Title: Cloning and sequencing of the structural region and expression of putative core
A/Reference number: JQ1584; MUID:92300349; PMID:1318944

A/Accession: JQ1585

A/Molecule type: genomic RNA
A/Residues: 1-15 <KUM>
A/Experimental source: strain U.K.

Query Match

Best Local Similarity 30.9%; Score 25; DB 2; Length 15;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVLPEVP 11
| : | : | : | : |
DB 9 PPLPEVP 15

RESULT 4

PA0088
protein QP200051 - fungus (Fusarium sporotrichioides) (fragment)
C/Species: Fusarium sporotrichioides
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C/Accession: PA0088
R/Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A/Reference number: PA0051
A/Accession: PA0088
A/Molecule type: protein
A/Residues: 1-15 <CHO>

Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 15;
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 EMPVLPEPPPEPV 13
| : | : | : | : |
DB 1 QKPDIPXDYP 11

RESULT 5

PS0455
superoxide dismutase (EC 1.15.1.1) (Mn) - rice (strain Nihonbare) (fragment)
C/Species: Oryza sativa (rice)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C/Accession: PS0455
R/Tsugita, A.
submitted to JIPID, April 1993
A/Reference number: PS0206
A/Accession: PS0455
A/Molecule type: protein
A/Residues: 1-15 <TSU>
A/Cross-references: UNIPROT:Q7M105
A/Experimental source: germ
C/Function:
A/Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C/Keywords: metalloprotein; oxidoreductase

Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 15;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 MPVLPEV 10
| : | : | : | : |
DB 6 LPLPEVD 12

RESULT 6

G85956
hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain EDL
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: G85956
R/Berna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
Miller, L.; Grobcock, E.O.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: G85956
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-17 <SR>
 A:Cross-references: UNIPROT:Q6X444; GB:AE005174; MID:912517539; PIDN:AAG58115.1; GSPDB:G
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: 24331

Query Match 29.6%; Score 24; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 8.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 VEPFP 13
 |||||
 DB 4 VSPFP 8

RESULT 7
 PC4371
 telomeric and tetraplex DNA binding protein qTBP42 I - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
 C:Accession: PC4371
 R:Sarig, G.; Weisman-Shomer, P.; Fry, M.
 Biochem. Biophys. Res. Commun. 237, 617-623, 1997
 A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CP
 A:Reference number: PC4371; MUID:97445086; PMID:9299414
 A:Accession: PC4371
 A:Molecule type: protein
 A:Residues: 1-16 <SR>
 C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 28.4%; Score 23; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEP 11
 |||||
 DB 5 PVEP 8

RESULT 8
 S17274
 ribosomal protein YmlJ5, mitochondrial, questionable - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 A:Variety: strain 07173
 C:Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
 C:Accession: S17274
 R:Grothman, L.; Graack, H.R.; Kruff, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.
 FEBS Lett. 284, 51-56, 1991
 A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from
 A:Reference number: S17255; MUID:91285106; PMID:2060626
 A:Accession: S17274
 A:Molecule type: protein
 A:Residues: 1-17 <SR>
 A:Cross-references: UNIPROT:P36530
 C:Comment: A coding region for this protein could not be identified in the genome of Sac
 C:Genetics:
 A:Genome: nuclear
 C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 27.8%; Score 22.5; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 7 LPVP-PPV 15
 |||||
 DB 8 LPVPVPPV 17

RESULT 9

A55149
 tetracenomycin A2 oxygenase (EC 1.-.-.-) - Streptomyces glaucescens (fragment)
 N:Alternate names: tcmA2 oxygenase; tcmA
 C:Species: Streptomyces glaucescens
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C:Accession: A55149
 R:Shen, B.; Hutchinson, C.R.
 J. Biol. Chem. 269, 30726-30733, 1994
 A:Title: Triple hydroxylation of tetracenomycin A2 to tetracenomycin C in Streptomyces

A2 oxygenase.
 A:Reference number: A55149; MUID:95074090; PMID:7982994
 A:Accession: A55149
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <SR>
 A:Cross-references: UNIPROT:Q7MOK6
 C:Genetics:
 A:Start codon: TTG
 C:Keywords: antibiotic biosynthesis; FAD; monomer; oxidoreductase

Query Match 27.2%; Score 22; DB 2; Length 11;
 Best Local Similarity 71.4%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EMPVLV 9
 |||||
 DB 5 EVPLV 11

RESULT 10
 G33160
 H+-transporting two-sector ATPase (EC 3.6.3.14) 9K chain - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 03-Jun-2002
 C:Accession: G33160
 R:Godinot, C.
 submitted to the Protein Sequence Database, February 1991
 A:Reference number: A33160
 A:Accession: G33160
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <GOD>
 C:Keywords: hydrolase

Query Match 27.2%; Score 22; DB 2; Length 14;
 Best Local Similarity 40.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 VLPVPPPV 15
 |||||
 DB 1 VAPVQVSP 10

RESULT 11
 B56884
 Pax-QNR, long form - quail (fragment)
 C:Species: Coturnix coturnix (quail)
 C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
 C:Accession: B56884
 R:Dozier, C.; Carriere, C.; Grevin, D.; Martin, P.; Quatmanns, B.; Stehelin, D.; Saule,
 Cell Growth Differ. 4, 281-289, 1993
 A:Title: Structure and DNA-binding properties of Pax-QNR, a paired box- and homeobox-con
 A:Reference number: A56884; MUID:93264300; PMID:8096617
 A:Accession: B56884
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-14 <DOZ>
 A:Cross-references: UNIPROT:007378; GB:X68169; MID:9311558; PIDN:CAA48271.1; PID:9311559

A:Experimental source: neuroretina cells
 C:Keywords: alternative splicing; retina

Query Match 27.2%; Score 22; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PVLPEPP 12
| | | |
1 PTPVSSR 8

DB

RESULT 12

PA0060
protein QF200037 - fungus (Fusarium sporotrichioides) (fragment)

C/Species: Fusarium sporotrichioides

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C/Accession: PA0060

R/Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

Submitted to JPLD, October 1994

A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi

A/Reference number: PA0051

A/Accession: PA0060

A/Molecule type: protein

A/Residues: 1-15 <CHO>

Query Match 27.2%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 PVEPP 13
| | | |
1 PLRPLP 6

DB

RESULT 13

ES5503
superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)

N/Alternate names: 21.3K bladder and kidney stone protein

C/Species: unidentified bacterium

C/Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004

C/Accession: ES5503

R/Binette, J.P.; Binette, M.B.

Submitted to the Protein Sequence Database, October 1996

A/Description: The proteins of kidney and gallbladder stones.

A/Reference number: AS5501

A/Accession: ES5503

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-16 <BIN>

A/Cross-references: UNIPROT:Q7M137

A/Experimental source: human bladder and kidney stones

C/Function: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C/Keywords: metalloprotein; oxidoreductase

Query Match 27.2%; Score 22; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.7e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MPVLPVE 10
| | | |
5 LPPLPYE 11

DB

RESULT 14

A23992
melanin-omochrome-stimulating hormone III - silkworm (fragment)

N/Alternate names: melanization and reddish coloration hormone III, MRCH III

C/Species: Bombyx mori (silkworm)

C/Date: 30-Jan-1988 #sequence_revision 30-Jan-1988 #text_change 09-Jul-2004

C/Accession: A23992

R/Matsumoto, S.; Isogai, A.; Suzuki, A.

FEBS Lett. 189, 115-118, 1985

A/Title: N-terminal amino acid sequence of an insect neurohormone, melanization and red

A/Reference number: A23992; MUID:85285612; PMID:3896851

A/Accession: A23992

A/Molecule type: protein

A/Residues: 1-16 <MAT>
A/Cross-references: UNIPROT:Q17211
C/Keywords: hormone

Query Match 27.2%; Score 22; DB 2; Length 16;
Best Local Similarity 37.5%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMPVLPVE 10
| | | |
5 DMPATPAD 12

DB

RESULT 15

hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) (clone hmg3.2) - potato (frag

C/Species: Solanum tuberosum (potato)

C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S56715

R/Bhattacharya, M.K.; Palva, N.L.; Dixon, R.A.; Korth, K.L.; Stermer, B.A.

Plant Mol. Biol. 28, 1-15, 1995

A/Title: Features of the hmg 1 subfamily of genes encoding HMG-CoA reductase in potato.

A/Reference number: S56710; MUID:95306778; PMID:7787174

A/Accession: S56715

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-18 <BHA>

A/Cross-references: UNIPROT:Q41458; EMBL:U34830; NID:9529524; PIDN:AAC37437.1; PID:95531

C/Suprafamily: hydroxymethylglutaryl-CoA reductase (NADPH)

C/Keywords: coenzyme A; oxidoreductase

Query Match 27.2%; Score 22; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVLPEPP 11
| | | |
7 PVKPLYP 13

DB

RESULT 16

S29166
quinoline oxidoreductase (EC 1.5.99.-) beta chain - Arthrobacter sp. (isolate Rue 61a)

C/Species: Arthrobacter sp.

A/Variety: isolate Rue 61a

C/Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C/Accession: S29166

R/de Beyer, A.; Lingens, F.

Biol. Chem. Hoppe-Seyler 374, 101-110, 1993

A/Title: Microbial metabolism of quinoline and related compounds. XVI. Quinoline oxidoreductase.

A/Reference number: S29165; MUID:93228843; PMID:8471177

A/Accession: S29166

A/Molecule type: protein

A/Residues: 1-18 <BEY>

A/Experimental source: isolate Rue 61a

C/Complex: heterohexamer; two alpha, two beta and two gamma chains

C/Function: catalyzes the oxidation of quinoline to 1H-4-oxoquinoline

A/Pathway: quinoline degradation

C/Keywords: FAD; flavoprotein; heterohexamer; molybdopterin; oxidoreductase

Query Match 27.2%; Score 22; DB 2; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 VEPPPV 15
| | | |
2 MHPFOFI 8

DB

RESULT 17

S6419

5

tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C:Accession: S66419
R:Kuwabara, T.
FEBS Lett. 371, 195-198, 1995
A:Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of spinacia oleracea
A:Reference number: S66419; PMID:95402209; PMID:7672127
A:Accession: S66419
A:Molecule type: protein
A:Residues: 1-9 <KDW>
A:Cross-references: UNIPROT:Q9T2K8; UNIPROT:Q41388

Query Match 25.9%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLTP 8
DB 2 PVLTP 5

RESULT 18
PS0452
32K protein 3306 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C:Accession: PS0452
R:Tangita, A.; Miyake, N.
submitted to JIPID, April 1993
A:Reference number: PS0208
A:Accession: PS0452
A:Molecule type: protein
A:Residues: 1-15 <TGS>
A:Experimental source: bran, strain Nihonbare
C:Comment: molecular weight 32K, pI 5.3.

Query Match 25.9%; Score 21; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 PPFPV 15
DB 6 PPFPV 10

RESULT 19
S20410
protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)
N:Alternate names: LHCI protein kinase
C:Species: chloroplast Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: S20410
R:Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.
FEBS Lett. 298, 33-35, 1992
A:Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cytochrome b6/f complex
A:Reference number: S20410; PMID:92183823; PMID:1544419
A:Accession: S20410
A:Molecule type: protein
A:Residues: 1-15 <GAL>
A:Cross-references: UNIPROT:Q9T2K8
C:Genetics:
A:Genome: chloroplast
C:Function:
A:Description: is responsible for the regulation of energy distribution between photosystems II and I
A>Note: does not exhibit redox-controlled activation
C:Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphotransferase

Query Match 25.9%; Score 21; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLTP 8

DB 2 PVLTP 5

RESULT 20
A20190
hypodermis B - early cattle grub (fragment)
C:Species: Hypoderma lineatum (early cattle grub)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C:Accession: A20190
R:Leclercq, A.; Tong, N.T.; Keil, B.
Eur. J. Biochem. 134, 261-267, 1983
A:Title: Hypodermis B, a trypsin-related enzyme from the insect Hypoderma lineatum.
A:Reference number: A20190; PMID:83261874; PMID:6307690
A:Accession: A20190
A:Molecule type: protein
A:Residues: 1-16 <LEC>
A:Cross-references: UNIPROT:P35588

Query Match 25.9%; Score 21; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 VBPPP 14
DB 9 IEDFPW 14

RESULT 21
E23734
insulin-like growth factor-binding protein 3 - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: E23734
R:Shimazaki, S.; Gao, L.; Shimomura, M.; Ling, N.
Mol. Endocrinol. 5, 938-948, 1991
A:Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-3
A:Reference number: A23734; PMID:92049376; PMID:1719383
A:Accession: E23734
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <SHI>

Query Match 25.9%; Score 21; DB 2; Length 17;
Best Local Similarity 57.1%; Pred. No. 2.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVLTPV 11
DB 9 PVLTPV 11

RESULT 22
A49237
45/47K antigen - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A49237
R:Romanin, F.; Laqueyrie, A.; Miltzer, P.; Pescher, P.; Chavaret, P.; Lagranderie, M.; Infect. Immun. 61, 742-750, 1993
A:Title: Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen complex, a major component of the cell wall
A:Reference number: A49237; PMID:93138802; PMID:8423100
A:Accession: A49237
A:Contents: BCG
A:Accession: A49237
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <ROM>
A:Cross-references: UNIPROT:P80069
A>Note: sequence extracted from NCBI backbone (NCBI:123246)

Query Match 25.9%; Score 21; DB 2; Length 17;
Best Local Similarity 57.1%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLPEP 11
 DB 4 PAPVPP 10

RESULT 23

A28060
 elastase inhibitor, leukocyte - horse (fragment)
 C/Species: Equus caballus (domestic horse)
 C/Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004
 C/Accession: A28060
 R/Porempa, J.; Dubin, A.; Marorek, W.; Travis, J.
 J.Biol. Chem. 263, 7364-7369, 1988
 A/Title: An elastase inhibitor from equine leukocyte cytosol belongs to the serpin super
 A/Reference number: A28060; MUID:88213423; PMID:3366785
 A/Accession: A28060
 A/Molecule type: protein
 A/Residues: 1-18 <POT>
 A/Cross-references: UNIPROT:P05619
 C/Superfamily: Serpin

Query Match 25.9%; Score 21; DB 2; Length 18;
 Best Local Similarity 35.7%; Pred. No. 2.8e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 4; Gaps 1;

QY 6 VLPEPP---PPV 15
 DB 4 LMPENFNADHPPI 17

RESULT 24

I78841
 thrombopoietin receptor - mouse (fragment)
 C/Species: Mus sp. (mouse)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C/Accession: I78841
 R/Alexander, W.S.; Dunn, A.R.
 Oncogene 10, 795-803, 1995
 A/Title: Structure and transcription of the genomic locus encoding murine c-Mpl, a recep
 A/Reference number: I58350; MUID:9516571; PMID:7862460
 A/Accession: I78841
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-18 <RBS>
 A/Cross-references: GB:S76842; NID:9912990; PIRN:AA833462.1; PID:9912991
 C/Genetics:
 A/Gene: c-mpl

Query Match 25.9%; Score 21; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 2.8e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 PVEPPFPV 15
 DB 2 PHGPAPV 9

RESULT 25

A61049
 halo-toxin - Pseudomonas syringae pv. mori
 C/Species: Pseudomonas syringae pv. mori
 A/Note: host mulberry tree
 C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
 C/Accession: A61049
 R/Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.;
 Chem. Lett. 00, 679-680, 1989
 A/Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri
 A/Reference number: A61049
 A/Accession: A61049
 A/Molecule type: protein
 A/Residues: 1-6 <KAJ>
 A/Note: sequence confirmed by synthesis

C/Comment: This toxin is one of the etiological agents of halo bright disease in mulberry
 C/Keywords: toxin

Query Match 24.7%; Score 20; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFP 13
 DB 1 PFP 3

RESULT 26

S6635
 alpha-2-macroglobulin isoform 1 - bovine (fragment)
 C/Species: Bos primigenius indicus (zebu cattle)
 C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S6635
 R/Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sotru
 FEBS Lett. 372, 93-95, 1995
 A/Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain o
 A/Reference number: S6634; MUID:96032553; PMID:7556651
 A/Accession: S6635
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-9 <DOL>
 A/Cross-references: UNIPROT:Q7M2N8

Query Match 24.7%; Score 20; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 EPFP 14
 DB 2 DEFP 6

RESULT 27

B59272
 peptide-N-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain -
 N/Alternate names: peptide N-glycosidase
 C/Species: Prunus dulcis var. baccata (sweet almond)
 C/Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
 C/Accession: B59272
 R/Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
 Eur. J. Biochem. 252, 118-123, 1998
 A/Title: Characterisation of peptide-N-(N-acetyl-beta-glucosaminyl)asparagine amidase
 A/Reference number: B59272; MUID:98181894; PMID:9523720
 A/Accession: B59272
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-10 <ALT>
 A/Cross-references: UNIPROT:P81898
 C/Keywords: hydrolase

Query Match 24.7%; Score 20; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 PVEPP 13
 DB 4 PLHDFP 9

RESULT 28

PA0028
 protein QA300042 - Arabidopsis thaliana (fragment)
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C/Accession: PA0028
 R/Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPD, July 1994
 A/Description: Separation and characterization of Arabidopsis proteins by two-dimension

A:Reference number: PA0001
A:Accession: PA0028
A:Molecule type: protein
A:Residues: 1-11 <KAM>
A:Experimental source: seed
C:Keywords: seed

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFP 13
DB 6 PFP 8

RESULT 29

PN0042
stathmin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 09-Jul-2004
C:Accession: PN0042

R/Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neur
A:Reference number: PN0041
A:Accession: PN0042

A:Molecule type: protein
A:Residues: 1-11 <KAT>
C:Species: Mus musculus (house mouse)
A:Experimental source: neuroblastoma cell
C:Comment: The molecular mass is 17,500 and the pI is 5.63. The amino-terminus is blocke
C:Keywords: brain

Query Match
Best Local Similarity 37.5%; Score 20; DB 2; Length 11;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 MPVLPVFP 11
DB 3 VPDPFPLSP 10

RESULT 30

B47415
mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 43K alpha chain - pig (fragment)
N:Alternate names: GDP-mannose pyrophosphorylase 43K alpha chain
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 25-Feb-1994 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C:Accession: B47415

R:Szumllo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.
J. Biol. Chem. 268, 17943-17950, 1993
A:Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and uct
A:Reference number: A47415; MUID:93352609; PMID:7688733
A:Accession: B47415

A:Molecule type: protein
A:Residues: 1-13 <SZU>
A:Experimental source: liver
C:Complex: The enzyme appears to be a heterodimer of alpha and beta chains.
C:Function:
A:Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP
A>Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ac
C:Keywords: blocked amino end, nucleotidyltransferase

Query Match
Best Local Similarity 60.0%; Score 20; DB 2; Length 13;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 PFPV 15
DB 8 PFPPL 12

RESULT 31

S21152
tryptophyllin-related peptide - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C:Accession: S21152

R:Mignogna, G.; Severini, C.; Simeone, M.; Negri, L.; Falconieri Brzjaner, G.; Kreil, G
FEBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of ti
A:Reference number: S21152; MUID:92339502; PMID:1633846
A:Accession: S21152

A:Molecule type: protein
A:Residues: 1-13 <MIG>
A:Cross-references: UNIPROT:Q7LZ51
A:Experimental source: skin

Query Match
Best Local Similarity 60.0%; Score 20; DB 2; Length 13;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PVPVFP 9
DB 9 PVPVFP 13

RESULT 32

H64008
hypothetical protein H10492 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998
C:Accession: H64008

R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, .
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.; Glodek, A.; Kelley, J.M.; Weidman, .
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95506530; PMID:7542800
A:Accession: H64008

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-14 <TIGR>
A:Cross-references: GB:U32731; GB:I42023; NID:G1573465; PID:G1573478; TIGR:H10492

Query Match
Best Local Similarity 42.9%; Score 20; DB 2; Length 14;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVPVFP 11
DB 6 PVPVFP 12

RESULT 33

PA0024
protein QA300050 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0024

R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimension
A:Reference number: PA0001
A:Accession: PA0024

A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Experimental source: seed

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 15;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFP 13

Db 6 PFP 8

RESULT 34

A49761

locustapyrokinin - migratory locust

C:Species: locusta migratoria (migratory locust)

C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004

C/Accession: A49761

R:Schroff, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.

Gen. Comp. Endocrinol. 81, 97-104, 1991

A:Title: Isolation, primary structure, and synthesis of locustapyrokinin: a myotropic peptide

A:Reference number: A49761; PMID:91224474; PMID:2026322

A:Accession: A49761

A:Molecule type: protein

A:Residues: 1-16 <SCH>

A:Cross-references: UNIPROT:P20404

C:Comment: This neuropeptide stimulates contractions in an isolated cockroach hindgut as

C:Superfamily: pyrokinin

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental

F:16/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 24.7%; Score 20; DB 1; Length 16;

Best Local Similarity 60.0%; Pred. No. 3.5e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PVPF 12

Db 8 PQPF 12

RESULT 35

A60551

leukocyte elastase (EC 3.4.21.37) - dog (fragment)

C:Species: Canis lupus familiaris (dog)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C/Accession: A60551

R:Axelsson, L.; Bergenfeldt, M.; Björk, P.; Olsson, R.; Ohlsson, K.

Scand. J. Clin. Lab. Invest. 50, 35-42, 1990

A:Title: Release of immunoreactive canine leukocyte elastase normally and in endotoxin A

A:Reference number: A60551; PMID:90193608; PMID:1690443

A:Accession: A60551

A:Molecule type: protein

A:Residues: 1-16 <AXB>

A:Cross-references: UNIPROT:Q8MJD1

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; leukocyte; lysosome; serine proteinase

Query Match 24.7%; Score 20; DB 2; Length 16;

Best Local Similarity 40.0%; Pred. No. 3.5e+03;

Matches 4; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 8 PVPF--PPVF 15

Db 6 PQPF 15

RESULT 36

A42576

steroid receptor complex Hsp56 60K component - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998

C/Accession: A42576

R:Yam, A.W.; Tomaselli, A.G.; Heinrichson, R.L.; Zurcher-Neely, H.; Ruff, V.A.; Johnson,

J. Biol. Chem. 267, 2868-2871, 1992

A:Title: The Hsp56 component of steroid receptor complexes binds to immobilized FK506 an

A:Reference number: A42576; PMID:92147620; PMID:1371107

A:Accession: A42576

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <YEM>

A:Experimental source: thymus
A>Note: sequence extracted from NCBI backbone (NCBI:80696)
C:Superfamily: human FK506-binding protein FKBP51; BKB-type peptidylprolyl isomerase ho
C:Keywords: steroid hormone receptor

Query Match 24.7%; Score 20; DB 2; Length 18;

Best Local Similarity 55.6%; Pred. No. 4e+03;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 VLPVPPFP 14

Db 9 VEPVBLFF 17

RESULT 37

I52614

u-plasminogen activator receptor precursor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004

C/Accession: I52614

R:Scoravja, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.

Blood 86, 624-635, 1995

A:Title: A conserved RXR- α less proximal promoter drives basal transcription from the uro

A:Reference number: I52614; PMID:95329719; PMID:7605992

A:Accession: I52614

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-18 <RES>

A:Cross-references: UNIPROT:Q03405; GB:S78532; NID:g999207; PIDN:AAD14289.1; PID:g42619f

A:Gene: uPAR

C:Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 24.7%; Score 20; DB 2; Length 18;

Best Local Similarity 60.0%; Pred. No. 4e+03;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLVP 9

Db 5 PLVPL 9

RESULT 38

A28027

protein P2 - curled-leaved tobacco (fragment)

C:Species: Nicotiana glauca (curled-leaved tobacco)

C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993

C/Accession: A28027

R:Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.

Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987

A:Title: Alterations in the phenotype of plant cells studied by NH₂-terminal amino acid

A:Reference number: A94167

A:Accession: A28027

A:Molecule type: protein

A:Residues: 1-18 <BAU>

A>Note: 14-Arg was also found

Query Match 24.7%; Score 20; DB 2; Length 18;

Best Local Similarity 33.3%; Pred. No. 4e+03;

Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 VLPVFP 11

Db 8 VLPVFP 13

RESULT 39

A40760

basic fibroblast growth factor, long form - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 09-Jul-2004

C/Accession: A40760

R:Nice, E.C.; Fabri, L.; Whitehead, R.H.; James, R.; Simpson, R.J.; Burgess, A.W.

J. Biol. Chem. 266, 14425-14430, 1991
A:Title: The major colonic cell mitogen extractable from colonic mucosa is an N terminal
A:Reference number: A40760; MID:91317799; PMID:1860849
A:Accession: A40760
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <NTC>
A:Cross-references: UNIPROT:Q7M2P3

Query Match 24.7%; Score 20; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 MPVLP 8
: |||
Db 14 LPALP 18

RESULT 40

B61218
alpha-glucanase - grass (Haynaldia villosa) (fragment)
C:Species: Haynaldia villosa, Daespyrum villosum
C:Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C:Accession: B61218
R:Shewry, P.R.; Sabelki, P.A.; Parmar, S.; Lafandra, D.
Biochem. Genet. 29, 207-211, 1991
A:Title: alpha-type prolamin are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia
A:Reference number: A61218; MID:91315394; PMID:1859356
A:Accession: B61218
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SHE>
A:Cross-references: UNIPROT:Q7M1F6
C:Keywords: seed; storage protein

Query Match 23.5%; Score 19; DB 2; Length 10;
Best Local Similarity 30.0%; Pred. No. 3e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMPTLPVPEP 11
: |||::|
Db 1 VRVPVQLQP 10

Search completed: June 7, 2005, 23:20:40
Job time : 14.9091 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 66 Seconds
(without alignments)
116.382 Million cell updates/sec

Title: US-10-691-157-5

Perfect score: 81
Sequence: 1 DLEMPYLVEPPFPV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1613378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	33.3	17	Q7MI13	Q7MI13 phaseolus v
2	27	33.3	18	Q9NSFO	Q9NSFO homo sapien
3	26	32.1	8	Q9TRX8	Q9TRX8 bos taurus
4	26	32.1	18	Q56610	Q56610 vibrio chol
5	25	30.9	9	Q9PEB5	Q9PEB5 kluyveromyc
6	25	30.9	12	Q83139	Q83139 barley stri
7	25	30.9	15	UC17_MAIZE	P80623 zea mays (m
8	24	29.6	8	NGIF_RAT	P82598 rattus norv
9	24	29.6	15	Q7MIU5	Q7MIU5 oryza sativ
10	24	29.6	16	Q64KC0	Q64KC0 sporophylla
11	24	29.6	17	Q9TRH5	Q9TRH5 bos taurus
12	24	29.6	17	Q8X4A4	Q8X4A4 escherichia
13	23	28.4	12	TM2A_METMA	P80652 methanosarc
14	23	28.4	13	SODM_ARTDA	P83389 arthrobostry
15	23	28.4	13	Q6GCD7	Q6GCD7 pleospora t
16	23	28.4	15	SODM_ENTAB	P22799 enterobacte
17	23	28.4	15	Q69EFJ3	Q69EFJ3 stemphylium
18	23	28.4	15	Q69EFJ3	Q69EFJ3 stemphylium
19	23	28.4	15	Q69GAL1	Q69GAL1 stemphylium
20	23	28.4	15	Q69GB9	Q69GB9 pleospora g
21	23	28.4	15	Q69GDB1	Q69GDB1 stemphylium
22	23	28.4	15	Q9TRQ1	Q9TRQ1 mus sp. bet
23	23	28.4	15	Q64KG2	Q64KG2 sporophylla
24	23	28.4	16	Q69G98	Q69G98 pleospora s
25	23	28.4	16	Q69GB3	Q69GB3 pleospora t
26	23	28.4	16	Q69GB3	Q69GB3 pleospora t
27	23	28.4	16	Q69GC2	Q69GC2 pleospora s
28	23	28.4	16	Q69GC5	Q69GC5 stemphylium
29	23	28.4	16	Q69GC8	Q69GC8 stemphylium
30	23	28.4	16	Q69GDB4	Q69GDB4 pleospora g
31	23	28.4	16	Q64KB4	Q64KB4 volatinia j

32	23	28.4	16	Q64KB8	Q64KB8 sporophylla
33	23	28.4	16	Q64KC6	Q64KC6 sporophylla
34	23	28.4	16	Q64KD0	Q64KD0 sporophylla
35	23	28.4	16	Q64KD2	Q64KD2 sporophylla
36	23	28.4	16	Q64KD8	Q64KD8 sporophylla
37	23	28.4	16	Q64KE0	Q64KE0 sporophylla
38	23	28.4	16	Q64KE2	Q64KE2 sporophylla
39	23	28.4	16	Q64KE4	Q64KE4 sporophylla
40	23	28.4	16	Q64KE8	Q64KE8 sporophylla
41	23	28.4	16	Q64KE2	Q64KE2 sporophylla
42	23	28.4	16	Q64KE6	Q64KE6 sporophylla
43	23	28.4	16	Q64KE8	Q64KE8 sporophylla
44	23	28.4	16	Q64KG0	Q64KG0 sporophylla
45	23	28.4	16	Q64KG6	Q64KG6 sporophylla
46	23	28.4	16	Q64KH0	Q64KH0 sporophylla
47	23	28.4	16	Q64KH4	Q64KH4 sporophylla
48	23	28.4	16	Q64KH6	Q64KH6 sporophylla
49	23	28.4	17	Q69G6A4	Q69G6A4 pleospora s
50	23	28.4	17	Q69G6A7	Q69G6A7 pleospora p
51	23	28.4	17	Q69GB6	Q69GB6 stemphylium
52	23	28.4	17	Q9UC43	Q9UC43 homo sapien
53	23	28.4	17	Q80X06	Q80X06 mus sp. abd
54	23	28.4	18	Q9BRH2	Q9BRH2 homo sapien
55	23	28.4	18	Q8CJD4	Q8CJD4 rattus norv
56	22.5	27.8	11	Q48933	Q48933 mycobacteri
57	22.5	27.8	11	Q79C20	Q79C20 mycobacteri
58	22.5	27.8	11	Q79C22	Q79C22 mycobacteri
59	22.5	27.8	17	YX35_YEAST	P36530 saccharomyc
60	22	27.2	9	P83157	P83157 anabaena sp
61	22	27.2	10	Q6A3T8	Q6A3T8 archanglopt
62	22	27.2	10	Q9QVJ5	Q9QVJ5 rattus sp.
63	22	27.2	10	Q9QVJ6	Q9QVJ6 rattus sp.
64	22	27.2	11	Q7M0K6	Q7M0K6 streptomyce
65	22	27.2	12	P82441	P82441 nicotiana t
66	22	27.2	13	Q6GVJ5	Q6GVJ5 burkholderi
67	22	27.2	14	P82326	P82326 pisum sativ
68	22	27.2	14	Q07378	Q07378 coturnix co
69	22	27.2	15	Q68CX4	Q68CX4 homo sapien
70	22	27.2	15	Q9HCX8	Q9HCX8 homo sapien
71	22	27.2	15	Q6UTP9	Q6UTP9 dimerostemm
72	22	27.2	15	Q71H02	Q71H02 andrena inc
73	22	27.2	15	P83076	P83076 bacillus ce
74	22	27.2	15	Q6LEB7	Q6LEB7 rattus norv
75	22	27.2	16	Q00497	Q00497 homo sapien
76	22	27.2	16	Q77489	Q77489 tupia glis
77	22	27.2	16	Q9T0Y6	Q9T0Y6 oryctolagus
78	22	27.2	16	Q38407	Q38407 bacterioph
79	22	27.2	16	Q6QVE1	Q6QVE1 phaseolus v
80	22	27.2	16	Q7M137	Q7M137 unidentified
81	22	27.2	16	Q9MMG6	Q9MMG6 sigma virus
82	22	27.2	17	Q9TRU8	Q9TRU8 bos taurus
83	22	27.2	18	Q9UCF9	Q9UCF9 homo sapien
84	22	27.2	18	Q41458	Q41458 solanum tub
85	22	27.2	18	Q9RSB0	Q9RSB0 arthrobaete
86	21	25.9	8	Q6R408	Q6R408 bubalus bub
87	21	25.9	9	Q9UMF3	Q9UMF3 homo sapien
88	21	25.9	9	Q9TRV0	Q9TRV0 antrophleura
89	21	25.9	10	PARE_PANRE	P82660 panagrellus
90	21	25.9	11	PVK3_BIACR	P83333 blaberus cr
91	21	25.9	11	PVK3_BIADU	P83334 blaptica du
92	21	25.9	11	PVK3_GROPO	P83335 gymnopadori
93	21	25.9	11	PVK3_LETMA	P83331 leucophaea
94	21	25.9	11	PVK3_NAUCI	P83332 nauphoeta c
95	21	25.9	13	YPS2_LACLC	P42021 lactococcus
96	21	25.9	14	Q71GK8	Q71GK8 andrena iml
97	21	25.9	14	Q85527	Q85527 chlamydia t
98	21	25.9	14	Q71I26	Q71I26 lactobacilli
99	21	25.9	14	Q9ZB42	Q9ZB42 streptococc
100	21	25.9	15	UC25_MAIZE	P80631 zea mays (m

ALIGNMENTS

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RESULT 1
Q7ML13 PRELIMINARY; PRT; 17 AA.
AC 07M13;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hydroxyproline-rich cell wall glycoprotein, 230K (Fragment).
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP SEQUENCE.
RX MEDLINE=96011753; PubMed=7548825;
RA Wojtaszek P., Trethowan J., Bolwell G.P.;
RT "Specificity in the immobilisation of cell wall proteins in response
RT to different elicitor molecules in suspension-cultured cells of French
RT bean (Phaseolus vulgaris L.).";
RL Plant Mol. Biol. 28:1075-1087(1995).
DR PIR; S59481; S59481.
FT NON_TER 1 17
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1929 MW; 7C0525B0179CE55 CRC64;

Query Match 33.3%; Score 27; DB 2; Length 17;
Best Local Similarity 46.7%; Pred. No. 1.9e+03;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 1 DLEMPVLPVPPFPV 15
DB 1 DMYLP--PVPPPPV 13

RESULT 2
Q9NSF0 PRELIMINARY; PRT; 18 AA.
AC Q9NSF0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MESPI (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Aultay C., Amstrong W., Ballbio A., Ectivill X., Gibson K.,
RA Leirich H., Pouscka A., Lundberg J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Carim L., Ectivill X., Escarceller M., Sunoy L.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; ALJ57535; CAB93427.1; -.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 18 AA; 2196 MW; 0ACBE7DA3E2849F0 CRC64;

Query Match 33.3%; Score 27; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 MPVLPVPPFP 13
DB 5 MPVLPVPPFP 14

RESULT 3
Q9TRX8 PRELIMINARY; PRT; 8 AA.
ID Q9TRX8

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AC Q9TRX8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Osteopontin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91282766; PubMed=1676261;
RA Prince C.W., Dickie D., Krumdieck C.L.;
RT "Osteopontin, a substrate for transglutaminase and factor XIII
RT activity.";
RL Biochem. Biophys. Res. Commun. 177:1205-1210(1991).
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 920 MW; 05DAFAF7632D767 CRC64;

Query Match 32.1%; Score 26; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.6e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 LPVPPFP 14
DB 1 LPVKPKXF 8

RESULT 4
Q56610 PRELIMINARY; PRT; 18 AA.
AC Q56610;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Acca (Fragment).
GN Name=acca;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6706;
RX MEDLINE=97074686; PubMed=8917113; DOI=10.1016/0378-1119(96)00155-2;
RA Franco A., Peir-Eu Y., Johnson J., Barry E.M., Guerra H., Maurer R.,
RA Morris J.G.;
RT "Cloning and characterization of dnaE, encoding the catalytic subunit
RT of replicative DNA polymerase III, from Vibrio cholerae strain
RT C6706.";
RL Gene 175:281-283 (1996).
DR EMBL; U30472; AAC4579.1; -.
FT NON_TER 18 18
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2154 MW; 18EBDAD212842EF CRC64;

Query Match 32.1%; Score 26; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLEMPVLPVE 10
DB 7 DFEKPIVELE 16

RESULT 5
Q9P8E5 PRELIMINARY; PRT; 9 AA.
ID Q9P8E5
AC Q9P8E5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

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DE HIS4 protein (Fragment).
GN Name=HIS4;
OS Kluyveromyces lacticis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL-Y1140;
RX MEDLINE=99448382; PubMed=10518937; DOI=10.1016/S0014-5793(99)01105-9;
RA Lamas-Macielas M., Esperanza Cerdan E., Freire-Picos M.A.;
RT "Kluyveromyces lacticis HIS4 transcriptional regulation: similarities
and differences to Saccharomyces cerevisiae HIS4 gene.";
RL FEBS Lett. 458:72-76(1999).
DR EMBL; AJ238494; CAB87125.1; -.
FT NON TER
SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

Query Match
Best Local Similarity 30.9%; Score 25; DB 2; Length 9;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPVLPV 9
DB 2 LPVVPV 7

RESULT 6
OB3139 PRELIMINARY; PRT; 12 AA.
ID OB3139
AC OB3139;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (strain CV17) genomic RNA-gamma, 5' leader.
OS Barley stripe mosaic virus (BSMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hordeivirus.
OX NCBI_TaxID=12337;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV17;
RX MEDLINE=91062385; PubMed=2247462;
RA Pety I.T., Edwards M.C., Jackson A.O.;
RT "Systemic movement of an RNA plant virus determined by a point
substitution in a 5' leader sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8894-8897(1990).
DR EMBL; M38633; AAA75527.1; -.
SQ SEQUENCE 12 AA; 1416 MW; 36A281207BC05047 CRC64;

Query Match
Best Local Similarity 30.9%; Score 25; DB 2; Length 12;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 MPVLPVPEPF 12
DB 4 MPVIVDSF 12

RESULT 7
UC17_MAIZE STANDARD; PRT; 15 AA.
ID UC17_MAIZE
AC P80623;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 32)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogonae; Zea.
OX NCBI_TaxID=4577;

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RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.5, its MW is: 42.7 kDa.
DR MaizeDB; P80623; COLEOPTILE.
DR MaizeDB; 123949; -.
KW Direct protein sequencing.
FT NON TER
FT NON TER
SQ SEQUENCE 15 AA; 1554 MW; COAFFP15FECECE8 CRC64;

Query Match
Best Local Similarity 30.9%; Score 25; DB 1; Length 15;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LEMPVLPVPEPF 11
DB 2 LSVFPAVAP 11

RESULT 8
NGIF_RAT
ID NGIF_RAT STANDARD; PRT; 8 AA.
AC P82598;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Non-arginase growth inhibitory factor (NGIF) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC STRAIN=Sprague-Dawley; TISSUE=liver;
RX MEDLINE=20198203; PubMed=10731662;
RA Kim K.-Y., Choi I., Kim S.-S.;
RT "Purification and characterization of a novel inhibitor of the
RT proliferation and hepatic stellate cells.";
RL J. Biochem. 127:23-27(2000).
CC -1- FUNCTION: Inhibitor of the proliferation of hepatic stellate cells
CC (HSC). Also inhibits the growth of bovine endothelial cells and
CC 3T6 fibroblasts.
KW Direct protein sequencing.
FT NON TER
SQ SEQUENCE 8 AA; 914 MW; 80A3676B02D76B1D CRC64;

Query Match
Best Local Similarity 29.6%; Score 24; DB 1; Length 8;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEPFP 12
DB 3 PVEPFP 7

RESULT 9
Q7MIU5 PRELIMINARY; PRT; 15 AA.
ID Q7MIU5
AC Q7MIU5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 'superoxide dismutase (EC 1.15.1.1) (Mn) (Fragment)'.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.

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OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RA Tsugita A.;
RL Submitted (APR-1993) to the PIR data bank.
DR PIR; PS0455; PS0455.
DR GO; GO:0004784; F:superoxide dismutase activity; IEA.
FT NON_TER 1 1
FT SEQUENCE 15 15
SQ SEQUENCE 15 AA; 1561 MW; 0596471D6F3DBEAE CRC64;

Query Match
Best Local Similarity 42.9%; Score 24; DB 2; Length 15;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 MPVLVPEPPFV 10
DB 6 LPILPYD 12

RESULT 10
Q6AKC0 PRELIMINARY; PRT; 16 AA.
ID Q6AKC0;
AC Q6AKC0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophylla telasco (chestnut-throated seedeater).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidae;
OC Fringillidae; Emberizinae; Sporophilla.
OX NCBI_TaxID=256699;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijmaer D.A., Sharpe N.M.M., Tubaro P.L., Lougheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophilla
RT (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
RW EMBL; AY387478; AAR26793.1; -.
KM Mitochondrion.
FT NON_TER 16 16
FT SEQUENCE 16 AA; 1902 MW; 0ADD11A3861D77C CRC64;

Query Match
Best Local Similarity 41.7%; Score 24; DB 2; Length 16;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLVPEPPFV 15
DB 1 MPQLNPFWLFI 12

RESULT 11
Q9TRH5 PRELIMINARY; PRT; 17 AA.
ID Q9TRH5;
AC Q9TRH5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Alpha-S1-casein homolog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Ruminantia; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=3231344; PubMed=1299613; DOI=10.1016/0014-5793(92)80664-3;
RA Neuteboom B., Gufferda M.G., Conti A.;

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RT "Isolation of a new ligand-carrying casein fragment from bovine
RT mammary gland microsomes.";
RL FEBS Lett. 305:189-191(1992).
SQ SEQUENCE 17 AA; 1950 MW; 8890EF0685A0537F CRC64;

Query Match
Best Local Similarity 71.4%; Score 24; DB 2; Length 17;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 VEPFPPFV 15
DB 2 VAPFPEV 8

RESULT 12
Q8X4A4 PRELIMINARY; PRT; 17 AA.
ID Q8X4A4;
AC Q8X4A4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Z4331 protein.
GN OrderedLocusNames=Z4331;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca U., Antcharman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RW EMBL; AE005528; AAG58115.1; -.
DR PIR; G85956; G85956.
KM Complete proteome.
FT SEQUENCE 17 AA; 1823 MW; 5A1C41BC7BF69D69 CRC64;

Query Match
Best Local Similarity 80.0%; Score 24; DB 2; Length 17;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 VEPFPP 13
DB 4 VSPFP 8

RESULT 13
TW2A METWA STANDARD; PRT; 12 AA.
ID TW2A METWA;
AC P80652;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
DE (EC 2.1.1.86) (NS-methyltetrahydromethanopterin--coenzyme M
DE methyltransferase 28 kDa subunit) (Fragment).
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE.
RC STRAIN=Goe1 / Goe1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=96370840; PubMed=8774736;
RA Ilendard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RA "Sodium ion translocation by NS-methyltetrahydromethanopterin;"

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RT coenzyme M methyltransferase from Methanosaarcina mazei G01
 RT reconstituted in ether lipid liposomes."
 RT Bur. J. Biochem. 239:857-864(1996).
 CC -1- FUNCTION: This enzyme complex catalyzes an intermediate step in
 CC methanogenesis, the formation of methyl-coenzyme M and
 CC tetrahydromethanopterin from coenzyme M and N5-methyl-
 CC tetrahydromethanopterin.
 CC -1- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
 CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
 CC (methylthio)ethanesulfonate.
 CC -1- SUBUNIT: Composed of six different subunits.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 KM Direct protein sequencing; Methanogenesis; Methyltransferase;
 KM transferase; Transmembrane.
 FT NON TER 12
 FT SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;
 SQ
 Query Match 28.4%; Score 23; DB 1; Length 12;
 Best Local Similarity 80.0%; Pred. No. 5.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 PVLPLV 9
 |||||
 Db 6 PVLPL 10
 RESULT 14
 SODM_ARTDA STANDARD; PRT; 13 AA.
 AC P83289;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Superoxide dismutase [Mn/Fe] (EC 1.15.1.1) (Fragment).
 OS Archaeobacter dactyloides (Nematode-trapping fungus).
 OC Bacteria; Fungi; Ascomycota; Pezizomycotina; Orbiliomycetes;
 OC Orbiliales; Orbiliaceae; mitosporic Orbiliaceae; Archaeobacteres.
 OX NCBI_TaxId=74499;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=072;
 RA Zhao M., Zhang K.;
 RL Submitted (FEB-2002) to Swiss-Prot.
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Binds 1 manganese or iron ion per subunit (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 CC family.
 CC InterPro: IPR001189; SODismutase.
 DR PROSITE: PS00088; SOD_MN; PARTIAL.
 KM Direct protein sequencing; Iron; Manganese; Metal-binding;
 KM Oxidoreductase.
 FT NON TER 13
 FT SEQUENCE 13 AA; 1515 MW; 69949202E642672B CRC64;
 SQ
 Query Match 28.4%; Score 23; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 6.2e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DE Hypothetical protein (Fragment).
 OS Pleospora trichoclinalcola.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; Pleospora.
 OX NCBI_TaxId=183473;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGS 36-118;
 RA Inderbitzin P., Berbee M.L.;
 RT "Mating type gene evolution in Pleospora, the sexual state of
 RT Stemphylium."
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY335167; AAR00945.1; -
 KM Hypothetical protein.
 FT NON TER 1
 FT SEQUENCE 13 AA; 1345 MW; 6AD166DF073972CB CRC64;
 SQ
 Query Match 28.4%; Score 23; DB 2; Length 13;
 Best Local Similarity 42.9%; Pred. No. 6.2e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 DLEMPVL 7
 ||:|:
 Db 4 DLEVPRT 10
 RESULT 16
 SODM_ENTAE STANDARD; PRT; 15 AA.
 AC P22799;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
 GN Name=soda;
 OS Enterobacter aerogenes (Enterobacter aerogenes).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Enterobacter.
 OX NCBI_TaxId=548;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=91248479; PubMed=136858;
 RA Kim S.W., Lee S.O., Lee T.H.;
 RL "Purification and characterization of superoxide dismutase from
 RT Aerobacter aerogenes."
 RT Agric. Biol. Chem. 55:101-108(1991).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Binds 1 iron ion per subunit (By similarity).
 CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 CC family.
 CC PIR: P0615; P0615.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; SOD_Fe_N; 1.
 DR PROSITE: PS00088; SOD_MN; PARTIAL.
 KM Direct protein sequencing; Iron; Metal-binding; Oxidoreductase.
 FT NON TER 15
 FT SEQUENCE 15 AA; 1756 MW; 352F3D949202E642 CRC64;
 SQ
 Query Match 28.4%; Score 23; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 7.2e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

AC Q69FU1: 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Stemphylium solani.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stemphylium.
 NCBI_TaxID=110364;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGS41-135;
 RA Inderbitzin P., Berbee M.L.;
 RT "Mating type gene evolution in Pleospora, the sexual state of
 RT Stemphylium.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY339855; AAR04451.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1547 MW; 84F7BBAD166DF45 CRC64;
 SC

Query Match 28.4%; Score 23; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 7.2e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7
 |::|:
 Db 3 DIEVPTI 9

RESULT 18

ID Q69FU3 PRELIMINARY; PRT; 15 AA.
 AC Q69FU3;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Stemphylium sarciniforme.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stemphylium.
 NCBI_TaxID=119934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGS38-121;
 RA Inderbitzin P., Berbee M.L.;
 RT "Mating type gene evolution in Pleospora, the sexual state of
 RT Stemphylium.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY339854; AAR04449.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1533 MW; 84EF1D8AD166DF45 CRC64;
 SC

Query Match 28.4%; Score 23; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 7.2e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7
 |::|:
 Db 3 DIEVPTI 9

RESULT 19

ID Q69GA1 PRELIMINARY; PRT; 15 AA.
 AC Q69GA1;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Stemphylium sp. EGS49-030.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stemphylium.
 NCBI_TaxID=235041;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGS 49-030;
 RA Inderbitzin P., Berbee M.L.;
 RT "Mating type gene evolution in Pleospora, the sexual state of
 RT Stemphylium.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY335179; AAR00981.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1542 MW; 84EF0ABAD166DF45 CRC64;
 SC

Query Match 28.4%; Score 23; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 7.2e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7
 |::|:
 Db 3 DIEVPTI 9

RESULT 20

ID Q69GB9 PRELIMINARY; PRT; 15 AA.
 AC Q69GB9;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Pleospora graciilariae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; Pleospora.
 NCBI_TaxID=91368;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGS 37-073;
 RA Inderbitzin P., Berbee M.L.;
 RT "Mating type gene evolution in Pleospora, the sexual state of
 RT Stemphylium.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY335173; AAR00963.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1512 MW; 84EF0ABAD166CF44 CRC64;
 SC

Query Match 28.4%; Score 23; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 7.2e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7
 |::|:
 Db 3 DIEVPTI 9

RESULT 21

ID Q69GD1 PRELIMINARY; PRT; 15 AA.
 AC Q69GD1;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Stemphylium sp. EGS08-174.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stemphylium.
 NCBI_TaxID=234989;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGS 08-174;
 RA Inderbitzin P., Berbee M.L.;
 RT "Mating type gene evolution in Pleospora, the sexual state of

OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stemphylium.
 NCBI_TaxID=235041;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGS 49-030;
 RA Inderbitzin P., Berbee M.L.;
 RT "Mating type gene evolution in Pleospora, the sexual state of
 RT Stemphylium.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY335179; AAR00981.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1542 MW; 84EF0ABAD166DF45 CRC64;
 SC

Query Match 28.4%; Score 23; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 7.2e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7
 |::|:
 Db 3 DIEVPTI 9

RESULT 20

ID Q69GB9 PRELIMINARY; PRT; 15 AA.
 AC Q69GB9;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Pleospora graciilariae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; Pleospora.
 NCBI_TaxID=91368;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGS 37-073;
 RA Inderbitzin P., Berbee M.L.;
 RT "Mating type gene evolution in Pleospora, the sexual state of
 RT Stemphylium.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY335173; AAR00963.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1512 MW; 84EF0ABAD166CF44 CRC64;
 SC

Query Match 28.4%; Score 23; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 7.2e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7
 |::|:
 Db 3 DIEVPTI 9

RESULT 21

ID Q69GD1 PRELIMINARY; PRT; 15 AA.
 AC Q69GD1;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Stemphylium sp. EGS08-174.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stemphylium.
 NCBI_TaxID=234989;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGS 08-174;
 RA Inderbitzin P., Berbee M.L.;
 RT "Mating type gene evolution in Pleospora, the sexual state of

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RT Stemphylium";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY335169; AAR00951.1; -.
KW Hypoetical protein.
FT NON TER
SQ SEQUENCE 15 AA; 1533 MW; 84EF1D8AD166DF45 CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 15;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7
DB 3 DIEVPFI 9

RESULT 22
Q9TNO1 PRELIMINARY; PRT; 15 AA.
ID Q9TNO1;
AC Q9TNO1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Beta 2M-class I-binding PEPTIDE-MAJOR histocompatibility complex H-2Kb-specific molecule POORLY associated with beta 2-microglobulin (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=94240094; PubMed=8183884;
RA Joyce S., Kuzushima K., Kepes G., Angelletti R.H., Nathenson S.G.;
RT "Characterization of an incompletely assembled major histocompatibility class I molecule (H-2Kb) associated with unusually long peptides: implications for antigen processing and presentation.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149 (1994).
FT NON TER
FT NON TER
SQ SEQUENCE 15 AA; 1754 MW; 2CEACDA0F1180DC7 CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 15;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DLEMPVL 9
DB 5 LQLPVVKV 12

RESULT 23
Q64KG2 PRELIMINARY; PRT; 15 AA.
ID Q64KG2;
AC Q64KG2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DS ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila cinnamomea (chestnut seedeater).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Passeroidea; Fringillidae; Emberizinae; Sporophila.
OX NCBI_TaxID=256690;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijmaer D.A., Sharpe N.M.M., Tubaro P.L., Lougheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0 (2004).
DR EMBL; AY387457; AAR26751.1; -.

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KW Mitochondrion.
FT NON TER
SQ SEQUENCE 15 AA; 1849 MW; 2D131A3861D99C5E CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 15;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPEVPFPFV 15
DB 1 MPQLNPWFPI 12

RESULT 24
Q69G98 PRELIMINARY; PRT; 16 AA.
ID Q69G98;
AC Q69G98;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypoetical protein (Fragment).
OS Pleospora sp. P327.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; OC Pleosporales; Pleosporaceae; Pleospora.
OX NCBI_TaxID=234982;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=P327;
RA Underhitzin P., Berbee M.L.;
RT "Mating type gene evolution in Pleospora, the sexual state of Stemphylium.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY335180; AAR00984.1; -.
KW Hypoetical protein.
FT NON TER
FT NON TER
SQ SEQUENCE 16 AA; 1662 MW; 54D36D8AD166DF07 CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 16;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7
DB 4 DIEVPFI 10

RESULT 25
Q69GB0 PRELIMINARY; PRT; 16 AA.
ID Q69GB0;
AC Q69GB0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DS Hypoetical protein (Fragment).
OS Pleospora etumuna.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; OC Pleosporales; Pleosporaceae; Pleospora.
OX NCBI_TaxID=235069;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=EGS 29-099;
RA Underhitzin P., Berbee M.L.;
RT "Mating type gene evolution in Pleospora, the sexual state of Stemphylium.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY335176; AAR00972.1; -.
KW Hypoetical protein.
FT NON TER
FT NON TER
SQ SEQUENCE 16 AA; 1632 MW; 54CF1D8AD166DF07 CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 16;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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OY 1 DLEMPVL 7
|:|:|:
Db 4 DLEVPTI 10

RESULT 26

OY 069GB3 PRELIMINARY; PRT; 16 AA.
AC 069GB3;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)
DE Hypothetical protein (Fragment).
OS Pleospora tomatonis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Pleospora.
OX NCBI_TaxId=235068;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGS 29-089;
RA Inderbitzin P., Berbee M.L.;
RT "Mating type gene evolution in Pleospora, the sexual state of Stemphylium."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY335175; AAR00969.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 16 AA; 1641 MW; 54CF0ABAD166DF07 CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 7.8e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 DLEMPVL 7
|:|:|:
Db 4 DLEVPTI 10

RESULT 27

OY 069GC2 PRELIMINARY; PRT; 16 AA.
AC 069GC2;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)
DE Hypothetical protein (Fragment).
OS Pleospora sp. EGS37-067.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Pleospora.
OX NCBI_TaxId=234979;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGS 37-067;
RA Inderbitzin P., Berbee M.L.;
RT "Mating type gene evolution in Pleospora, the sexual state of Stemphylium."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY335172; AAR00960.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 16 AA; 1641 MW; 54CF0ABAD166DF07 CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 7.8e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 DLEMPVL 7
|:|:|:
Db 4 DLEVPTI 10

RESULT 28

OY 069GC5 PRELIMINARY; PRT; 16 AA.
AC 069GC5;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)
DE Hypothetical protein (Fragment).
OS Stemphylium sp. EGS48-089.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Pleospora.
OX NCBI_TaxId=235021;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGS 48-089;
RA Inderbitzin P., Berbee M.L.;
RT "Mating type gene evolution in Pleospora, the sexual state of Stemphylium."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY335171; AAR00957.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 16 AA; 1632 MW; 54CF1D8AD166DF07 CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 7.8e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 DLEMPVL 7
|:|:|:
Db 4 DLEVPTI 10

RESULT 29

OY 069GC8 PRELIMINARY; PRT; 16 AA.
AC 069GC8;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)
DE Hypothetical protein (Fragment).
OS Stemphylium sp. EGS48-074.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Pleospora.
OX NCBI_TaxId=235018;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGS 48-074;
RA Inderbitzin P., Berbee M.L.;
RT "Mating type gene evolution in Pleospora, the sexual state of Stemphylium."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY335170; AAR00954.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 16 AA; 1632 MW; 54CF1D8AD166DF07 CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 7.8e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 DLEMPVL 7
|:|:|:
Db 4 DLEVPTI 10

RESULT 30

OY 069GD4 PRELIMINARY; PRT; 16 AA.
AC 069GD4;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)
DE Hypothetical protein (Fragment).

OS Pleospora gigaspora.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Pleospora.
OX NCBI_TaxID=235067;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGS 37-017;
RA Inderbitzin P., Berbee M.L.;
RT "Mating type gene evolution in Pleospora, the sexual state of
RT Stemphylium."
RL Submitted (Jul-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY35168; AAR00948.1; --
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 16 AA; 1641 MW; 54CF0ABAD166DF07 CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 7.8e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 DLEMPVL 7
|||:
Db 4 DIEVPTI 10

RESULT 31

OS 064KB4 PRELIMINARY; PRT; 16 AA.
AC 064KB4;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Volactinia jaccarina (blue-black grassquit).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Volatinia.
OX NCBI_TaxID=135452;
RN [1]
RP SEQUENCE FROM N.A.
RA Liljemaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
RT (Aves: Passeriformes)."
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387481; AAR26799.1; --
DR EMBL; AY387482; AAR26801.1; --
KW Mitochondrion.
FT NON TER 16
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 MPVLPEPPPPV 15
|||:
Db 1 MPOLNPMPWFFI 12

RESULT 32

OS 064KB8 PRELIMINARY; PRT; 16 AA.
AC 064KB8;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila zeilichi (Narosky's seedeater).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
OX NCBI_TaxID=256700;
RN [1]
RP SEQUENCE FROM N.A.
RA Liljemaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
RT (Aves: Passeriformes)."
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387479; AAR26799.1; --
DR EMBL; AY387480; AAR26797.1; --
KW Mitochondrion.
FT NON TER 16
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 MPVLPEPPPPV 15
|||:
Db 1 MPOLNPMPWFFI 12

RESULT 33

OS 064KC6 PRELIMINARY; PRT; 16 AA.
AC 064KC6;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila ruficollis (dark-throated seedeater).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
OX NCBI_TaxID=200161;
RN [1]
RP SEQUENCE FROM N.A.
RA Liljemaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
RT (Aves: Passeriformes)."
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387475; AAR26787.1; --
DR EMBL; AY387476; AAR26789.1; --
DR EMBL; AY387477; AAR26791.1; --
KW Mitochondrion.
FT NON TER 16
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 MPVLPEPPPPV 15
|||:
Db 1 MPOLNPMPWFFI 12

RESULT 34

OS 064KD0 PRELIMINARY; PRT; 16 AA.
AC 064KD0;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila palustris (marsh seedeater).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
OX NCB1_TaxID=256698;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijtmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387473; AAR26783.1; -.
DR EMBL; AY387474; AAR26785.1; -.
KM Mitochondrion.
FT NON TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match      28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPVEPPFPV 15
   ||| | | | |
Db 1 MPQLNPNPWFPI 12

RESULT 35
O64K02 PRELIMINARY; PRT; 16 AA.
AC O64K02;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila nigricollis (yellow-bellied seedeater).
OC Mitochondrion.
OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
OX NCB1_TaxID=138930;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijtmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387472; AAR26781.1; -.
KM Mitochondrion.
FT NON TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match      28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPVEPPFPV 15
   ||| | | | |
Db 1 MPQLNPNPWFPI 12

RESULT 36
O64K08 PRELIMINARY; PRT; 16 AA.
AC O64K08;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila minuta (ruddy-breasted seedeater).
OC Mitochondrion.
OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.

```

```

OX NCB1_TaxID=256697;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijtmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387469; AAR26775.1; -.
DR EMBL; AY387470; AAR26777.1; -.
DR EMBL; AY387471; AAR26779.1; -.
KM Mitochondrion.
FT NON TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match      28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPVEPPFPV 15
   ||| | | | |
Db 1 MPQLNPNPWFPI 12

RESULT 37
O64KE0 PRELIMINARY; PRT; 16 AA.
AC O64KE0;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila melanogaster (black-bellied seedeater).
OC Mitochondrion.
OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
OX NCB1_TaxID=256696;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijtmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387468; AAR26773.1; -.
KM Mitochondrion.
FT NON TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match      28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPVEPPFPV 15
   ||| | | | |
Db 1 MPQLNPNPWFPI 12

RESULT 38
O64KE2 PRELIMINARY; PRT; 16 AA.
AC O64KE2;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila luctuosa (black-and-white seedeater).
OC Mitochondrion.
OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
OX NCB1_TaxID=256695;

```



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RN [1]
RP SEQUENCE FROM N.A.
RA Lijmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387467; AAR26771.1; -.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 16;
Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPVEPPFPV 15
DB 1 MPQLNPMPFP 12

RESULT 39
O64KE4 PRELIMINARY; PRT; 16 AA.
AC O64KE4;
DC 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila leucoptera (white-bellied seedeater).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
NCBI_TaxID=25694;
OX NCB1_TaxID=25694;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387466; AAR26769.1; -.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 16;
Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPVEPPFPV 15
DB 1 MPQLNPMPFP 12

RESULT 40
O64KE8 PRELIMINARY; PRT; 16 AA.
AC O64KE8;
DC 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila hypoxantha (tawny-bellied seedeater).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
NCBI_TaxID=25693;
OX NCB1_TaxID=25693;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;

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```

RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387464; AAR26765.1; -.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 16;
Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPVEPPFPV 15
DB 1 MPQLNPMPFP 12

Search completed: June 7, 2005, 23:18:59
Job time : 68 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 59.2 Seconds

(without alignments)
71.864 Million cell updates/sec

Title: US-10-691-157-6

Perfect score: 62

Sequence: 1 MPQNPYKLPQM 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	62	100.0	11 4 AAB72505	Aab72505 Colostyrin
2	62	100.0	11 4 AAB59311	Aab59311 Ewe colos
3	62	100.0	11 4 AAB72251	Aab72251 Colostyrin
4	62	100.0	11 4 AAB72537	Aab72537 Colostyrin
5	62	100.0	11 5 AAO14582	Aao14582 Neural ce
6	62	100.0	11 5 AAM51041	Aam51041 Colostyrin
7	62	100.0	11 5 AAE20233	Aae20233 Colostyrin
8	62	100.0	11 5 ADN60300	Adn60300 Constitue
9	62	100.0	11 8 ADS74387	AdS74387 Ovine col
10	62	100.0	12 2 AAB59342	Aab59342 Ewe colos
11	60	48.4	8 2 AAB60468	Aab60468 Antiprol
12	60	48.4	8 2 AAR60461	Aar60461 Antiprol
13	60	48.4	11 2 AAR21944	Aar21944 Substance
14	30	48.4	11 2 AAM92718	Aam92718 Human tac
15	30	48.4	15 7 ABR84651	AbR84651 Human ant
16	29	46.8	15 5 AAW00884	Aaw00884 Epstei
17	29	46.8	15 5 AAB99000	Aab99000 Phospheno
18	29	46.8	15 5 AAE20383	Aae20383 Epstei
19	29	46.8	15 5 ABB08787	Abb08787 Human gly
20	29	46.8	15 5 ABR44016	AbR44016 E. coli T
21	28	45.2	7 2 AAY08887	Aay08887 C. linden
22	28	45.2	9 2 AAY48162	Aay48162 Immunogen
23	28	45.2	9 7 ADK23699	Adk23699 Human 98P
24	28	45.2	10 7 ADK24080	Adk24080 Human 98P
25	28	45.2	10 7 ADK24948	Adk24948 Human 98P

26	45.2	11 2 AAR28392	Aar28392 Bradykini
27	45.2	12 3 AAY93148	Aay93148 Rat G-pro
28	45.2	12 4 AAB60026	Aab60026 Internali
29	45.2	12 4 AAG67753	Aag67753 Amino aci
30	45.2	12 6 ABU60819	Abu60819 Peptide p
31	45.2	12 6 ABP97049	Abp97049 Human RPR
32	45.2	12 6 ABP54416	Abp54416 Human RF
33	45.2	12 7 ADA88861	Ada88861 Internali
34	45.2	12 8 ADJ87494	Adj87494 RPR C-re
35	45.2	12 8 ADQ94363	Adq94363 MrgC11 li
36	45.2	14 4 AAM97397	Aam97397 Human pep
37	45.2	15 2 AAR97958	Aar97958 Japan ced
38	45.2	18 5 AAB09233	Aab09233 Transcrip
39	45.2	18 2 AAY03842	Aay03842 Activatio
40	45.2	18 4 AAB48367	Aab48367 Human CTR
41	45.2	18 4 AAB60901	Aab60901 Human CTR
42	45.2	18 5 AAB07299	Abb07299 Chimeric
43	45.2	18 5 ABB09233	Abb09233 Human Oct
44	45.2	18 6 ABG76153	Abg76153 Human Oct
45	45.2	18 7 ADI00396	Adi00396 Human CTR
46	43.5	6 2 AAM04274	Aam04274 Milk deri
47	43.5	8 5 ABB09499	Abb09499 Substance
48	43.5	10 4 AAB91451	Aab91451 Tachykini
49	43.5	11 2 AAR28445	Aar28445 Neurokini
50	43.5	11 2 AAR42649	Aar42649 Neurokini
51	43.5	11 4 AAB91409	Aab91409 Tachykini
52	43.5	11 5 ABB09496	Abb09496 Substance
53	43.5	12 2 AAM15279	Aam15279 Salmonell
54	43.5	12 7 ADC36089	Adc36089 Chemokine
55	43.5	12 7 ADC42837	Adc42837 Modulator
56	43.5	15 2 AAR47036	Aar47036 Apolipop
57	43.5	15 2 AAR97957	Aar97957 Japan ced
58	43.5	17 7 ABR62371	AbR62371 Apolipop
59	41.9	8 8 ADK51384	Adk51384 EBV EBNA2
60	41.9	8 8 ADK51385	Adk51385 EBV EBNA2
61	41.9	9 5 ABG68026	Abg68026 Human ADP
62	41.9	9 6 ADA24181	Ada24181 Alzheimer
63	41.9	9 7 ADD23602	Add23602 Breast ca
64	41.9	9 8 ADJ58442	Adj58442 Peptide p
65	41.9	9 8 ADJ58441	Adj58441 Peptide p
66	41.9	9 8 ADQ70435	Adq70435 Cancer re
67	41.9	9 8 ADQ71135	Adq71135 Cancer re
68	41.9	9 8 ADQ71658	Adq71658 Cancer re
69	41.9	9 8 ADQ68309	Adq68309 Cancer re
70	41.9	9 8 ADQ68675	Adq68675 Cancer re
71	41.9	9 8 ADQ69717	Adq69717 Cancer re
72	41.9	9 8 ADQ69360	Adq69360 Cancer re
73	41.9	9 8 ADQ70358	Adq70358 Cancer re
74	41.9	9 8 ADQ72110	Adq72110 Cancer re
75	41.9	9 8 ADQ70083	Adq70083 Cancer re
76	41.9	9 8 ADQ71948	Adq71948 Cancer re
77	41.9	9 8 ADQ69011	Adq69011 Cancer re
78	41.9	9 8 ADQ69637	Adq69637 Cancer re
79	41.9	9 8 ADQ71923	Adq71923 Cancer re
80	41.9	10 2 AAR67100	Aar67100 Anti-tumo
81	41.9	10 2 ADK39992	Adk39992 PNA molec
82	41.9	10 8 ADQ69538	Adq69538 Cancer re
83	41.9	10 8 ADQ72778	Adq72778 Cancer re
84	41.9	10 8 ADQ68849	Adq68849 Cancer re
85	41.9	10 8 ADQ68481	Adq68481 Cancer re
86	41.9	10 8 ADQ70256	Adq70256 Cancer re
87	41.9	10 8 ADQ73198	Adq73198 Cancer re
88	41.9	10 8 ADQ69834	Adq69834 Cancer re
89	41.9	10 8 ADQ69188	Adq69188 Cancer re
90	41.9	10 8 ADQ70609	Adq70609 Cancer re
91	41.9	10 8 ADQ69200	Adq69200 Cancer re
92	41.9	10 8 ADQ70607	Adq70607 Cancer re
93	41.9	10 8 ADQ68495	Adq68495 Cancer re
94	41.9	10 8 ADQ69889	Adq69889 Cancer re
95	41.9	10 8 ADQ68845	Adq68845 Cancer re
96	41.9	10 8 ADQ69124	Adq69124 Cancer re
97	41.9	10 8 ADQ69544	Adq69544 Cancer re
98	41.9	10 8 ADQ70538	Adq70538 Cancer re

99 26 41.9 10 8 ADQ70255
100 26 41.9 10 8 ADQ69906

Adq70255 Cancer re
Adq69906 Cancer re

ALIGNMENTS

RESULT 1

AAB72505
ID AAB72505 standard; peptide; 11 AA.

AC AAB72505;

DT 09-MAY-2001 (first entry)

XX Colostriin peptide #6.

KW Dermatological; oxidative stress regulator; colostriin.

OS Unidentified.

PN WO200112650-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022665.

PR 17-AUG-1999; 99US-0149310P.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Stanton GJ, Hughes TK, Boldogh I;

DR MPI; 2001-218342/22.

PT Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostriin, its

PT constituent peptide, analog or their combinations.

PS Claim 6; Page 25; 48pp; English.

XX The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostriin, or its constituent peptide (e.g. the present peptide), CC to change the level of an oxidizing species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient

XX Sequence 11 AA;

Query Match 100.0%; Score 62; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPQNFYKLPQM 11

DB 1 MPQNFYKLPQM 11

RESULT 2
AAB59311
ID AAB59311 standard; peptide; 11 AA.

AC AAB59311;

DT 21-MAR-2001 (first entry)

XX Ewe colostriin peptide fragment A-2.

KW Sheep; colostriin; proline rich polypeptide; colostrum; immune disorder;

KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

OS Ovis sp.

PN WO200075173-A2.

PD 14-DEC-2000.

PF 02-JUN-2000; 2000WO-GB002128.

PR 02-JUN-1999; 99GB-00012852.

PA (REGG-) REGEN THERAPEUTICS PLC.

PI Georgiades JA;

DR MPI; 2001-071058/08.

PT Peptides having an N-terminal amino acid sequence isolated from colostriin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques.

PS Claim 7; Page 27; 63pp; English.

XX The present invention provides the sequences of a number of peptides found in ewe's colostriin. Colostriin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques

XX Sequence 11 AA;

Query Match 100.0%; Score 62; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPQNFYKLPQM 11

DB 1 MPQNFYKLPQM 11

RESULT 3

AAB72251
ID AAB72251 standard; peptide; 11 AA.

AC AAB72251;

DT 14-MAY-2001 (first entry)

XX Colostriin derived cytokine inducing peptide SEQ ID 6.

KW Colostriin; immune response; cytokine; blood cell proliferation;

KW central nervous system disorder; neurological disorder; mental disorder; dementia; neurodegenerative disease; Alzheimer's disease; psychosis;

XX neurosis; infection.

OS Synthetic.

PN WO200111937-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022818.

PR 17-AUG-1999; 99US-0149311P.

PA (REGG-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2001-202804/20.
XX Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostriatin as an immunological
PT regulator.
XX
XX
PS Claim 1; Page 34; 50pp; English.
XX
XX Sequences AAB72246 - AAB72275 represent peptides derived from colostriatin,
CC a proline rich polypeptide aggregate contained in colostrum. The peptides
CC have immune response modulatory activity, and are capable of inducing
CC cytokines. Colostriatin and its derived peptides are useful for inducing
CC cytokine production, for modulating an immunological response and for
CC inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 62; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNFYKLPQM 11
DB 1 MPQNFYKLPQM 11

RESULT 4
AAB72537
ID AAB72537 standard; peptide; 11 AA.
XX
AC AAB72537;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostriatin peptide #6.
XX
KW Neuroprotective; neural cell differentiation regulator; colostriatin;
XX colostrum.
XX
OS Unidentified.
XX
PN WO200112651-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US022774.
XX
PR 17-AUG-1999; 99US-0149633P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Boldogh I;
XX
PI WPI; 2001-226545/23.
XX
DR WPI; 2001-226545/23.
XX
PT Use of colostriatin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating damaged
PT neural cells in a patient.
XX
PS Claim 6; Page 21; 35pp; English.
XX
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostriatin and
CC colostriatin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostriatin is a polypeptide complex found in colostrum
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 62; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNFYKLPQM 11
DB 1 MPQNFYKLPQM 11

RESULT 5
AA014582
ID AA014582 standard; peptide; 11 AA.
XX
XX AA014582;
AC
XX 27-MAY-2002 (first entry)
XX
DT
XX
DB Neural cell regulatory colostriatin peptide 6.
XX
KW Neural cell differentiation; neural cell regulator; colostriatin peptide;
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
KW neural cell treatment.
XX
XX Unidentified.
OS
XX
FH Key Location/Qualifiers
FT Modified-site 11 /note="Optional C-terminal amide"
PT
XX
PN WO200213851-A1.
XX
PD 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US022777.
XX
XX 17-AUG-2000; 2000WO-US022777.
XX
PR 17-AUG-2000; 2000WO-US022777.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Boldogh I, Stanton JG, Hughes TK,
XX
PI WPI; 2002-269152/31.
XX
DR WPI; 2002-269152/31.
XX
PT Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostriatin, its constituent peptide and/or
PT analog..
XX
PS Claim 7; Page 21; 37pp; English.
XX
XX The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostriatin peptide) in order to change the
CC cells in morphology to form neural cells. Colostriatin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostriatin peptide used in
CC the method of the invention
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 62; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNFYKLPQM 11
DB 1 MPQNFYKLPQM 11

RESULT 6
AAM51041

ID AAM51041 standard; peptide, 11 AA.
XX
AC AAM51041;
XX
DT 30-MAY-2002 (first entry)
XX
DE Colostriin constituent peptide.
XX
KW Colostriin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 11 /note="optional C-terminal amidation"
FT
XX
PN WO200213849-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022775.
XX
PR 17-AUG-2000; 2000WO-US022775.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX (REGG-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
XX WPI; 2002-269150/31.
XX
PT Modulation of blood cell proliferation in a patient involves use of blood
PT cell regulator selected from colostriin, its constituent peptide and/or
PT analog.
XX
XX Claim 1; Page 34; 54pp; English.
XX
PS The present sequence is that of a colostriin constituent peptide that is
XX preferred for use as an immunological regulator and as a blood cell
XX regulator in claimed methods of the invention. Methods are claimed for:
CC inducing a cytokine in a cell by contact with an immunological regulator,
CC where the cell is present in a cell culture, a tissue, an organ or an
CC organism, and the cell is mammalian, including human; modulating an
CC immune response in a cell by contact with the immunological regulator
CC under conditions effective to induce a cytokine; modulating an immune
CC response in a patient by administering an immunological regulator under
CC conditions effective to induce a cytokine, where the immunological
CC regulator is administered topically or as part of a dietary supplement,
CC and where the immune response is specific or non specific, an interferon
CC response or an antibody response; modulating blood cell proliferation by
CC contacting blood cells with a blood cell regulator, where the blood cells
CC are present in a cell culture or an organism, are mammalian or human, and
CC where the blood cells are increased in number or differentiated; and a
CC method for modulating blood cell proliferation in a patient. A claimed
CC cytokine-inducing composition comprises a pharmaceutical carrier and an
CC active agent such as the present peptide. Cytokines induced by this
CC peptide in human leucocyte cultures include interferon-gamma, tumour
CC necrosis factor-alpha, interleukin-6 and interleukin-10
XX
SQ Sequence 11 AA:
Query Match 100.0%; Score 62; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFYKLPOM 11
| | | | | | | | | | |
DB 1 MPONFYKLPOM 11

RESULT 7
AAE20233

ID AAE20233 standard; peptide, 11 AA.
XX
AC AAE20233;
XX
DT 18-JUN-2002 (first entry)
XX
DE Colostriin constituent peptide #6.
XX
KW Blood cell regulator; colostriin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnery.
XX
XX Unidentified.
XX
OS
XX
FH Key Location/Qualifiers
FT Modified-site 11 /note="Optionally C-terminal amide"
FT
XX
PN WO200213850-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022776.
XX
PR 17-AUG-2000; 2000WO-US022776.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
XX WPI; 2002-269151/31.
XX
PT Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostriin, its
PT constituent peptide and/or analog.
XX
XX Claim 6; Page 25; 51pp; English.
XX
PS The invention relates to a composition which comprises a blood cell
XX regulator selected from colostriin, its constituent peptide and/or
XX analogue. The invention is used for modulating the oxidative stress level
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
CC organ, or organism; or for treating oxidative damage to the skin of a
CC patient e.g. animal or human; to modulate oxidative stress during/ after
CC a premature birth or normal birth, preventing/delaying aging in a
CC patient; enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostriin constituent peptide
XX
SQ Sequence 11 AA:
Query Match 100.0%; Score 62; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFYKLPOM 11
| | | | | | | | | | |
DB 1 MPONFYKLPOM 11

RESULT 8
ADN60300
ID ADN60300 standard; peptide, 11 AA.
XX

AC ADN60300;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Constituent peptide of colostrinin SEQ ID NO:6.
 XX
 KW modulator; colostrinin; intracellular signaling molecule modulator;
 KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;
 KW DNA damage; beta-amyloid; retinoic acid; cytoskeletal; 4HNE inhibitor;
 KW 4HNE-protein adduct formation reduction;
 KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;
 KW c-Jun NH2-terminal kinase inhibition.
 XX
 OS Synthetic.
 XX
 PN WO2004037851-A2.
 XX
 PD 06-MAY-2004.
 XX
 PF 22-OCT-2003; 2003WO-US033423.
 XX
 PR 22-OCT-2002; 2002US-0420369P.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA (BOLD/) BOLDOGH I.
 PA (STAN/) STANTON J G.
 PA (GEOR/) GEORGIADIS J A.
 PA (HUGH/) HUGHES T K.
 PA (KRUZ/) KRUZEL M.
 XX
 PI Bolldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;
 XX
 DR MPI; 2004-365494/34.
 XX
 PT Use of colostrinin for e.g. modulating an intracellular signaling
 PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a
 PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
 PT a cell.
 XX
 PS Claim 6; SEQ ID NO 6; 46pp; English.
 XX
 CC The present invention describes the use of a modulator selected from
 CC colostrinin, its constituent peptide, its active analogue, and a
 CC combination of these, for modulating an intracellular signaling molecule
 CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
 CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
 CC The modulator has cytoskeletal activity, and can be used as a 4HNE
 CC inhibitor. The modulator is useful in the manufacture of a medicament for
 CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated
 CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,
 CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.
 CC Colostrinin, or its constituent peptide or active analogue is useful for
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
 CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
 CC The present sequence represents a synthetic constituent peptide of
 CC colostrinin, which can be used as a modulator in the present invention.
 XX
 SQ Sequence 11 AA;
 XX

Query Match 100.0%; Score 62; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFYKLPQM 11
 |||||
 DB 1 MPONFYKLPQM 11

RESULT 9
 ADS74387
 ID ADS74387 standard; peptide; 11 AA.
 XX

AC ADS74387;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Ovine colostrinin peptide.
 XX
 KW Colostrum; colostrinin; sheep; peptide purification.
 KW Ovis aries.
 XX
 PN WO2004081038-A1.
 XX
 PD 23-SEP-2004.
 XX
 PF 10-MAR-2004; 2004WO-GB001014.
 XX
 PR 11-MAR-2003; 2003GB-00005552.
 XX
 PR 08-MAR-2004; 2004GB-00005190.
 XX
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;
 XX
 DR MPI; 2004-677519/66.
 XX
 PT Recovering peptides such as colostrinin from mammalian colostrum, by
 PT mixing colostrum with alcohol to form alcohol phase containing peptides
 PT and precipitate, separating alcohol phase from precipitate, and
 PT recovering alcohol phase.
 XX
 PS Disclosure; SEQ ID NO 2; 41pp; English.
 XX
 CC The present sequence is that of a peptide that can be recovered from
 CC ovine colostrum using the method of the invention. The invention
 CC provides a method for the recovery of peptides (especially colostrinin)
 CC from colostrum in substantially pure, biologically active form and in
 CC high yield. The method involves mixing the colostrum with an alcohol to
 CC form an alcohol phase containing the colostrinin and a precipitate
 CC containing higher molecular weight caseins and other proteins. Best
 CC results are obtained using methanol or ethanol of at least 80%, and
 CC preferably up to 100%, purity. The alcohol phase is then separated from
 CC the precipitate, and the colostrinin is separated from the alcohol,
 CC preferably by evaporation, to form a colostrinin-rich phase, which is
 CC recovered. A precipitation agent, such as ammonium sulfate, may be added
 CC either to the alcohol phase or, preferably, to the colostrinin-rich phase
 CC to induce precipitation of the colostrinin peptides. The method is
 CC generally applicable to the separation of peptides from fluids containing
 CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic
 CC acids.
 XX
 SQ Sequence 11 AA;
 XX

Query Match 100.0%; Score 62; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFYKLPQM 11
 |||||
 DB 1 MPONFYKLPQM 11

RESULT 10
 AAB59342
 ID AAB59342 standard; peptide; 12 AA.
 XX
 AC AAB59342;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Ewe colostrinin peptide fragment derived sequence #2.
 XX
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX

XX Ovis sp.
 OS WO200075173-A2.
 PN 14-DEC-2000.
 PD 02-JUN-2000; 2000WO-GB002128.
 XX 02-JUN-1999; 99GB-00012852.
 PR (REGS-) REGEN THERAPEUTICS PLC.
 XX Georgiades JA;
 PI WPI; 2001-071058/08.
 DR Peptides having an N-terminal amino acid sequence isolated from
 PT colostrin for treating e.g. disorders of the central nervous system and
 PT immune system, viral and bacterial infections, and diseases characterized
 PT by amyloid plaques.
 XX
 PS Claim 8; Page 27; 63pp; English.
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques
 CC
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 62; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPONFYKLPQM 11
 Db 2 MPONFYKLPQM 12
 RESULT 11
 AAR60468
 ID AAR60468 standard; peptide; 8 AA.
 AC AAR60468;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 DE Antiproliferative peptide to transplantable human B-cell lymphoma.
 KW antiproliferative; transplant; B-cell lymphoma line SUP-B8; Burkitt's;
 KW inhibit clonal expansion; induce apoptosis; anti-idiotype; IgM lambda;
 KW inhibit cell proliferation; peptidomimetics; cell surface receptor;
 KW immunoglobulin superfamily; treatment; neoplasia; identification;
 KW induce replication; therapy; clonal anergy; modulate tyrosine kinase.
 XX
 OS Synthetic.
 XX
 PN WO9418345-A1.
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-US001319.
 PR 05-FEB-1993; 93US-00014426.
 PR 15-NOV-1993; 93US-00153341.
 XX
 PA (AFY-) AFFYMAX TECHNOLOGIES NV.

PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 XX Reneschler MF, Levy R, Bhatt RR, Dower WJ;
 XX WPI; 1994-279762/34.
 DR Identifying anti-proliferative peptide(s) which specifically bind to
 PT immunoglobulin super-family species idiotype - esp. to inhibit B-cell
 PT lymphoma and leukocytic leukaemia cell proliferation, for anti-idiotype
 PT therapy.
 XX
 PS Claim 7; Page 45; 69pp; English.
 CC AAR60400-73 are peptide ligands which bind to purified IgM lambda
 CC receptor of the human Burkitt's lymphoma cell line SUP-B8. Peptides
 CC AAR60414 to AAR60473 were biotinylated and linked to streptavidin. The
 CC peptides were identified with the use of filamentous phage libraries
 CC displaying random peptides. Corresponding synthetic peptides bound
 CC specifically to this Ig receptor, and blocked the binding of an anti-
 CC idiotype antibody. The ligands, when conjugated to form dimers or
 CC tetramers, induced cell death by apoptosis in vitro at nanomolar
 CC concentrations. This effect was associated with the specific stimulation
 CC of intracellular protein tyrosine phosphorylation. The peptides of the
 CC invention can be used individually, as complexes of cross-linked peptides
 CC or can be conjugated to deliver toxins or radionuclides to neoplastic
 CC cells bearing the specific Ig receptor. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 CC
 SQ Sequence 8 AA;
 Query Match 48.4%; Score 30; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPONFYK 7
 Db 1 MPEDFYR 7
 RESULT 12
 AAR60461
 ID AAR60461 standard; peptide; 8 AA.
 AC AAR60461;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 DE Antiproliferative peptide to transplantable human B-cell lymphoma.
 KW antiproliferative; transplant; B-cell lymphoma line SUP-B8; Burkitt's;
 KW inhibit clonal expansion; induce apoptosis; anti-idiotype; IgM lambda;
 KW inhibit cell proliferation; peptidomimetics; cell surface receptor;
 KW immunoglobulin superfamily; treatment; neoplasia; identification;
 KW induce replication; therapy; clonal anergy; modulate tyrosine kinase.
 XX
 OS Synthetic.
 XX
 PN WO9418345-A1.
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-US001319.
 PR 05-FEB-1993; 93US-00014426.
 PR 15-NOV-1993; 93US-00153341.
 XX
 PA (AFY-) AFFYMAX TECHNOLOGIES NV.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 XX Reneschler MF, Levy R, Bhatt RR, Dower WJ;
 XX WPI; 1994-279762/34.
 DR

XX Identifying anti-proliferative peptide(s) which specifically bind to
 PT immunoglobulin super-family species idotype - esp. to inhibit B-cell
 PT lymphoma and leukocytic leukaemia cell proliferation, for anti-idiotypic
 PT therapy.
 XX
 PS Claim 7; Page 45; 69pp; English.
 CC AAR60400-73 are peptide ligands which bind to purified IgM lambda
 CC receptor of the human Burkitt's lymphoma cell line SUP-B8. Peptides
 CC AAR60414 to AAR60473 were biotinylated and linked to streptavidin. The
 CC peptides were identified with the use of filamentous phage libraries
 CC displaying random peptides. Corresponding synthetic peptides bound
 CC specifically to this Ig receptor, and blocked the binding of an anti-
 CC idotypic antibody. The ligands, when conjugated to form dimers or
 CC tetramers, induced cell death by apoptosis in vitro at nanomolar
 CC concentrations. This effect was associated with the specific stimulation
 CC of intracellular protein tyrosine phosphorylation. The peptides of the
 CC invention can be used individually, as complexes of cross-linked peptides
 CC or can be conjugated to deliver toxins or radionuclides to neoplastic
 CC cells bearing the specific Ig receptor. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 CC
 SQ Sequence 8 AA;
 Query Match 48.4%; Score 30; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 0;
 QY 1 PQNPFYK 7
 ||:|:
 1 MEDEFYR 7
 DB
 RESULT 13
 AAR21944
 ID AAR21944 standard; protein; 11 AA.
 XX
 AC AAR21944;
 XX
 DT 25-JUN-1992 (first entry)
 XX
 DE Substance P [Pro 11].
 XX
 KM Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's syndrome;
 KM hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 OS
 PN WO9202248-A.
 XX
 PD 20-FEB-1992.
 XX
 PF 27-JUL-1990; 90US-00559173.
 XX
 PR 27-JUL-1990; 90US-00559173.
 XX
 PA (CHIL-) CHILDRENS MED CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI; 1992-079804/10.
 XX
 PT Treatment of neuronal accumulation of beta-amyloid - using tachykinin
 PT agonists e.g. substance P, physalaemin and neurokinin B, for treating
 PT Alzheimer's disease, downs syndrome, etc.
 XX
 PS Claim 10; Page 21; 35pp; English.
 CC The peptide is the tachykinin agonist substance P with a Proline residue
 CC substituted at position 11. The peptide was synthesised by standard solid
 CC phase synthesis. Neuronal accumulation of beta-amyloid may be treated by
 CC administration of tachykinin agonists. The peptide can reduce the

CC neurotoxic effects of a beta-amyloid related polypeptide on cultured
 CC neurons. The peptide and its analogues are useful for controlling
 CC diseases characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome. See also AAR21932-75
 XX
 SQ Sequence 11 AA;
 Query Match 48.4%; Score 30; DB 2; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 2;
 QY 2 PQNPFYKLP 9
 ||:|:
 4 PQQFGLP 11
 DB
 RESULT 14
 AAR92718
 ID AAR92718 standard; peptide; 11 AA.
 XX
 AC AAR92718;
 XX
 DT 20-MAR-2003 (revised)
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #64.
 XX
 KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KM hereditary cerebral haemorrhage; non-inherited congenital angiodysplasia.
 XX
 OS Homo sapiens.
 OS
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 29-JUL-1991; 91US-00737371.
 XX
 PR 27-JUL-1990; 90US-00559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells.
 XX
 PS Disclosure; Col 37-38; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiodysplasia with cerebral
 CC haemorrhage. AAR92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments. (Updated on 20-MAR-2003 to correct PF
 CC field.)
 XX
 SQ Sequence 11 AA;
 Query Match 48.4%; Score 30; DB 2; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 2;
 QY 2 PQNPFYKLP 9
 ||:|:
 4 PQQFGLP 11
 DB

RESULT 15
 ABR84651
 ID ABR84651 standard; peptide; 15 AA.
 XX
 AC ABR84651;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human antigenic SGA-1M peptide fragment #1.
 XX
 KM Human, SGA-1M; cancer; antigen; cytostatic; breast cancer;
 KM ovarian cancer; skin cancer; lymphoid system; thyroid cancer;
 KM pancreatic cancer; stomach cancer; lung cancer.
 XX
 OS Homo sapiens.
 XX
 FN WO2003065873-A2.
 XX
 PD 14-AUG-2003.
 XX
 PF 03-FEB-2003; 2003WO-US002974.
 XX
 PR 01-FEB-2002; 2002US-0353826P.
 XX
 PA (SEAT-) SEATTLE GENETICS INC.
 XX
 PI Petroziello JM, Law C, Wahl AF;
 XX
 DR WPI; 2003-731465/69.
 XX
 PT Diagnosing or staging cancer in a subject by detecting or measuring a SGA
 PT -1M gene product in a sample derived from the subject.
 XX
 PS Example; Page 184; Opp; English.
 CC The present invention relates to a method of diagnosing or staging cancer
 CC in a subject, which comprises detecting or measuring a SGA-1M gene
 CC product in a sample derived from the subject, where elevated levels of
 CC the SGA-1M gene product compared to a non-cancerous sample or
 CC predetermined standard value for a non-cancerous sample indicates the
 CC presence or advanced stage of cancer in the subject. Also provided is the
 CC human SGA-1M gene, its two open reading frames and the two encoded
 CC proteins. The method is useful for diagnosing or staging cancer in a
 CC subject, and comprises detecting or measuring a SGA-1M gene product in a
 CC sample derived from the subject, where elevated levels of the SGA-1M gene
 CC product compared to a non-cancerous sample or predetermined standard
 CC value for a non-cancerous sample indicates the presence or advanced stage
 CC of cancer. The SGA-1M gene product is also useful for vaccinating a
 CC subject against cancer. It is particularly linked to breast, ovarian,
 CC skin, thyroid, pancreatic, stomach and lung cancer, and cancers of the
 CC lymphoid system. The present sequence is a fragment of the protein of the
 CC invention
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 48.4%; Score 30; DB 7; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPONFYKLPQ 10
 ||:|
 DB 5 MPETFSNLPR 14

XX
 DE Epstein Barr virus EBNA-2 p276-290.
 XX
 KM Adeno-associated virus; vector; liposome; transfection; dendritic cell;
 KM EBV; EBNA-2; adoptive immunotherapy; tumour associated antigen.
 XX
 OS Human herpesvirus 4.
 XX
 FN WO9703703-A1.
 XX
 PD 06-FEB-1997.
 XX
 PF 19-JUL-1996; 96WO-US012012.
 XX
 PR 21-JUL-1995; 95US-0001312P.
 PR 01-NOV-1995; 95US-0007184P.
 PR 01-DEC-1995; 95US-00566286.
 XX
 PA (RHON) RHONE POULENC RORER PHARM INC.
 XX
 PI Philip R, Lebikowski JS;
 XX
 DR WPI; 1997-145208/13.
 XX
 PT Adeno-associated virus:liposome complexes for transfecting dendritic
 PT cells - for inducing immune response, useful for treating e.g. neoplasia
 PT or infections.
 XX
 PS Example 5; Page 58; 134pp; English.
 CC Tumour associated antigens (AAW13660-61, AAW0878-903) can be loaded into
 CC dendritic cells and used to induce antitumour immunity. Alternatively,
 CC the dendritic cells are transfected with adeno associated virus plasmid
 CC DNA (which includes DNA encoding the tumour associated antigen) complexed
 CC with cationic liposomes. The antigen loaded or transfected dendritic
 CC cells can be used to generate tumour antigen-specific cytotoxic T
 CC lymphocytes for use in adoptive immunotherapy in a patient having the
 CC corresponding tumour. A suitable antigen comprises amino acids 276-290
 CC (AAW00884) of Epstein Barr virus EBNA-2. (Updated on 27-AUG-2003 to
 CC correct OS field.)
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 46.8%; Score 29; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 POFYKLPQM 11
 ||:|
 DB 4 PTVFYNIIPM 13

RESULT 17
 ABB99000
 ID ABB99000 standard; peptide; 15 AA.
 XX
 AC ABB99000;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Phosphoenol pyruvate dependent glycosylphosphate transferase 9.02 peptide.
 XX
 KM Phosphoenol pyruvate dependent glycosylphosphate transferase 9.02; cancer;
 KM cytostatic; HIV infection; anti-HIV; enzyme.
 XX
 OS Unidentified.
 XX
 FN CN1363668-A.
 XX
 PD 14-AUG-2002.
 XX
 PF 05-JAN-2001; 2001CN-00105052.
 XX

PR 05-JUN-2001; 2001CN-00105052.
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-751782/82.
XX
XX Poly(amide-phosphoenolpyruvate-dependent glycosylphosphate transferase
PT 9.02 and polynucleotide for coding it.
XX
XX
XX Example 5; Page 20 (disclosure); 33pp; Chinese.
XX
XX The present invention relates to phosphoenol pyruvate dependent
CC glycosylphosphate transferase 9.02 (see ABB98999). The protein can be
CC used for treating diseases such as cancer and HIV infection. The present
CC sequence is an N-terminal peptide fragment of the protein, which was used
CC in an example from the invention
XX
XX Sequence 15 AA;
SQ
Query Match 46.8%; Score 29; DB 5; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 MPONFYKLPQ 10
DB 1 MPANFYQIVQ 10
RESULT 18
AAE20383
ID AAE20383 standard; peptide; 15 AA.
AC AAE20383;
XX
XX 07-AUG-2003 (revised)
DT 18-JUN-2002 (first entry)
XX
XX Epstein-Barr virus tumour associated antigen (TAA) peptide epitope #2.
DE
XX Gene-delivery compound; single-chain binding polypeptide; SCBP;
KW nucleic acid-binding moiety; NABM; lipid-associating moiety; IAM;
KW gene therapy; targeted gene delivery; tumour associated antigen; TAA;
KW epitope.
XX
XX Cercopithecine herpesvirus 15.
OS
XX WO200200914-A2.
PN
XX 03-JAN-2002.
PD
XX 25-JUN-2001; 2001WO-US020182.
PF
XX 23-JUN-2000; 2000US-0213653P.
PR
XX
XX (HUST/) HUSTON J S.
PA (WILS/) WILS P.
PA (QUAN/) QUAN Z.
PA (LAUR/) LAURENT O.
PA (MARASCO/) MARASCO W A.
PA (SCHER/) SCHERMAN D.
XX
XX Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
PI WPI; 2002-268789/31.
DR
XX
XX Gene-delivery compound for targeted gene delivery, comprises single-chain
PT binding polypeptide having effector segment with cysteinyl residue and
PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
PT residue.
XX
XX Disclosure; Page 28; 96pp; English.

XX
XX The invention relates to gene-delivery compound comprising a single-chain
CC binding polypeptide (SCBP) having at least one effector segment having a
CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
CC associating moiety (IAM) coupled to SCBP by the residue. Gene-delivery
CC compound is useful for targeted gene delivery for treating diseases by
CC gene therapy. The present sequence is Epstein-Barr virus tumour
CC associated antigen (TAA) peptide epitope. TAA may be targeted by the
CC SCBP of the present invention. (Updated on 07-AUG-2003 to correct OS
CC field.)
XX
XX Sequence 15 AA;
SQ
Query Match 46.8%; Score 29; DB 5; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 POFYFYKLPQM 11
DB 4 PTVFYNIIPM 13
RESULT 19
ABB08787
ID ABB08787 standard; peptide; 15 AA.
AC ABB08787;
XX
XX 22-MAY-2002 (first entry)
DT
XX
XX Human glycosyl-phosphatidyl inositol glycan F10.89 peptide.
DE
XX Human; glycosyl-phosphatidyl inositol glycan F10.89;
KW embryonic development malformation; immunological dysfunction;
KW hormonal metabolic disturbance.
XX
XX Homo sapiens.
OS
XX CN1326960-A.
PN
XX 19-DEC-2001.
PD
XX 05-JUN-2000; 2000CN-00116326.
PF
XX 05-JUN-2000; 2000CN-00116326.
PR
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX WPI; 2002-206969/27.
DR
XX
XX New polypeptide-glycosyl-phosphatidyl inositol glycan F10.89 and
PT polynucleotide encoding the polypeptide.
PT
XX
XX Example 5; Page 20 (disclosure); 35pp; Chinese.
PS
XX The invention relates to human glycosyl-phosphatidyl inositol glycan
CC F10.89, the polynucleotide encoding this polypeptide and DNA recombinant
CC processes to produce the polypeptide. The present invention also
CC discloses the method of applying the polypeptide in treating various
CC diseases, such as embryonic development malformation, immunological
CC dysfunction disease and hormonal metabolic disturbance disease. The
CC present invention also discloses the antagonist for resisting the
CC polypeptide and its treatment effect. The present invention also
CC discloses the application of the polynucleotide for encoding glycosyl-
CC phosphatidyl inositol glycan F10.89. The present sequence is that of the
CC N-terminal peptide from human glycosyl-phosphatidyl inositol glycan
CC F10.89, useful in examples of the invention
XX
XX Sequence 15 AA;
SQ
Query Match 46.8%; Score 29; DB 5; Length 15;

Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 FYKLPPOM 11
|:|:|
DB 9 FVKLPOM 15

RESULT 20

ABR44016
ID ABR44016 standard; peptide; 15 AA.

XX ABR44016;

DT 04-AUG-2003 (first entry)

DE E. coli TNase N-terminal fragment.

KM Bacterium; L-cysteine; cystathionine-beta-lyase; drug; cosmetic; food;
TNase; enzyme.

XX Escherichia coli.

XX EP1298200-A2.

XX 02-APR-2003.

PF 17-SEP-2002; 2002RP-00020588.

PR 28-SEP-2001; 2001JP-00302008.

PA (AJIN) AJINOMOTO CO INC.

PI Takagi H, Wada M, Nakamori S;

DR WPI; 2003-423253/40.

XX New bacterium belonging to genus Escherichia which is modified so that

PT cystathionine-beta-lyase activity is reduced/eliminated, useful for

PT producing L-cysteine useful in the field of drugs, cosmetics and foods.

PS Example 1; Page 10; 28pp; English.

CC The invention relates to a bacterium belonging to the genus Escherichia

CC which has the ability to produce L-cysteine and which is modified so that

CC cystathionine-beta-lyase activity is reduced or eliminated. The bacterium

CC is useful for producing L-cysteine which is useful in the field of drugs,

CC cosmetics and foods. The present sequence represents an E. coli TNase N-

CC terminal fragment

CC Sequence 15 AA;

QY 3 ONPYKLPPOM 11
|:|:|
DB 2 ENFKLPPOM 10

RESULT 21

AA08887
ID AA08887 standard; protein; 7 AA.

XX AA08887;

DT 19-AUG-1999 (first entry)

DE C. lindemuthianum chitin deacetylase C-terminal fragment.

KM Chitin deacetylase; N-acetyl aminosugar; hypotensive; antibacterial;

KM anti-osteoporotic; antitumour; cholesterol reduction; chitin; chitosan;

KW food; animal feed; thickener; blood pressure; treatment; osteoporosis;

KM gout; hyperurinaemia; Bifidus bacteria.

OS Colletotrichum lindemuthianum.

XX DE19810349-A1.

XX 10-JUN-1999.

XX 10-MAR-1998; 98DE-01010349.

XX 02-DEC-1997; 97JP-00345737.

XX (NORO) NAT FOOD RES INST MIN AGRIC.

XX Hamamatsu S, Hayashi K, Tokuyasu K, Mori Y;

XX WPI; 1999-338951/29.

XX Nucleic acid encoding bacterial chitin deacetylase useful for generating

XX chitosan.

XX Example 1; Page 5; 14pp; German.

XX This invention describes a novel protein and its encoding nucleic acid

XX deacetylase activity on the N-acetyl group of N-acetyl aminosugars which

XX has been isolated from Colletotrichum lindemuthianum. The protein of the

XX invention has hypotensive, antibacterial, anti-osteoporotic, antitumour

XX and cholesterol reducing activity. The products of the invention can be

XX used to convert chitin to chitosan. Chitosan is used in foods or animal

XX feeds, particularly as a thickener, and in pharmaceuticals, to reduce

XX cholesterol levels or blood pressure, in treatment of gout,

XX hyperurinaemia and osteoporosis; for stimulating growth of Bifidus

XX bacteria while suppressing Escherichia coli and Clostridium perfringens,

XX and as antitumour agent. The protein of the invention is also used to

XX produce chitosan oligosaccharides from chitin oligosaccharides and for

XX removing N-acetyl from other amino sugars, making it suitable for

XX synthesis of new sugar chains

XX Sequence 7 AA;

QY 2 PGNFYK 7
|:|:|
DB 1 PGNFYK 6

RESULT 22

AA48162
ID AA48162 standard; peptide; 9 AA.

XX AA48162;

DT 01-DEC-1999 (first entry)

DE Immunogenic peptide having a human leukocyte antigen binding motif #2773.

KM Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;

KM immune response; T cell activation; major histocompatibility complex;

KM cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;

KM prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;

KM vaccine; immunisation.

XX Synthetic.

XX Homo sapiens.

XX WO9945954-A1.

XX 16-SEP-1999.

PF 13-MAR-1998; 98WO-US005039.
 XX
 PR 13-MAR-1998; 98WO-US005039.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Kubo RT, Sidney J, Cells B, Grey HM, Southwood S;
 XX WPI, 1999-551214/46.
 DR
 XX
 PT New immunogenic peptides with HLA binding motif, useful in treatment and
 PT diagnosis of cancers and viral diseases.
 XX
 PS Claim 1; Page 140; 150pp; English.
 XX
 CC AAY5390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above
 CC
 SQ Sequence 9 AA;
 QY
 Query Match 45.2%; Score 28; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 2 PONYKYL 8
 2 PONYLYTL 8
 RESULT 23
 ADK23699
 ID ADK23699 standard; peptide; 9 AA.
 XX
 AC ADRK23699;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human 98P4B6 derived motif-bearing CTL peptide epitope #6.
 XX
 KW human; 98P4B6; STEAP-2; cancer; breast; colon; lung; kidney; prostate;
 KW gene therapy; genetic abnormality; transgenic; knockout animal;
 KW cytostatic; epitope.
 XX
 OS Homo sapiens.
 XX
 PN WO2003087306-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 04-APR-2003; 2003WO-US010462.
 XX
 PR 05-APR-2002; 2002US-0370387P.
 PR 06-JUN-2002; 2002US-00165044.
 PR 20-DEC-2002; 2002US-0435480P.
 XX

PA (AGEN-) AGENSYS INC.
 XX
 PI Challita-Bid PM, Raitano AB, Paris M, Ge W, Jakobovits A;
 XX
 DR WPI; 2003-903158/82.
 XX
 PT A composition comprising 98P4B6 proteins and nucleic acid molecules for
 PT detecting, preventing, prognosing and/or treating cancers that express
 PT 98P4B6 (e.g. pancreatic, prostatic or lung cancer).
 XX
 PS Claim 1; Page 143; 616pp; English.
 XX
 CC This invention relates to a novel human gene 98P4B6 (also known as STEAP-
 CC 2, six transmembrane epithelial antigen of prostate-2) located on
 CC chromosome 7q21 and the encoded protein and variants derived thereof.
 CC Specifically, it refers to the expression pattern of this gene in adult
 CC normal tissues and its aberrant over-expression in various cancers
 CC including breast, colon, lung, kidney and prostate. The present invention
 CC describes compositions and methods useful for detecting, preventing,
 CC prognosing and/or treating cancers that express 98P4B6. Furthermore, the
 CC polynucleotide can be used for gene therapy purposes, for monitoring
 CC genetic abnormalities and for generating transgenic or 'knockout'
 CC animals, which can be useful for the development and screening of
 CC therapeutically useful reagents. The encoded proteins may also be used in
 CC generating antibodies and vaccines, as well as in identifying ligands and
 CC cellular constituents that bind to 98P4B6 gene products. Accordingly,
 CC these compositions exhibit cytostatic activities. This peptide sequence
 CC is a motif bearing CTL peptide epitope derived from a human 98P4B6
 CC protein variant of the invention.
 CC
 SQ Sequence 9 AA;
 QY
 Query Match 45.2%; Score 28; DB 7; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 4 NPYKLP 9
 3 DPKLP 8
 RESULT 24
 ADK24080
 ID ADK24080 standard; peptide; 10 AA.
 XX
 AC ADRK24080;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human 98P4B6 derived motif-bearing CTL peptide epitope #387.
 XX
 KW human; 98P4B6; STEAP-2; cancer; breast; colon; lung; kidney; prostate;
 KW gene therapy; genetic abnormality; transgenic; knockout animal;
 KW cytostatic; epitope.
 XX
 OS Homo sapiens.
 XX
 PN WO2003087306-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 04-APR-2003; 2003WO-US010462.
 XX
 PR 05-APR-2002; 2002US-0370387P.
 PR 06-JUN-2002; 2002US-00165044.
 PR 20-DEC-2002; 2002US-0435480P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Challita-Bid PM, Raitano AB, Paris M, Ge W, Jakobovits A;
 XX
 DR WPI; 2003-903158/82.
 XX

PT A composition comprising 98P4B6 proteins and nucleic acid molecules for
 PT detecting, preventing, prognosing and/or treating cancers that express
 PT 98P4B6 (e.g. pancreatic, prostatic or lung cancer).

PS Claim 1; Page 146; 616pp; English.

XX This invention relates to a novel human gene 98P4B6 (also known as STEAP-
 CC 2, six transmembrane epithelial antigen of prostate-2) located on
 CC chromosome 7q21 and the encoded protein and variants derived thereof.
 CC Specifically, it refers to the expression pattern of this gene in adult
 CC normal tissues and its aberrant over-expression in various cancers
 CC including breast, colon, lung, kidney and prostate. The present invention
 CC describes compositions and methods useful for detecting, preventing,
 CC prognosing and/or treating cancers that express 98P4B6. Furthermore, the
 CC polynucleotide can be used for gene therapy purposes, for monitoring
 CC genetic abnormalities and for generating transgenic or 'knockout'
 CC animals, which can be useful for the development and screening of
 CC therapeutically useful reagents. The encoded proteins may also be used in
 CC generating antibodies and vaccines, as well as in identifying ligands and
 CC cellular constituents that bind to 98P4B6 gene products. Accordingly,
 CC these compositions exhibit cytostatic activities. This peptide sequence
 CC is a motif bearing CTL peptide epitope derived from a human 98P4B6
 CC protein variant of the invention.

SQ Sequence 10 AA;

Query Match 45.2%; Score 28; DB 7; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.5e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFYKLP 9
 :|||:-|
 Db 3 DFYKIP 8

RESULT 25

ADK24948
 ID ADK24948 standard; peptide; 10 AA.

AC ADK24948;

DT 06-MAY-2004 (first entry)

DE Human 98P4B6 derived motif-bearing CTL peptide epitope #1058.

XX human; 98P4B6; STEAP-2; cancer; breast; colon; lung; kidney; prostate;
 KW gene therapy; genetic abnormality; transgenic; knockout animal;
 KW cytostatic; epitope.

XX Homo sapiens.

OS Homo sapiens.

PN WO2003087306-A2.

PD 23-OCT-2003.

PF 04-APR-2003; 2003WO-US010462.

PR 05-APR-2002; 2002US-0370387P.

PR 06-JUN-2002; 2002US-00165044.

PR 20-DEC-2002; 2002US-0435480P.

PA (AGEN-) AGENSYS INC.

PI Challita-Eid PM, Raitano AB, Faris M, Ge W, Jakobovits A;

DR WPI; 2003-903158/82.

PT A composition comprising 98P4B6 proteins and nucleic acid molecules for
 PT detecting, preventing, prognosing and/or treating cancers that express
 PT 98P4B6 (e.g. pancreatic, prostatic or lung cancer).

PS Claim 1; Page 152; 616pp; English.

CC This invention relates to a novel human gene 98P4B6 (also known as STEAP-
 CC 2, six transmembrane epithelial antigen of prostate-2) located on
 CC chromosome 7q21 and the encoded protein and variants derived thereof.
 CC Specifically, it refers to the expression pattern of this gene in adult
 CC normal tissues and its aberrant over-expression in various cancers
 CC including breast, colon, lung, kidney and prostate. The present invention
 CC describes compositions and methods useful for detecting, preventing,
 CC prognosing and/or treating cancers that express 98P4B6. Furthermore, the
 CC polynucleotide can be used for gene therapy purposes, for monitoring
 CC genetic abnormalities and for generating transgenic or 'knockout'
 CC animals, which can be useful for the development and screening of
 CC therapeutically useful reagents. The encoded proteins may also be used in
 CC generating antibodies and vaccines, as well as in identifying ligands and
 CC cellular constituents that bind to 98P4B6 gene products. Accordingly,
 CC these compositions exhibit cytostatic activities. This peptide sequence
 CC is a motif bearing CTL peptide epitope derived from a human 98P4B6
 CC protein variant of the invention.

SQ Sequence 10 AA;

Query Match 45.2%; Score 28; DB 7; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.5e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFYKLP 9
 :|||:-|
 Db 4 DFYKIP 9

RESULT 26

AAR28392
 ID AAR28392 standard; peptide; 11 AA.

AC AAR28392;

DT 25-MAR-2003 (revised)

DT 18-MAR-1993 (first entry)

DE Bradykinin receptor antagonist CT-0008.

XX Bradykinin receptor antagonist; heterodimer; higher oligomer; potency;
 KW duration; CP-0088; burns; migraine; shock CNS injury; asthma; rhinitis;
 KW premature labour; inflammatory arthritis; homodimer;

XX inflammatory bowel disease.

OS Synthetic.

XX key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /label= N1e

PN WO9217201-A1.

PD 15-OCT-1992.

PF 30-MAR-1992; 92WO-US002431.

PR 01-APR-1991; 91US-00677391.

PR 27-MAR-1992; 92US-00859582.

PA (CORT-) CORTECH INC.

PI Cheronis JC, Blodgett JK, Whalley ET, Eubanks SR, Allen LG;
 PI Nguyen KT;

DR WPI; 1992-365995/44.
 XX Bradykinin antagonists comprising linked bradykinin antagonist chains -
 PT are for treatment of post-operative pain, asthma and aseptic shock.
 XX
 PS Disclosure; Page 76; 109pp; English.
 XX
 CC The sequence given is a bradykinin receptor antagonist which can form
 CC homo- or heterodimers or higher oligomers. It demonstrates greater
 CC potency and/or duration of action than the parent peptide itself.
 CC Bradykinin receptors antagonists such as this can be used in the
 CC treatment of burns, perioperative pain, migraine and other forms of pain,
 CC shock CNS injury, asthma, rhinitis, premature labour, inflammatory
 CC arthritis, inflammatory bowel disease etc. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 11 AA;
 Query Match 45.2%; Score 28; DB 2; Length 11;
 Best Local Similarity 71.4%; Pred. No. 3.8e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PONEFKL 8
 DB 4 PONEFWL 10
 RESULT 27
 AA93148
 ID AA93148 standard; peptide; 12 AA.
 XX
 AC AA93148;
 XX
 DT 06-DEC-2000 (first entry)
 XX
 DE Rat G-protein coupled receptor protein rGRT022-derived peptide #1.
 XX
 KW G-protein coupled receptor; human; bovine; nervous system disorder; rat;
 KM mouse; somatostatin excretion.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 12
 FT /note="C-terminal amide"
 XX
 PN WO200029441-A1.
 XX
 PD 25-MAY-2000.
 XX
 PP 11-NOV-1999; 99WO-JP006283.
 XX
 PS 13-NOV-1998; 98JP-00323759.
 PR 08-MAR-1999; 99JP-00060030.
 PR 14-APR-1999; 99JP-00106812.
 PR 14-JUN-1999; 99JP-00166672.
 PR 04-AUG-1999; 99JP-00224640.
 PR 14-SEP-1999; 99JP-00259818.
 XX
 CC (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Watanabe T, Kikuchi K, Terao Y, Shintani Y, Hinuma S, Fukushima S;
 PI Fujii R, Hosoya M, Kitada C;
 XX
 DR WPI; 2000-387747/33.
 XX
 PT G protein coupled receptor protein and antibodies to it for treatment and
 PT diagnosis of nerve diseases.
 XX
 PS Example 7; Page 128; 184pp; Japanese.
 XX
 CC The invention relates to the isolation of novel G-protein coupled
 CC receptor (GPCR) genes and their encoded proteins. This sequence

CC 'represents a peptide derived from the rat GPCR protein clone rGRT022 and
 CC was used in an acidification rate assay. The DNAs and proteins are used
 CC for the treatment, prevention and diagnosis of disorders of the nervous
 CC system. The proteins and its fragments are also promoters of somatostatin
 CC excretion
 XX
 SQ Sequence 12 AA;
 Query Match 45.2%; Score 28; DB 3; Length 12;
 Best Local Similarity 55.6%; Pred. No. 4.2e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPONEFKLP 9
 DB 1 MPHSFANLP 9
 RESULT 28
 AAB60026
 ID AAB60026 standard; peptide; 12 AA.
 XX
 AC AAB60026;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Internalising peptide SEQ ID NO: 41.
 XX
 KW Internalising peptide; transport; apoptosis; arthritis; cancer;
 KM stem cell; cell differentiation; immune response stimulation;
 KW HIV vaccine.
 XX
 OS Synthetic.
 XX
 PN WO200115511-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 31-AUG-2000; 2000WO-US024034.
 XX
 PR 01-SEP-1999; 99US-0151980P.
 PR 13-MAR-2000; 2000US-0188944P.
 XX
 PA (UVP1-) UNIV PITTSBURGH.
 XX
 PI Robbins PD, Mi Z, Frizzell R, Glorioso JC, Gambotto A;
 XX
 DR WPI; 2001-273309/28.
 XX
 PT Peptides that facilitate uptake and cytoplasmic and/or nuclear transport
 PT of proteins, DNA and viruses, useful, e.g. for facilitating uptake of
 PT antigens in immunogenic compositions.
 XX
 PS Claim 1; Page 122; 129pp; English.
 XX
 CC The present invention provides the sequences of 75 peptides which
 CC facilitate the uptake and transport of viruses, proteins and nucleic
 CC acids. These internalising peptides can be used for transport into the
 CC cytoplasm or the nucleus. They are useful for facilitating uptake into
 CC the cell, inducing apoptosis, for example in the treatment of arthritis
 CC and cancer, to expand a population of stem cells or differentiated cells,
 CC to stimulate cell differentiation, facilitate the integration of AA9 into
 CC the genome of a cell, and to stimulate an immune response, for example in
 CC the case of a HIV vaccine. The present sequence is one of the peptides of
 CC the invention
 XX
 SQ Sequence 12 AA;
 Query Match 45.2%; Score 28; DB 4; Length 12;
 Best Local Similarity 44.4%; Pred. No. 4.2e+02;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 3 QNPFYKLPM 11
 :||:|::

Db 4 KNFFWLPEL 12

RESULT 29
AAG67753
ID AAG67753 standard; peptide; 12 AA.

AC AAG67753;
XX
DT 10-DEC-2001 (first entry)
XX
DE Amino acid sequence of synthetic peptide.
XX
KW Human; prolactin secretion; hypovarianism; sperm development;
KW osteoporosis; lactation disorder; hypothyroidism; kidney failure;
KW menopause; hyperprolactinemia; pituitary tumor; diencophalon tumour;
KW menstrual disorder; stress; autoimmune disease; prolactinoma; sterility;
KW impotence; amenorrhea; lactorrhea; hyperpituitarism;
KW Sheehan's syndrome Chaiti-Frommel syndrome; Argonz-del Castillo syndrome;
KW Liphoma; Forbes-Albright syndrome; spermatogenesis disorder.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 12 /note="amide attached to residue"
XX
PN WO200166134-A1.
XX
PD 13-SEP-2001.
XX
PF 06-MAR-2001; 2001WO-JP001716.
XX
PR 06-MAR-2000; 2000JP-00065752.
PR 07-DEC-2000; 2000JP-00378001.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Matsumoto Y, Watanabe T, Hinuma S, Habata Y, Yoshida H;
DR WPI; 2001-596812/67.
XX
PT New polypeptide, useful as a vasotrophic, tranquilizing, immunosuppressive
PT and gynecological agent comprises the prolactin secretion regulator.
XX
PS Example 1; Page 94; 180pp; Japanese.
XX
CC The specification describes a human polypeptide which is a prolactin
CC secretion regulating agent. The prolactin secretion regulating agent
CC polypeptide and polynucleotide are used for the treatment and prevention
CC of hypovarianism, sperm under development, osteoporosis, menopause,
CC lactation disorders, hypothyroidism, kidney failure, hyperprolactinemia,
CC pituitary tumor, diencophalon tumour, menstrual disorders, stress,
CC autoimmune disease, prolactinoma, sterility, impotence, amenorrhea,
CC lactorrhea, hyperpituitarism, Chaiti-Frommel syndrome, Argonz-del Castillo
CC syndrome, Forbes-Albright syndrome, Liphoma, Sheehan's syndrome and
CC spermatogenesis disorders. The present peptide was used in the course of
CC the invention
XX
SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 4; Length 12;
Best Local Similarity 55.6%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9
| : | | |
| : | | |
DB 1 MPHSFANLP 9

RESULT 30
ABU60819
ID ABU60819 standard; peptide; 12 AA.

XX AC ABU60819;
XX
DT 06-MAY-2003 (first entry)
XX
DE Peptide production by gene recombination associated peptide #3.
XX
KW Peptide production; low-molecular peptide; Kiss-1; GPR8 ligand;
KW gene recombination.
XX
OS Homo sapiens.
XX
PN WO200292829-A1.
XX
PD 21-NOV-2002.
XX
PF 16-MAY-2002; 2002WO-JP004735.
XX
PR 17-MAY-2001; 2001JP-00147341.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Nishimura O, Suenaga M, Ito T, Kitada C;
DR WPI; 2003-129302/12.
XX
PT Process for producing peptides e.g. Kiss-1 peptide and GPR8 ligand for
PT subsequent applications by gene recombination technique through tandem
PT repeats to provide precursor protein with specific cleavage sites.
XX
PS Disclosure; Page 52; 87pp; Japanese.
XX
CC The invention describes a method of producing a peptide comprising the
CC excision of the N and C-terminals of a target peptide with enzymes or
CC chemically through the attached cleavage sites repeated by ligation in a
CC precursor protein. The method is for producing (low-molecular) peptides
CC e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by the
CC gene recombination technique through tandem repeats to provide a
CC precursor protein with specific cleavage sites. With this method, peptide
CC production can be carried out easily to provide large quantities of the
CC required peptides. This is the amino acid sequence of a peptide
CC associated with the peptide production method of the invention
XX
SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 6; Length 12;
Best Local Similarity 55.6%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9
| : | | |
| : | | |
DB 1 MPHSFANLP 9

RESULT 31
ABP97049
ID ABP97049 standard; peptide; 12 AA.

AC ABP97049;
XX
DT 23-JUN-2003 (first entry)
XX
DE Human RFRP-3 peptide SEQ ID NO:39.
XX
KW RFRP-3; prolactin secretion promoter; secretion; prolactin; GPCR;
KW G protein-coupled receptor; gynaecological; osteopathic; cytostatic;
KW immunomodulator; antiinfertility; vasotrophic; hypovarianism; menopause;
KW prolactin secretion-related disease; spermatoc hypoplasia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 12

/label= amidated

FT XX WO2003018795-A1.
 XX XX 06-MAR-2003.
 XX XX 22-AUG-2002; 2002WO-JP008466.
 XX XX 24-AUG-2001; 2001JP-00254826.
 PR (TAKEDA) TAKEDA CHEM IND LTD.
 PA
 XX Hinuma S, Yoshida H, Habata Y, Hosoya M, Kikada C;
 PI
 DR WPI: 2003-268422/26.
 DR N-PSDB; ACC49304.
 CC Novel RFRP-3 peptides and encoded DNAs, applicable in diagnosis of and
 PT developing drugs for treating prolactin secretion-related diseases e.g.
 PT hypovarianism, spermatoc hypoplasia and menopause.
 CC Example; Page 107, 197pp; Japanese.
 XX
 CC The present invention describes RFRP-3 peptides. RFRP-3 is a G protein-
 CC coupled receptor (GPCR) which is a prolactin secretion promoter. RFRP-3
 CC has gynaecological, osteopathic, cytostatic, immunomodulator, vasotropic
 CC and antiinfective activities. The RFRP-3 peptides and their encoded
 CC DNAs can be used in the diagnosis of and developing drugs for treating
 CC prolactin secretion-related diseases e.g. hypovarianism, spermatoc
 CC hypoplasia and menopause. The developed drugs are safe with low toxicity.
 CC The present sequence represents a human RFRP-3 peptide, which is used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 12 AA:

Query Match 45.2%; Score 28; DB 6; Length 12;
 Best Local Similarity 55.6%; Pred. No. 4.2e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 MFQNFYKLP 9
 ||: ||
 DB 1 MPHSPANLP 9

RESULT 32

ABP54416
 ID ABP54416 standard; peptide; 12 AA.
 XX
 AC ABP54416;
 XX
 DT 21-JAN-2003 (first entry)

XX Human RF amide peptide related sequence SEQ ID NO:3.
 DE
 XX
 XX
 KW Rf amide peptide; cytostatic; antiinfective; prolactin-related disease;
 KW hyperprolactinemia; infertility; Chiari-Frommel syndrome; cancer;
 KW Forbes-Albright syndrome.
 KW
 XX Homo sapiens.
 OS
 XX WO200246405-A1.
 PN
 XX 13-JUN-2002.
 PD
 XX 06-DEC-2001; 2001WO-JP010668.
 PF
 XX 07-DEC-2000; 2000JP-00373125.
 PR
 XX (TAKEDA) TAKEDA CHEM IND LTD.
 PA
 XX Suenaga M, Yamada T, Nishimura O,
 PI
 DR WPI: 2003-018538/01.

DR N-PSDB; ABQ83409.
 XX
 XX
 PT Producing an RF amide peptide for treating prolactin-related diseases,
 PT comprises obtaining a fusion protein or peptide using a transformant then
 PT cleaving the peptide bond in the amino acid side of a cysteine residue.
 XX
 XX
 PS Claim 6; Page 81; 100pp; Japanese.

CC The present invention describes a method for producing an RF amide
 CC peptide (I) which can be a partial peptide of a polypeptide selected from
 CC the amino acid sequences given in ABP5442 to ABP5447, by cleaving a
 CC peptide bond in the amino acid side of the cysteine residue of a fusion
 CC protein or polypeptide linked to the N-terminal of a protein or
 CC polypeptide with cysteine at its N-terminal and optionally an oxidisable
 CC methionine residue. (I) has cytostatic and antiinfective activities.
 CC The method can be used for producing a peptide which is used for
 CC preventing or treating prolactin-related diseases, e.g.
 CC hyperprolactinemia, infertility, Chiari-Frommel syndrome, Forbes-Albright
 CC syndrome and cancer. The method is used for large-scale industrial
 CC production of the peptide. The present sequence represents a specifically
 CC claimed peptide from the present invention
 CC
 XX
 SQ Sequence 12 AA:

Query Match 45.2%; Score 28; DB 6; Length 12;
 Best Local Similarity 55.6%; Pred. No. 4.2e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 MFQNFYKLP 9
 ||: ||
 DB 1 MPHSPANLP 9

RESULT 33

ADA88861
 ID ADA88861 standard; peptide; 12 AA.
 XX
 AC ADA88861;
 XX
 DT 20-NOV-2003 (first entry)

XX Internalised peptide pep35 SEQ ID NO:41.
 DE
 XX
 XX
 KW internalising peptide; cytostatic; antiinflammatory; immunomodulator;
 KW antiarthritic; cytoplasmic transport; nuclear transport;
 KW peptide-cargo complex; apoptosis; arthritic; tumour; differentiation;
 KW immune response; vaccine; inflammation; necrosis; transplantation;
 KW cystic fibrosis; lung inflammation; gene therapy.
 KW
 XX Synthetic.
 OS
 XX WO2003068942-A2.
 PN
 XX 21-AUG-2003.
 PD
 XX 12-FEB-2003; 2003WO-US004632.
 PF
 XX 13-FEB-2002; 2002US-00075869.
 PR
 XX (UVP1-) UNIV PITTSBURGH.
 PA
 XX Robbins PD, Mi Z, Fritzel R, Glorioso JC, Gambotto A, Mai JC;
 PI
 DR WPI: 2003-697526/66.
 DR
 XX New internalising peptides, useful for facilitating the delivery, uptake
 XX and cytoplasmic and/or nuclear transport of proteins, DNA or viruses into
 XX a target cell, for inducing apoptosis in arthritic or tumor cells, or in
 XX gene therapy.
 XX Example 3; Page 19; 171pp; English.
 PS
 CC The present invention describes an internalising peptide (I) comprising

CC any one of 14 fully defined amino acid sequences (designated PI-P14, see
CC ADA8896 to ADA8906, and ADA8917 to ADA8919). (1) has cytostatic,
CC antiinflammatory, immunomodulator and antiarthritic activities. The
CC internalising peptides are useful for facilitating the delivery, uptake
CC and cytoplasmic end/or nuclear transport of cargo, e.g. proteins, DNA or
CC viruses, into a target cell. The internalising peptides and peptide-cargo
CC complexes from the present invention are also useful for inducing
CC apoptosis in cells (e.g. arthritic cells or tumor cells), expanding a
CC population of stem cell or differentiated cells, stimulating the
CC differentiation of a population of stem cells, facilitating the
CC integration of adeno-associated virus DNA into the genome of a cell,
CC stimulating or eliciting an immune response in a subject, facilitating
CC the delivery of immunogens (e.g. vaccines), inhibiting the inflammatory
CC process, protecting tissue from apoptosis or necrosis during tissue
CC isolation prior to transplantation, facilitating transfer of proteins and
CC peptides to the lung for the treatment of cystic fibrosis or lung
CC inflammation, or in gene therapy. The present sequence represents a
CC peptide used in the exemplification of the present invention.

SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 7; Length 12;
Best Local Similarity 44.4%; Pred. NO. 4.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 QNFYKLPQM 11
: ||: ||:
DB 4 KNFFWLPPEL 12

RESULT 34

ADJ87494
ID ADJ87494 standard; peptide; 12 AA.

AC ADJ87494;

DT 06-MAY-2004 (first entry)

DE RFRP C-terminal peptide SEQ ID NO.13.

XX RFRP: myopathy; behavioural abnormality; RFRP: receptor protein OT77022;
XX neuroprotective; ophthalmological; cardiact; haemostatic;
XX immunostimulant; nephrotoxic; anabolic; anorectic; antidepressant;
XX tranquiliser; anticonvulsant; nootropic; muscular; adrenal dysfunction;
XX twitching; aggressive behaviour; abnormal gait; hyperthermia;
XX leukopenia; thrombopenia; increased voluntary behaviour;
XX muscle depression; neurasthenia; eye disease; kidney disease; myasthenia;
XX heart disease; blood disorder; appetite loss; obesity; depression;
XX anxiety; epilepsy; emotional disorder.

OS Unidentified.

PN WO2004014414-A1.

PD 19-FEB-2004.

PF 07-AUG-2003; 2003WO-JP010078.

PR 09-AUG-2002; 2002JP-00232684.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Kasuga H, Hinuma S, Miyashita H, Matsuoaka K;

PS WPI; 2004-191658/18.

XX The invention relates to novel compounds for treatment and prevention of
XX myopathy, adrenal dysfunction, leukopenia and behavioral abnormalities.
XX Disclosure; SEQ ID NO 13; 180pp; Japanese.

CC The invention relates to novel compounds for treatment and prevention of

CC diseases including myopathy and behavioural abnormalities contain RFRP or
CC receptor protein OT77022 or their partial peptides or DNA encoding them.
CC A compound of the invention has neuroprotective, ophthalmological,
CC cardiact, haemostatic, immunostimulant, nephrotoxic, anabolic,
CC anorectic, antidepressant, tranquiliser, anticonvulsant, nootropic, and
CC muscular-gen. activity. The compounds are useful for prevention,
CC treatment, diagnosis and investigation of diseases including myopathy,
CC adrenal dysfunction, twitching, aggressive behaviour, abnormal gait,
CC hyperthermia, leukopenia, thrombopenia, increased voluntary behaviour,
CC muscle depression, neurasthenia, eye disease, kidney disease, myasthenia,
CC heart disease, blood disorders, appetite loss, obesity, depression,
CC anxiety, epilepsy and emotional disorders. The present sequence is used
CC in the exemplification of the invention.

SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 8; Length 12;
Best Local Similarity 55.6%; Pred. NO. 4.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 MPQNFYKLP 9
: ||: ||:
DB 1 MPHSFANLP 9

RESULT 35

ADQ94363
ID ADQ94363 standard; peptide; 12 AA.

AC ADQ94363;

DT 23-SEP-2004 (first entry)

DE MrgC11 ligand screen related RFRP-1 peptide.

XX analgesic; G-protein-coupled receptor; MrgC11; pain perception; pain;
XX animal model; structure based ligand identification; diagnostic marker;
XX sensory perception; chronic pain; allodynia; hyperalgesia; glaucoma;
XX MrgC11 ligand screen.

OS Unidentified.

PN US2004121410-A1.

PD 24-JUN-2004.

PF 20-DEC-2002; 2002US-00327387.

PR 20-DEC-2002; 2002US-00327387.

PA (ANDE/) ANDERSON D J.

PA (DONG/) DONG X.

PA (ZYLK/) ZYLKA M.

PA (HANS/) HAN S.

PA (SIMO/) SIMON M.

PI Anderson DJ, Dong X, Zylka M, Han S, Simon M;

PS WPI; 2004-505997/48.

XX Novel G-protein coupled receptor called MrgC11 polypeptide, useful for
XX identifying agents that alter pain perception in mammal.

XX Example 2; Page 29; 40pp; English.

XX The invention describes an isolated G-protein-coupled receptor (MrgC11)
XX polypeptide (1) comprising a sequence of 322 amino acids fully defined in
XX the specification. (1) is useful for identifying a compound that can be
XX used to alter pain perception in a mammal, involves contacting test
XX compounds with at least a portion of (1), identifying the test compounds
XX that form complexes with (1), measuring the effect of the test compounds
XX identified in above step, in an animal model of pain, and identifying
XX test compounds that alter pain perception in the animal model as useful

CC in altering pain perception in a mammal, where (I) is a native MrgC11
CC polypeptide. The test compounds identified in the above method enhance or
CC decrease the perception of pain. The test compounds are chosen from
CC peptides, peptide mimetics, antibodies, small organic molecules and small
CC inorganic molecules, preferably binding peptides. The peptides are anchored to a
CC solid support by specifically binding an immobilised antibody. The test
CC compounds are contained in a cellular extract prepared from cells known
CC to express (I) or from dorsal root ganglion cells. (I) is useful for
CC identifying a compound that binds (I), and for identifying agonist or
CC antagonist of (I). (I) is useful as an antigen to raise polyclonal or
CC monoclonal antibodies, as a therapeutic target, target for structure
CC based ligand identification, and as a diagnostic marker for diagnosing
CC changes in sensory perception, in patients suffering from disease such as
CC chronic pain, allodynia, hyperalgesia and glaucoma. This is the amino
CC acid sequence of a peptide used in a screening of potential mouse G-
CC protein-coupled receptor MrgC11 ligands.

SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 8; Length 12;
Best Local Similarity 55.6%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 MPONFYKLP 9
||:|
DB 1 MPHSFANLP 9

RESULT 36

AAM97397
ID AAM97397 standard; peptide; 14 AA.

AAM97397;

24-JAN-2002 (first entry)

Human peptide #672 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KM neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KM amyloid protein; angiotensin; apoptosis related protein; cadherin;
KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KM complement related protein; cytochrome; kinase; cytokine; interferon;
KM interleukin; G-protein coupled receptor; thioesterase; inflammation;
KM multifactorial disease; autoimmune disease; infection;
KM nervous system disease.

XX Homo sapiens.

OS WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035498.

XX 28-DEC-1999; 99US-0173419P.

XX 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX Shimketa RA, Leach M,

XX WPI; 2001-465210/50.

XX polymorphic nucleic acids encoding e.g. amylase, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.

PS Disclosure; Page 3815; 4143pp; English.

XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,

CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesin, cytokines,
CC interleukin, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms

SQ Sequence 14 AA;

Query Match 45.2%; Score 28; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PONFYKL 8
||:|
DB 4 PONSXYKL 10

RESULT 37

AAR97958
ID AAR97958 standard; peptide; 15 AA.

AAR97958;

16-AUG-1996 (first entry)

Japan cedar pollen mature allergen Cry j II amino acids 436-450.

XX Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
KM Sugi pollinosis; diagnosis; treatment.

XX Cryptomeria japonica.

XX JP08047392-A.

XX 20-FEB-1996.

XX 07-NOV-1994; 94JP-00297840.

XX 05-NOV-1993; 93JP-00276773.

XX 26-MAY-1994; 94JP-00134868.

XX (MEIP) MEIJI MILK PROD CO LTD.

XX WPI; 1996-166249/17.

XX Japan cedar pollen allergen Cry j II epitope - comprises at least part of

XX specified 460 aminoacid protein.

XX Disclosure; Fig 5; 17pp; Japanese.

XX AAR97871-R97960 are overlapping peptides used for the epitope mapping of
CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
CC peptides of it are useful in the diagnosis, prevention and treatment of
CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant
CC regions of the allergen were identified using the overlapping peptides of
CC the full epitope derived from a Cry j II antigen-specific T cell line.
CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460
XX amino acid allergen are the most allergenic of the 90 peptides tested

SQ Sequence 15 AA;

Query Match 45.2%; Score 28; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

OY 1 MFQNFYKLPQ 10
 ||| : |||
 DB 5 MFOEY--PQ 12

RESULT 38

AAW03529
 ID AAW03529 standard; peptide; 18 AA.

XX AAW03529;

DT 17-FEB-1997 (first entry)

DE Transcriptional activation motif from human Oct-2 protein.

XX Chimaeric protein; transcription activation; cleavage;

KW transcription repression; gene therapy; therapeutic protein; phenotype;

KM prophylactic protein; gene expression.

OS Homo sapiens.

PN WO9620951-A1.

PD 11-JUL-1996.

PF 29-DEC-1995; 95WO-US016982.

PR 29-DEC-1994; 94US-00366083.

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Pomerantz JL, Sharp PA, Pabo CO;

DR WPI; 1996-33938/33.

PT New chimaeric protein contg. two or more DNA binding domains - opt. also

PT domain that activates or represses transcription or cleaves target DNA,

PT and DNA encoding them, useful in gene therapy.

PS Example 4; Page 18; 74pp; English.

CC New chimaeric proteins which selectively bind DNA with Kd 10(-8) or

CC better, comprise at least one composite DNA-binding region comprising a

CC continuous polypeptide chain of 2 or more component polypeptide domains,

CC at least 2 of these being mutually heterologous and additionally may also

CC comprise at least one transcription activating or repressing domain (TAD

CC or TRD), or a DNA cleaving domain (DCD), these domains being able to bind

CC to DNA sequences linked to the target DNA sequence. Genes encoding such

CC proteins are useful in gene therapy to correct/compensate for abnormal

CC gene expression, to direct expression of therapeutic/prophylactic

CC proteins or RNA and generally to modify cell phenotype. The chimaeric

CC proteins are used to express, repress or cleave the target. This

CC transcription activating domain was derived from the human Oct-2 protein

XX SQ Sequence 18 AA;

DT 18-JUN-1999 (first entry)

DE Activation domain of human CTF.
 XX Chimeric; transcription activator; DNA-binding domain; cytotoxicity;
 KW proliferation; immune response; inflammatory response; clotting; p55;
 KW hormonal regulation; activation domain; human.

OS Homo sapiens.

PN WO9910508-A1.

PD 04-MAR-1999.

PF 27-AUG-1997; 97WO-US015219.

PR 27-AUG-1997; 97WO-US015219.

PA (ARIA-) ARIAD GENE THERAPEUTICS INC.

PI Sridaran N;

DR WPI; 1999-190623/16.

PT Nucleic acid encoding chimeric transcription activator protein - which

PT activates transcription of a gene in a cell.

PS Disclosure; Page 21; 90pp; English.

CC The invention relates to a nucleic acid encoding a chimeric transcription

CC activator protein which activates transcription of a gene to which the

CC chimeric transcription activator protein is targeted. The nucleic acid

CC contains at least one composite transcription activation domain

CC comprising a continuous polypeptide region containing two or more

CC component polypeptide regions, at least two of which are mutually

CC heterologous and do not occur in nature in the same gene product, and at

CC least one additional domain comprising a DNA-binding domain. The chimeric

CC proteins can be used to inhibit a transcriptional regulation protein or

CC inhibit the translation of an inhibitor of a cellular pathway. The

CC proteins can involve homing, cytotoxicity, proliferation, immune

CC response, inflammatory response, clotting or dissolving of clots,

CC hormonal regulation etc. By using the chimeric constructs, the production

CC of a specific protein is increased by stimulating expression of the

CC endogenous gene encoding the protein, with the absence of an immune

CC reaction against the protein, thereby resulting in a more efficient

CC treatment of the subject

XX SQ Sequence 18 AA;

DT 20-APR-2001 (first entry)

DE Human CTF protein activation domain motif.

KW Fusion protein; transcription factor; ligand binding domain; OCA-B; OAD;

KW transcription activation domain; gene therapy; therapeutic protein;

KW B cell specific transcriptional co-activator; cytokine; interleukin;

XX erythropoietin; tissue plasminogen activator; clotting factor; CTF.

XX OS Homo sapiens.

RESULT 40

AAW03842
 ID AAW03842 standard; protein; 18 AA.

XX AAW03842;

DT 20-APR-2001 (first entry)

DE Human CTF protein activation domain motif.

KW Fusion protein; transcription factor; ligand binding domain; OCA-B; OAD;

KW transcription activation domain; gene therapy; therapeutic protein;

KW B cell specific transcriptional co-activator; cytokine; interleukin;

XX erythropoietin; tissue plasminogen activator; clotting factor; CTF.

XX OS Homo sapiens.

PN WO20078951-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 16-JUN-2000; 2000MO-US016620.
 XX
 PR 18-JUN-1999; 99US-0140289P.
 XX
 PA (ARIA-) ARIAD GENE THERAPEUTICS INC.
 XX
 PI Natesan S;
 XX
 DR WPI; 2001-102722/11.
 XX
 XX
 PT New recombinant nucleic acid encoding chimeric transcription activator,
 PT useful to effect transcription of target genes in transgenic cells or
 PT organisms, comprising ligand binding domain and OCA-B activation domain.
 XX
 PS Disclosure; Page 16; 55pp; English.
 XX
 CC The invention relates to a recombinant nucleic acid (I) encoding a fusion
 CC protein (chimeric transcription factor) that comprises a ligand binding
 CC domain and a transcription activation domain which contains all or a part
 CC of an OCA-B (a B cell specific transcriptional co-activator) activation
 CC domain (OAB). (I) is useful for rendering a cell capable of expressing a
 CC target gene in a ligand-dependent manner. The method involves transducing
 CC a cell in vitro or in vivo, with (I) which encodes the fusion protein
 CC that stimulates, in a ligand dependent manner, the transcription of a
 CC target gene operably linked to a transcription control sequence
 CC recognized by the fusion protein. (I) and vectors, virus and cells
 CC containing (I) are useful for rendering a host organism capable of
 CC regulating expression of a target gene such as a therapeutic protein,
 CC antisense sequence or ribozyme of interest. The therapeutic proteins such
 CC as cytokines (interleukin-2, IL-4, IL-12) when expressed can involve
 CC homing, cytotoxicity, proliferation, immune response, inflammatory
 CC response, clotting or dissolving of clots or hormonal regulation etc.,
 CC and thus are useful in gene therapy techniques. The method is useful for
 CC increasing the efficacy of many gene therapy strategies by substantially
 CC elevating the expression of a therapeutic target gene allowing expression
 CC to reach therapeutically effective levels. Transcription factors encoded
 CC by (I) are also useful in the large scale production of recombinant
 CC proteins such as erythropoietin, tissue plasminogen activator, clotting
 CC factors, antibodies etc. Also, the factors encoded by (I) are useful in a
 CC range of biological experiments in which precise control over a target
 CC gene is desired. The present sequence represents an activation domain
 CC peptide motif from human CTF
 XX
 SQ Sequence 18 AA;

Query Match 45.2%; Score 28; DB 4; Length 18;
 Best Local Similarity 71.4%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 NPYKLPO 10
 ||:||||
 Db 1 NPLQLPO 7

Search completed: June 7, 2005, 23:10:53
 Job time : 62.2 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:57:32 ; Search time 15 Seconds

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54.743 Million cell updates/sec

Title: US-10-691-157-6

Perfect score: 62

Sequence: 1 MPQNRXKLPQM 11

Scoring table: BLOSUM62

Searched: Gapd 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 183464

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : Issued Patents AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	11	4	US-09-641-803-6
2	30	48.4	8	1	US-08-014-426-53
3	30	48.4	8	1	US-08-014-426-60
4	30	48.4	8	5	PCT-US94-01319-53
5	30	48.4	8	5	PCT-US94-01319-60
6	30	48.4	11	2	US-07-737-371E-64
7	29	46.8	15	4	US-09-000-003A-11
8	28	45.2	18	3	US-08-920-610-4
9	28	45.2	18	3	US-09-140-149-2
10	28	45.2	18	3	US-08-672-213-4
11	28	45.2	18	3	US-08-973-131-31
12	28	45.2	18	4	US-09-615-917-2
13	27	43.5	15	4	US-08-480-190-271
14	27	43.5	15	4	US-08-488-379-271
15	27	43.5	15	4	US-08-475-399A-271
16	27	43.5	15	4	US-08-077-255A-271
17	27	43.5	15	5	PCT-US93-07545-271
18	26	41.9	10	2	US-08-934-222-93
19	26	41.9	10	2	US-08-933-402-93
20	26	41.9	10	2	US-09-207-621-93
21	26	41.9	10	2	US-08-532-818-93
22	26	41.9	10	3	US-09-231-797-93
23	26	41.9	10	3	US-08-934-224-93
24	26	41.9	10	3	US-08-933-843-93
25	26	41.9	10	3	US-08-934-223-93
26	26	41.9	10	3	US-09-413-492-93
27	26	41.9	11	2	US-08-704-655-18

28	41.9	11	4	US-09-920-174-3	Sequence 3, Appl
29	41.9	11	4	US-09-920-195A-3	Sequence 3, Appl
30	41.9	16	3	US-08-462-436-22	Sequence 22, Appl
31	41.9	16	3	US-08-465-275-22	Sequence 22, Appl
32	41.9	16	4	US-08-640-877-22	Sequence 22, Appl
33	41.9	16	4	US-09-799-576A-22	Sequence 22, Appl
34	41.9	16	4	US-09-799-540-22	Sequence 22, Appl
35	40.3	8	2	US-08-765-061-9	Sequence 2, Appl
36	40.3	8	3	US-09-514-739-2	Sequence 2, Appl
37	40.3	10	1	US-07-954-213-4	Sequence 4, Appl
38	40.3	10	2	US-08-765-061-7	Sequence 7, Appl
39	40.3	11	2	US-07-737-371E-39	Sequence 39, Appl
40	40.3	11	2	US-07-737-371E-40	Sequence 40, Appl
41	40.3	11	4	US-09-579-883B-12	Sequence 12, Appl
42	40.3	12	1	US-08-275-983B-17	Sequence 17, Appl
43	40.3	12	3	US-08-794-002-10	Sequence 10, Appl
44	40.3	12	3	US-08-854-039B-10	Sequence 10, Appl
45	40.3	12	4	US-08-765-702B-10	Sequence 10, Appl
46	40.3	15	2	US-08-637-418-9	Sequence 9, Appl
47	40.3	15	2	US-08-637-418-10	Sequence 10, Appl
48	40.3	16	1	US-07-954-213-12	Sequence 12, Appl
49	40.3	16	3	US-07-861-458C-134	Sequence 134, Appl
50	38.7	5	4	US-09-608-892-36	Sequence 36, Appl
51	38.7	7	2	US-08-968-676-69	Sequence 69, Appl
52	38.7	7	4	US-09-261-894A-69	Sequence 69, Appl
53	38.7	8	4	US-09-266-764-26	Sequence 26, Appl
54	38.7	8	4	US-09-239-043D-52	Sequence 52, Appl
55	38.7	8	4	US-09-239-043D-823	Sequence 823, Appl
56	38.7	8	4	US-09-239-043D-1597	Sequence 1597, Appl
57	38.7	9	1	US-08-024-253-18	Sequence 18, Appl
58	38.7	9	2	US-08-629-291A-27	Sequence 27, Appl
59	38.7	9	2	US-08-658-335B-27	Sequence 27, Appl
60	38.7	9	3	US-08-159-339A-367	Sequence 367, Appl
61	38.7	9	3	US-07-987-264-6	Sequence 6, Appl
62	38.7	9	3	US-09-492-543-73	Sequence 73, Appl
63	38.7	9	4	US-09-492-543-101	Sequence 101, Appl
64	38.7	9	4	US-09-406-640-27	Sequence 27, Appl
65	38.7	9	4	US-09-239-043D-47	Sequence 47, Appl
66	38.7	9	4	US-09-239-043D-803	Sequence 803, Appl
67	38.7	9	4	US-09-239-043D-1591	Sequence 1591, Appl
68	38.7	9	4	US-09-239-043D-1842	Sequence 1842, Appl
69	38.7	9	4	US-09-971-020A-20	Sequence 20, Appl
70	38.7	9	4	US-09-971-020A-22	Sequence 22, Appl
71	38.7	10	4	US-09-239-043D-1194	Sequence 1194, Appl
72	38.7	10	4	US-09-239-043D-2291	Sequence 2291, Appl
73	38.7	11	2	US-07-737-371E-20	Sequence 20, Appl
74	38.7	11	2	US-07-737-371E-21	Sequence 21, Appl
75	38.7	11	2	US-07-737-371E-22	Sequence 22, Appl
76	38.7	11	2	US-07-737-371E-23	Sequence 23, Appl
77	38.7	11	2	US-07-737-371E-24	Sequence 24, Appl
78	38.7	11	2	US-07-737-371E-27	Sequence 27, Appl
79	38.7	11	2	US-07-737-371E-37	Sequence 37, Appl
80	38.7	11	2	US-07-737-371E-55	Sequence 55, Appl
81	38.7	11	2	US-07-737-371E-65	Sequence 65, Appl
82	38.7	11	4	US-09-239-043D-107	Sequence 107, Appl
83	38.7	11	4	US-09-239-043D-957	Sequence 957, Appl
84	38.7	11	4	US-09-239-043D-1676	Sequence 1676, Appl
85	38.7	11	6	5411935-8	Patent No. 5411935
86	38.7	12	2	US-08-811-492-145	Sequence 145, Appl
87	38.7	12	2	US-08-811-492-147	Sequence 147, Appl
88	38.7	12	2	US-08-811-492-147	Sequence 147, Appl
89	38.7	13	4	US-09-927-734C-10	Sequence 10, Appl
90	38.7	13	4	US-08-637-418-19	Sequence 19, Appl
91	38.7	15	2	US-08-637-418-20	Sequence 20, Appl
92	38.7	15	3	US-08-101-624-19	Sequence 19, Appl
93	38.7	15	3	US-08-596-257A-10	Sequence 10, Appl
94	38.7	15	3	US-08-479-744A-19	Sequence 19, Appl
95	38.7	15	3	US-08-860-339-10	Sequence 10, Appl
96	38.7	15	3	US-08-280-757B-19	Sequence 19, Appl
97	38.7	15	3	US-09-227-357-539	Sequence 539, Appl
98	38.7	15	4	US-09-370-644B-10	Sequence 10, Appl
99	38.7	15	4	US-09-425-762-19	Sequence 19, Appl
100	38.7	15	4	US-09-573-629-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-641-803-6
Sequence 6, Application US/09641803
Patent No. 6500798
GENERAL INFORMATION:
APPLICANT: STANTON, G. John
APPLICANT: HUGHES, Thomas K.
APPLICANT: BOLOGH, Istvan
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
FILE REFERENCE: 265.00220101
CURRENT APPLICATION NUMBER: US/09/641,803
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 60/149,310
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 11
TYPE: PRP
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-6

Query Match 100.0%; Score 62; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNFYKLPQM 11
| | | | | | | | | | | |
DB 1 MPQNFYKLPQM 11

RESULT 2
US-08-014-426-53
Sequence 53, Application US/08014426
Patent No. 5512435
GENERAL INFORMATION:
APPLICANT: Renschler, Markus F.
APPLICANT: Levy, Ronald
APPLICANT: Bhatt, Ramesh
APPLICANT: Dower, William
TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,426
FILING DATE: 05-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 5490A-204
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-014-426-53

Query Match 48.4%; Score 30; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNFYK 7
| | | | | : | |
DB 1 MPEDFYR 7

RESULT 3
US-08-014-426-60
Sequence 60, Application US/08014426
Patent No. 5512435
GENERAL INFORMATION:
APPLICANT: Renschler, Markus F.
APPLICANT: Levy, Ronald
APPLICANT: Bhatt, Ramesh
APPLICANT: Dower, William
TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,426
FILING DATE: 05-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 5490A-204
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-014-426-60

Query Match 48.4%; Score 30; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNFYK 7
| | | | | : | |
DB 1 MPEDFYR 7


```
RESULT 4
PCT-US94-01319-53
; Sequence 53, Application PC/TUS9401319
; GENERAL INFORMATION:
; APPLICANT: Renschler, Markus F.
; APPLICANT: Levy, Ronald
; APPLICANT: Bharti, Ramesh
; APPLICANT: Dower, William
; TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE
; TITLE OF INVENTION: PEPTIDES
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01319
; FILING DATE: 04-FEB-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,426
; FILING DATE: 05-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 5490A-204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; PCT-US94-01319-53

Query Match          48.4%; Score 30; DB 5; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 MPONFYK 7
DB      1 MPEDFYR 7

RESULT 5
PCT-US94-01319-60
; Sequence 60, Application PC/TUS9401319
; GENERAL INFORMATION:
; APPLICANT: Renschler, Markus F.
; APPLICANT: Levy, Ronald
; APPLICANT: Bharti, Ramesh
; APPLICANT: Dower, William
; TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE
; TITLE OF INVENTION: PEPTIDES
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
```

```
STATE: California
COUNTRY: US
ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01319
; FILING DATE: 04-FEB-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,426
; FILING DATE: 05-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 5490A-204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; PCT-US94-01319-60
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Query Match          48.4%; Score 30; DB 5; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 MPONFYK 7
DB      1 MPEDFYR 7
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```
RESULT 6
US-07-737-371E-64
; Sequence 64, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-64

Query Match 48.4%; Score 30; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PNFYKLP 9
|||:
Db 4 PQFFGLP 11

RESULT 7
US-09-000-003A-11
Sequence 11, Application US/09000003A
Patent No. 6652850
GENERAL INFORMATION:
APPLICANT: Philip, Ramla
Lebkowski, Jane S.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRAL LIPOSOMES AND
THEIR USE IN TRANSFECTING DENDRITIC CELLS TO STIMULATE
SPECIFIC IMMUNITY
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Alexis Barron, Esq.
STREET: Suite 2600 Aramark Tower, 1101 Market Street
CITY: Philadelphia
STATE: PA
COUNTRY: United States of America
ZIP: 19107
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,003A
FILING DATE: 15-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12012
FILING DATE: 19-JUL-1996
APPLICATION NUMBER: US 60/001,312
FILING DATE: 21-JUL-1995
APPLICATION NUMBER: US 60/007,184
FILING DATE: 01-NOV-1995
APPLICATION NUMBER: US 08/566,286
FILING DATE: 01-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barron, Alexis
REGISTRATION NUMBER: 22,702
REFERENCE/DOCKET NUMBER: 20,846-K USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 923-4466
TELEFAX: (215) 923-2189
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-000-003A-11

Query Match 46.8%; Score 29; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PNFYKLPQM 11
|||:
Db 4 PTVFYNIPPM 13

RESULT 8
US-08-920-610-4
Sequence 4, Application US/08920610
Patent No. 6015709
GENERAL INFORMATION:
APPLICANT: Natesan, Sridaran
TITLE OF INVENTION: TRANSCRIPTIONAL ACTIVATORS AND
COMPOSITIONS AND USES RELATED THERETO
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: FOLEY, HONG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,610
FILING DATE: 27-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: APV-006.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-920-610-4

Query Match 45.2%; Score 28; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NPFYKLPQ 10
|||:
Db 1 NPLQLPQ 7

RESULT 9
US-09-140-149-2
Sequence 2, Application US/09140149
Patent No. 6117680
GENERAL INFORMATION:
APPLICANT: Natesan, Sridaran
APPLICANT: Gilman, Michael Z
TITLE OF INVENTION: No. 6117680e1 Compositions and Methods for Regulation of
FILE REFERENCE: 363C
CURRENT APPLICATION NUMBER: US/09/140,149
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 08/918,401

EARLIER FILING DATE: 1997-08-26
EARLIER APPLICATION NUMBER: 08/920,610
EARLIER FILING DATE: 1997-08-27
EARLIER APPLICATION NUMBER: 09/126,009
EARLIER FILING DATE: 1998-07-29
EARLIER APPLICATION NUMBER: PCT/US97/15219
EARLIER FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-140-149-2

Query Match 45.2%; Score 28; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFKLPQ 10
Db 1 NFKLPQ 7

RESULT 10
US-08-672-213-4
Sequence 4, Application US/08672213
Patent No. 6306649

GENERAL INFORMATION:
APPLICANT: GILMAN, Michael Z.
APPLICANT: NATESAN, Sridaran
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
TITLE OF INVENTION: FACTORS IN GENE THERAPY
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Gene Therapeutics, Inc.
STREET: 26 Landsdowne Street
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139-4234

COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,213
FILING DATE: 27-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,553
FILING DATE: 27-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,614
FILING DATE: 29-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, David L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: ARIAD 346B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-494-0400
TELEFAX: 617-494-0208
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-213-4

Query Match 45.2%; Score 28; DB 3; Length 18;

Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFKLPQ 10
Db 1 NFKLPQ 7

RESULT 11
US-08-973-131-31
Sequence 31, Application US/08973131
Patent No. 6326166
GENERAL INFORMATION:
APPLICANT: Pomerantz, Joel L.
APPLICANT: Pado, Carl O.
TITLE OF INVENTION: Chimeric DNA-binding proteins
FILE REFERENCE: APV-022.02
CURRENT APPLICATION NUMBER: US/08/973,131
CURRENT FILING DATE: 1998-03-16
EARLIER APPLICATION NUMBER: PCT/US95/16982
EARLIER FILING DATE: 1995-12-29
EARLIER APPLICATION NUMBER: 08/366,083
EARLIER FILING DATE: 1994-12-29
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 18
TYPE: PRT
ORGANISM: human
US-08-973-131-31

Query Match 45.2%; Score 28; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFKLPQ 10
Db 1 NFKLPQ 7

RESULT 12
US-09-615-917-2
Sequence 2, Application US/09615917
Patent No. 6479653
GENERAL INFORMATION:
APPLICANT: Natesan, Sridaran
APPLICANT: Gilman, Michael Z.
TITLE OF INVENTION: No. 6479653el Compositions and Methods for Regulation of
TITLE OF INVENTION: Transcription
FILE REFERENCE: 363C continuation
CURRENT APPLICATION NUMBER: US/09/615,917
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 08/918,401
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 08/920,610
PRIOR FILING DATE: 1997-08-27
PRIOR APPLICATION NUMBER: 09/126,009
PRIOR FILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: 09/140,149
PRIOR FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-615-917-2

Query Match 45.2%; Score 28; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 NFKYLPQ 10
|||
Db 1 NFKYLPQ 7

RESULT 13

US-08-480-190-271
; Sequence 271, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 271:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-480-190-271

Query Match 43.5%; Score 27; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 NFKYLPQ 10
|||
Db 2 NFKYLPQ 8

RESULT 14

US-08-488-379-271
; Sequence 271, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley

APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 271:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-08-488-379-271

Query Match 43.5%; Score 27; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 NFKYLPQ 10
|||
Db 2 NFKYLPQ 8

RESULT 15

US-08-475-399A-271
; Sequence 271, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 271:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-271

Query Match
Best Local Similarity 43.5%; Score 27; DB 4; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 NRYKLPQ 10
|||
2 NRYSPQ 8

Db

RESULT 16
US-08-077-255A-271
Sequence 271, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906

TELEX: 200154
INFORMATION FOR SEQ ID NO: 271:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-271

Query Match
Best Local Similarity 43.5%; Score 27; DB 4; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 NRYKLPQ 10
|||
2 NRYSPQ 8

Db

RESULT 17
PCT-US93-07545-271
Sequence 271, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 271:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-271

Query Match
Best Local Similarity 43.5%; Score 27; DB 5; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 NRYKLPQ 10
|||
2 NRYSPQ 8

Db

RESULT 18
US-08-934-222-93
; Sequence 93, Application US/08934222
; Patent No. 5928896
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,222
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-222-93
Query Match 41.9%; Score 26; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 PONFYKLP 9
DB 2 PNNLDKLP 9
RESULT 19
US-08-933-402-93
; Sequence 93, Application US/08933402
; Patent No. 5948887
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA

ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,402
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-402-93
Query Match 41.9%; Score 26; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 PONFYKLP 9
DB 2 PNNLDKLP 9
RESULT 20
US-09-207-621-93
; Sequence 93, Application US/09207621
; Patent No. 5952465
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,621
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741

FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-207-621-93

Query Match 41.9%; Score 26; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PNNFYKLP 9
DB 2 PNNLDKLP 9

RESULT 21
US-08-532-818-93
Sequence 93, Application US/08532818
Patent No. 5965698
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSES: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-532-818-93

Query Match 41.9%; Score 26; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 PNNFYKLP 9
DB 2 PNNLDKLP 9

DB 2 PNNLDKLP 9

RESULT 22
US-09-231-797-93
Sequence 93, Application US/09231797
Patent No. 6084066
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSES: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,797
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-231-797-93

Query Match 41.9%; Score 26; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PNNFYKLP 9
DB 2 PNNLDKLP 9

RESULT 23
US-08-934-224-93
Sequence 93, Application US/08934224
Patent No. 6100044
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSES: Foley & Lardner
STREET: Suite 500, 3000 K Street NW

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,224
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-224-93

Query Match 41.9%; Score 26; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PGNFYKLP 9
| | | |
Db 2 PNNLDKLP 9

RESULT 24
US-08-933-843-93
Sequence 93, Application US/08933843
Patent No. 6111069
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,843
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-933-843-93

Query Match 41.9%; Score 26; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PGNFYKLP 9
| | | |
Db 2 PNNLDKLP 9

RESULT 25
US-08-934-223-93
Sequence 93, Application US/08934223
Patent No. 6147189
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,223
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-223-93

Query Match 41.9%; Score 26; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PNFYKLP 9
DB 2 PNNLDKLP 9

RESULT 26
US-09-413-492-93
; Sequence 93, Application US/09413492
; Patent No. 6258550
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Plank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/413,492
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Iacason, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-413-492-93

Query Match 41.9%; Score 26; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PNFYKLP 9
DB 2 PNNLDKLP 9

RESULT 27
US-08-704-655-18
; Sequence 18, Application US/08704655
; Patent No. 5869453
; GENERAL INFORMATION:
; APPLICANT: Moss, Denis J.
; APPLICANT: Burrows, Scott R.

APPLICANT: Khanna, Rajiv
APPLICANT: Kerr, Vebberly M.
APPLICANT: Burrows, Jacqueline M.
APPLICANT: Sunbrier, Andreas
TITLE OF INVENTION: Cytotoxic T Cell Epitopes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,655
FILING DATE: 13-SEP-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU95/00140
FILING DATE: 16-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: FBRC002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (712) 789-2679
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-704-655-18

Query Match 41.9%; Score 26; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 FYKLPQM 11
DB 3 FYNIRPP 9

RESULT 28
US-09-920-174-3
; Sequence 3, Application US/09920174
; Patent No. 6699477
; GENERAL INFORMATION:
; APPLICANT: KHANNA, RAJIV
; APPLICANT: KERR, BEVERLEY M.
; APPLICANT: MISKO, IHOR S.
; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FBRC:008USC2
; CURRENT APPLICATION NUMBER: US/09/920,174
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/920,175
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/194,450
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-920-174-3

Query Match 41.9%; Score 26; DB 4; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 FYKLPOM 11
Db 3 FYNIPPM 9

RESULT 29
US-09-920-195A-3
Sequence 3, Application US/09920195A
Patent No. 6703024
GENERAL INFORMATION:
APPLICANT: KHANNA, RAJIV
APPLICANT: KERR, BEVERLEY M.
APPLICANT: MISKO, IHOR S.
APPLICANT: MOSS, DENIS J.
APPLICANT: BURROWS, SCOTT R.
TITLE OF INVENTION: EBV CTL EPITOPES
FILE REFERENCE: FBRC:008USC1
CURRENT APPLICATION NUMBER: US/09/920,195A
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 09/194,450
PRIOR FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-920-195A-3

Query Match 41.9%; Score 26; DB 4; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 FYKLPOM 11
Db 3 FYNIPPM 9

RESULT 30
US-08-462-436-22
Sequence 22, Application US/08462436
Patent No. 6001823
GENERAL INFORMATION:
APPLICANT: HULTGREN, SCOTT
TITLE OF INVENTION: A NEW METHOD FOR THE TREATMENT AND
TITLE OF INVENTION: PROPHYLAXIS OF BACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,436

FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13455
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,035
FILING DATE: 18-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HULTGREN-1C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-436-22

Query Match 41.9%; Score 26; DB 3; Length 16;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9
Db 9 QDHYKMP 15

RESULT 31
US-08-465-275-22
Sequence 22, Application US/08465275
Patent No. 6153396
GENERAL INFORMATION:
APPLICANT: HULTGREN, SCOTT
APPLICANT: KUEHN, META
APPLICANT: XU, Zheng
APPLICANT: OGG, Derek
APPLICANT: HARRIS, Mark
APPLICANT: LEPISTO, Matci
APPLICANT: KILBERG, Jan
APPLICANT: JONES, Charles H.
TITLE OF INVENTION: TREATMENT OR PROPHYLAXIS OF DISEASES
TITLE OF INVENTION: CAUSED BY PILUS-FORMING BACTERIA
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,275
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,035
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/13455
FILING DATE: 18-NOV-1994
ATTORNEY/AGENT INFORMATION:

NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 016921-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-275-22

Query Match 41.9%; Score 26; DB 3; Length 16;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9
|:|:|
Db 9 QDHYKMP 15

RESULT 32
US-08-640-877-22
Sequence 22, Application US/08640877
Patent No. 6420127
GENERAL INFORMATION:
APPLICANT: HULJGREN, Scott
APPLICANT: KUEHN, Meta
APPLICANT: XU, Zheng
APPLICANT: OGG, Derek
APPLICANT: HARRIS, Mark
APPLICANT: LEPISTO, Matti
APPLICANT: JONES, Charles H.
TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,877
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/13455
FILING DATE: 18-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 016921-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-640-877-22

Query Match 41.9%; Score 26; DB 4; Length 16;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9
|:|:|
Db 9 QDHYKMP 15

RESULT 33
US-09-799-576A-22
Sequence 22, Application US/09799576A
Patent No. 6548255
GENERAL INFORMATION:

APPLICANT: HULJGREN, Scott
APPLICANT: KUEHN, Meta
APPLICANT: XU, Zheng
APPLICANT: OGG, Derek
APPLICANT: HARRIS, Mark
APPLICANT: LEPISTO, Matti
APPLICANT: JONES, Charles H.
TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,576A
FILING DATE: 07-Mar-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/640,877
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: WO PCT/US94/13455
FILING DATE: 18-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 016921-164
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-799-576A-22

Query Match 41.9%; Score 26; DB 4; Length 16;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9
|:|:|
Db 9 QDHYKMP 15

```
RESULT 34
; US-09-799-540-22
; Sequence 22, Application US/09799540
; Patent No. 6596504
; GENERAL INFORMATION:
; APPLICANT: HULTIGREN, Scott
; APPLICANT: KUEHN, Meta
; APPLICANT: XU, Zheng
; APPLICANT: OGG, Derek
; APPLICANT: HARRIS, Mark
; APPLICANT: LEPISTO, Matti
; APPLICANT: KJHLBERG, Jan
; APPLICANT: JONES, Charles H.
; TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DONNE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22113-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/799,540
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/640,877
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 016921-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-799-540-22

Query Match          41.9%; Score 26; DB 4; Length 16;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3 QNFYKLP 9
       |:|:|:|
       9 QDHYKMP 15

DB

RESULT 35
; US-08-765-061-9
; Sequence 9, Application US/08765061
; Patent No. 5935796
; GENERAL INFORMATION:
; APPLICANT: FOSANG, AMANDA J
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND COMPOSITIONS
; TITLE OF INVENTION: RELATING TO THE PROTEOGLYCAN PROTEINS OF CARTILAGE
; TITLE OF INVENTION: BREAKDOWN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRIFFITH HACK
; STREET: 509 ST KILDA ROAD
```

```
; CITY: MELBOURNE
; STATE: VICTORIA
; COUNTRY: AUSTRALIA
; ZIP: 3004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,061
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PM6668
; FILING DATE: 07-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SANTER, VIVIEN B
; REFERENCE/DOCKET NUMBER: PP4262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: +61 3 9243 8300
; TELEFAX: +61 3 9 243 8333/4
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; US-08-765-061-9

Query Match          40.3%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 MPONEY 6
       |:|:|:|
       2 IPENPF 7

DB

RESULT 36
; US-09-514-739-2
; Sequence 2, Application US/09514739
; Patent No. 6379946
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Tenor, Jennifer L
; APPLICANT: Cliche, Todd A
; APPLICANT: Petell, James K.
; APPLICANT: Strickland, James A
; APPLICANT: Orr, Gregory L
; APPLICANT: Faltig, Raymond
; APPLICANT: Binstlim, Scott
; TITLE OF INVENTION: INSECTICIDAL PROTEIN TOXINS FROM XENORHABDUS
; FILE REFERENCE: 50585A
; CURRENT APPLICATION NUMBER: US/09/514,739
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: 09/072,264
; EARLIER FILING DATE: 1998-05-04
; EARLIER APPLICATION NUMBER: 60/045,641
; EARLIER FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Xenorhabdus Wi
; US-09-514-739-2
```

Query Match 40.3%; Score 25; DB 3; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 QNFYKLP 9
: : : : :
Db 2 QNFYKLP 8

RESULT 37

US-07-954-213-4
; Sequence 4, Application US/07954213
; Patent No. 5387504

GENERAL INFORMATION:

APPLICANT: Mumford, Richard A.

APPLICANT: Laik, Michael W.

APPLICANT: Bayne, Ellen B.K.

APPLICANT: Hoerner, Lori A.

TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AND ASSAY SYSTEM

TITLE OF INVENTION: FOR DETECTING STROMELYSIN CLEAVAGE PRODUCTS

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 E. Lincoln Avenue

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/954,213

FILING DATE: 19920930

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Wallen, John W.III

REGISTRATION NUMBER: 35,403

REFERENCE/DOCKET NUMBER: 18842

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3905

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-954-213-4

Query Match 40.3%; Score 25; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFY 6
: : : : :
Db 2 IPENFF 7

RESULT 38

US-08-765-061-7

; Sequence 7, Application US/08765061

; Patent No. 5935796

GENERAL INFORMATION:

APPLICANT: POSANG, AMANDA J

TITLE OF INVENTION: DIAGNOSTIC METHODS AND COMPOSITIONS

TITLE OF INVENTION: RELATING TO THE PROTEOLYCAN PROTEINS OF CARTILAGE

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: GRIFFITH HACK

STREET: 509 ST KILDA ROAD

CITY: MELBOURNE

STATE: VICTORIA

COUNTRY: AUSTRALIA

ZIP: 3004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/765,061

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PM6668

FILING DATE: 07-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: SANTER, VIVIAN B

REFERENCE/DOCKET NUMBER: FP4262

TELECOMMUNICATION INFORMATION:

TELEPHONE: +61 3 9243 8300

TELEFAX: +61 3 9 243 8333/4

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: C-terminal

US-08-765-061-7

Query Match 40.3%; Score 25; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFY 6
: : : : :
Db 2 IPENFF 7

RESULT 39

US-07-737-371E-39

; Sequence 39, Application US/07737371E

; Patent No. 5876948

GENERAL INFORMATION:

APPLICANT: Yankner, Bruce A.

TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/737,371E

FILING DATE: 29-JUL-1991

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/559,172

FILING DATE: 27-JUL-1990

ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29, 066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-39

Query Match 40.3%; Score 25; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|||
Db 4 PQCFYAL 10

RESULT 40
US-07-737-371E-40
Sequence 40, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29, 066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-40

Query Match 40.3%; Score 25; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|||
Db 4 PQCFYPL 10

Search completed: June 7, 2005, 23:23:17
Job time : 17 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 23:00:52 ; Search time 49.5 Seconds
(without alignments)
85.185 Million cell updates/sec

Title: US-10-691-157-6
Perfect score: 62
Sequence: 1 MPQWRYKLPQM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 309695

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10F_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	11	US-10-281-652-6	Sequence 6, Appli
2	62	100.0	11	US-10-691-157-6	Sequence 6, Appli
3	62	100.0	11	US-10-691-330-6	Sequence 6, Appli
4	29	46.8	10	US-10-062-710-83	Sequence 83, Appli
5	29	45.8	15	US-09-888-721-10	Sequence 10, Appli
6	28	45.2	12	US-10-075-869-41	Sequence 41, Appli
7	28	45.2	12	US-10-366-493-41	Sequence 41, Appli
8	28	45.2	12	US-10-432-585-3	Sequence 3, Appli
9	28	45.2	12	US-10-719-587-39	Sequence 39, Appli
10	28	45.2	12	US-10-477-712B-7	Sequence 7, Appli
11	28	45.2	12	US-10-487-634-39	Sequence 39, Appli

12	45.2	12	US-10-926-893-41	Sequence 41, Appli	
13	28	45.2	18	US-09-852-370-31	Sequence 31, Appli
14	28	45.2	18	US-10-002-244-4	Sequence 4, Appli
15	27	43.5	12	US-10-649-873-111	Sequence 111, App
16	26	41.9	9	US-10-014-340-803	Sequence 803, App
17	26	41.9	9	US-10-845-391-53	Sequence 53, Appli
18	26	41.9	11	US-09-920-174-3	Sequence 3, Appli
19	26	41.9	11	US-09-920-195A-3	Sequence 3, Appli
20	26	41.9	11	US-10-752-380-3	Sequence 3, Appli
21	26	41.9	15	US-10-125-869A-43	Sequence 43, Appli
22	26	41.9	15	US-10-125-869A-119	Sequence 119, App
23	26	41.9	15	US-10-462-262-267	Sequence 267, App
24	26	41.9	15	US-10-462-262-343	Sequence 343, App
25	26	41.9	16	US-09-799-576A-22	Sequence 22, Appli
26	26	41.9	16	US-09-799-540-22	Sequence 22, Appli
27	26	41.9	16	US-09-799-608-22	Sequence 22, Appli
28	26	41.9	16	US-09-798-932-22	Sequence 22, Appli
29	26	41.9	17	US-09-799-680-22	Sequence 22, Appli
30	26	41.9	17	US-09-745-078A-21	Sequence 21, Appli
31	26	41.9	17	US-09-962-756-1205	Sequence 1205, App
32	26	41.9	17	US-09-962-756-1757	Sequence 1757, App
33	26	41.9	17	US-09-962-756-1911	Sequence 1911, App
34	26	41.9	17	US-10-374-624-21	Sequence 21, Appli
35	26	41.9	17	US-10-253-471-1205	Sequence 1205, App
36	26	41.9	17	US-10-253-471-1757	Sequence 1757, App
37	26	41.9	17	US-10-253-493-1205	Sequence 1205, App
38	26	41.9	17	US-10-253-493-1757	Sequence 1757, App
39	26	41.9	17	US-10-253-493-1911	Sequence 1911, App
40	26	41.9	18	US-09-745-078A-20	Sequence 20, Appli
41	26	41.9	18	US-10-374-624-20	Sequence 20, Appli
42	25	40.3	18	US-09-943-944E-140	Sequence 140, App
43	25	40.3	8	US-09-756-283A-42	Sequence 42, Appli
44	25	40.3	8	US-09-756-283A-58	Sequence 58, Appli
45	25	40.3	8	US-09-756-283A-69	Sequence 69, Appli
46	25	40.3	8	US-09-756-283A-90	Sequence 90, Appli
47	25	40.3	8	US-09-756-283A-96	Sequence 96, Appli
48	25	40.3	8	US-10-078-968-2	Sequence 2, Appli
49	25	40.3	8	US-10-931-637-2	Sequence 2, Appli
50	25	40.3	8	US-10-684-346-31	Sequence 31, Appli
51	25	40.3	9	US-10-245-871-107	Sequence 107, App
52	25	40.3	9	US-10-253-286-107	Sequence 107, App
53	25	40.3	9	US-10-823-253-6	Sequence 6, Appli
54	25	40.3	9	US-10-823-253-20	Sequence 20, Appli
55	25	40.3	9	US-10-883-020-32	Sequence 32, Appli
56	25	40.3	9	US-10-726-332-202	Sequence 202, App
57	25	40.3	10	US-10-007-761-41	Sequence 41, Appli
58	25	40.3	10	US-10-843-731-41	Sequence 41, Appli
59	25	40.3	10	US-11-028-539-103	Sequence 103, App
60	25	40.3	11	US-10-119-528-31	Sequence 31, Appli
61	25	40.3	11	US-10-343-654-27	Sequence 27, Appli
62	25	40.3	11	US-10-718-071-9	Sequence 9, Appli
63	25	40.3	11	US-09-813-653-27	Sequence 27, Appli
64	25	40.3	12	US-09-845-612B-10	Sequence 10, Appli
65	25	40.3	12	US-10-468-496-670	Sequence 670, App
66	25	40.3	12	US-10-468-496-671	Sequence 671, App
67	25	40.3	12	US-10-468-496-672	Sequence 672, App
68	25	40.3	13	US-10-468-496-673	Sequence 673, App
69	25	40.3	13	US-10-468-496-674	Sequence 674, App
70	25	40.3	13	US-10-468-496-675	Sequence 675, App
71	25	40.3	13	US-10-468-496-676	Sequence 676, App
72	25	40.3	13	US-10-468-496-677	Sequence 677, App
73	25	40.3	13	US-10-468-496-678	Sequence 678, App
74	25	40.3	13	US-10-468-496-679	Sequence 679, App
75	25	40.3	13	US-10-468-496-680	Sequence 680, App
76	25	40.3	13	US-10-468-496-681	Sequence 681, App
77	25	40.3	13	US-10-468-496-682	Sequence 682, App
78	25	40.3	13	US-10-468-496-683	Sequence 683, App
79	25	40.3	13	US-10-468-496-684	Sequence 684, App
80	25	40.3	13	US-10-468-496-685	Sequence 685, App
81	25	40.3	13	US-10-468-496-686	Sequence 686, App
82	25	40.3	13	US-10-468-496-687	Sequence 687, App
83	25	40.3	13	US-10-468-496-688	Sequence 688, App
84	25	40.3	13	US-10-468-496-689	Sequence 689, App

85	24	38.7	6	17	US-10-808-187-2401	Sequence 2401, Ap
86	24	38.7	7	10	US-09-261-894-69	Sequence 69, Appl
87	24	38.7	8	15	US-10-408-133-26	Sequence 26, Appl
88	24	38.7	8	17	US-10-654-601-52	Sequence 52, Appl
89	24	38.7	8	17	US-10-654-601-823	Sequence 823, Appl
90	24	38.7	8	17	US-10-654-601-1597	Sequence 1597, Ap
91	24	38.7	9	8	US-08-344-824-331	Sequence 331, Appl
92	24	38.7	9	9	US-09-749-831-6	Sequence 6, Appl1
93	24	38.7	9	9	US-09-835-948-73	Sequence 73, Appl
94	24	38.7	9	14	US-09-835-948-101	Sequence 101, Appl
95	24	38.7	9	14	US-10-172-587-27	Sequence 27, Appl
96	24	38.7	9	14	US-10-172-587-73	Sequence 73, Appl
97	24	38.7	9	14	US-10-172-587-101	Sequence 101, Appl
98	24	38.7	9	15	US-10-428-335-92	Sequence 92, Appl
99	24	38.7	9	15	US-10-428-335-133	Sequence 133, Appl
100	24	38.7	9	16	US-10-469-125-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1

US-10-281-652-6
; Sequence 6, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265, 00220101
; CURRENT FILING DATE: 2002-10-28
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-6

Query Match 100.0%; Score 62; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFYKLPOM 11
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DB 1 MPONFYKLPOM 11

RESULT 2

US-10-691-157-6
; Sequence 6, Application US/10691157
; Publication No. US20040266681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265, 00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-157-6

Query Match 100.0%; Score 62; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFYKLPOM 11
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DB 1 MPONFYKLPOM 11

RESULT 3

US-10-691-330-6
; Sequence 6, Application US/10691330
; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: Bolldogh, Istvan
; APPLICANT: Stanton, G. John
; APPLICANT: Hughes, Thomas K., Jr.
; APPLICANT: Krusel, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265,00390101
; CURRENT APPLICATION NUMBER: US/10/691,330
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-330-6

Query Match 100.0%; Score 62; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFYKLPOM 11
|||||

DB 1 MPONFYKLPOM 11

RESULT 4

US-10-062-710-83
; Sequence 83, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank O.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Pai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes

FILE OF INVENTION: Via Peptide Vaccines
FILE REFERENCE: 3781-001-27
CURRENT APPLICATION NUMBER: US/10/062,710
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/310,498
PRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 83
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV CTL-Epitopes
US-10-062-710-83

Query Match 46.8%; Score 29; DB 14; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PQNFYKL 8
DB 1 PDNFYKL 7

RESULT 5
US-09-888-721-10
Sequence 10, Application US/09888721
Patent No. US2002013290A1
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Wils, Pierre
APPLICANT: Zhu, Quan
APPLICANT: Laurent, Olivier
APPLICANT: Marasco, Wayne A.
APPLICANT: Schertman, Daniel
TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
FILE REFERENCE: 23611-A USA
CURRENT APPLICATION NUMBER: US/09/888,721
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/213,653
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 15
TYPE: PRT
ORGANISM: Epstein-Barr Virus
US-09-888-721-10

Query Match 46.8%; Score 29; DB 9; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PQNFYKL 11
DB 4 PTFYFNIPPM 13

RESULT 6
US-10-075-869-41
Sequence 41, Application US/10075869
Publication No. US20030104622A1
GENERAL INFORMATION:
APPLICANT: Robbins, Paul D.
APPLICANT: Mi, Zhibao
APPLICANT: Fritzeil, Raymond
APPLICANT: Gambotto, Joseph C.
APPLICANT: Gambotto, Andrea
TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT
FACILITATE UPTAKE AND CYTOPLASMIC AND/OR NUCLEAR TRANSPORT
TITLE OF INVENTION: OF PROTEINS, DNA AND VIRUSES

FILE REFERENCE: AP32573-AAA 072396,0237
CURRENT APPLICATION NUMBER: US/10/075,869
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/151,980
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: 60/188,944
PRIOR FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: random peptide library
US-10-075-869-41

Query Match 45.2%; Score 28; DB 14; Length 12;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKL 11
DB 4 KNFPLPEL 12

RESULT 7
US-10-366-493-41
Sequence 41, Application US/10366493
Publication No. US20030219826A1
GENERAL INFORMATION:
APPLICANT: Robbins, Paul D.
APPLICANT: Mi, Zhibao
APPLICANT: Fritzeil, Raymond
APPLICANT: Gambotto, Joseph C.
APPLICANT: Gambotto, Andrea
APPLICANT: Mai, Jeffrey C.
TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT FACILITATE UPTAKE AND CYTOPLASMIC
TITLE OF INVENTION: OF PROTEINS, DNA AND VIRUSES
FILE REFERENCE: AP32573-A-A-A-A 072396,0246
CURRENT APPLICATION NUMBER: US/10/366,493
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 10/075,869
PRIOR FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 09/653,182
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/188,944
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/151,980
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pep 35
US-10-366-493-41

Query Match 45.2%; Score 28; DB 15; Length 12;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKL 11
DB 4 KNFPLPEL 12

RESULT 8
US-10-432-585-3
Sequence 3, Application US/10432585

/ Publication No. US20040029215A1
/ GENERAL INFORMATION:
/ APPLICANT: SUENAGA, Masato
/ APPLICANT: YAMADA, Takao
/ APPLICANT: NISHIMURA, Osamu
/ TITLE OF INVENTION: Method of Production for RFRP
/ FILE REFERENCE: 2829 USOP
/ CURRENT APPLICATION NUMBER: US/10/432,585
/ CURRENT FILING DATE: 2003-05-23
/ PRIOR APPLICATION NUMBER: JP 2000-373125
/ PRIOR FILING DATE: 2000-12-07
/ NUMBER OF SEQ ID NOS: 30
/ SEQ ID NO 3
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Human
US-10-432-585-3

Query Match 45.2%; Score 28; DB 15; Length 12;
Best Local Similarity 55.6%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9
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Db 1 MPHSFANLP 9

RESULT 9
US-10-719-587-39
/ Sequence 39, Application US/10719587
/ Publication No. US20040132073A1
/ GENERAL INFORMATION:
/ APPLICANT: Takeda Chemical Industries, Ltd.
/ TITLE OF INVENTION: Novel G protein-coupled receptor protein, its DNA and ligand ther
/ FILE REFERENCE: 2368USOP-CIP
/ CURRENT APPLICATION NUMBER: US/10/719,587
/ CURRENT FILING DATE: 2003-11-21
/ PRIOR APPLICATION NUMBER: US 09/831,758
/ PRIOR FILING DATE: 2001-05-11
/ PRIOR APPLICATION NUMBER: PCT/JP99/06283
/ PRIOR FILING DATE: 1999-11-11
/ PRIOR APPLICATION NUMBER: JP 10-323759
/ PRIOR FILING DATE: 1998-11-13
/ PRIOR APPLICATION NUMBER: JP 11-060030
/ PRIOR FILING DATE: 1999-03-08
/ PRIOR APPLICATION NUMBER: JP 11-106812
/ PRIOR FILING DATE: 1999-04-14
/ PRIOR APPLICATION NUMBER: JP 11-166672
/ PRIOR FILING DATE: 1999-06-14
/ PRIOR APPLICATION NUMBER: JP 11-221640
/ PRIOR FILING DATE: 1999-08-04
/ PRIOR APPLICATION NUMBER: JP 11-259818
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 62
/ SEQ ID NO 39
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
US-10-719-587-39

Query Match 45.2%; Score 28; DB 16; Length 12;
Best Local Similarity 55.6%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9
||:|
Db 1 MPHSFANLP 9

RESULT 10
US-10-477-712B-7

/ Sequence 7, Application US/10477712B
/ Publication No. US20040185525A1
/ GENERAL INFORMATION:
/ APPLICANT: Takeda Chemical Industries, Ltd.
/ TITLE OF INVENTION: A Method for Producing A Peptide
/ FILE REFERENCE: OKA-0213
/ CURRENT APPLICATION NUMBER: US/10/477,712B
/ CURRENT FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: JP 2001-147341
/ PRIOR FILING DATE: 2001-05-17
/ NUMBER OF SEQ ID NOS: 85
/ SEQ ID NO 7
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Human
US-10-477-712B-7

Query Match 45.2%; Score 28; DB 16; Length 12;
Best Local Similarity 55.6%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9
||:|
Db 1 MPHSFANLP 9

RESULT 11
US-10-487-634-39
/ Sequence 39, Application US/10487634
/ Publication No. US20040241165A1
/ GENERAL INFORMATION:
/ APPLICANT: HINUMA, Shuji
/ APPLICANT: YOSHIDA, Hiroaki
/ APPLICANT: HASEGAWA, Yugo
/ APPLICANT: HOSOTA, Masaki
/ APPLICANT: KITADA, Chieko
/ TITLE OF INVENTION: Novel RFRP-3 And Its DNA
/ FILE REFERENCE: 2944USOP
/ CURRENT APPLICATION NUMBER: US/10/487,634
/ CURRENT FILING DATE: 2004-02-24
/ PRIOR APPLICATION NUMBER: PCT/JP02/08466
/ PRIOR FILING DATE: 2002-08-22
/ PRIOR APPLICATION NUMBER: JP 2001-254826
/ PRIOR FILING DATE: 2001-08-24
/ NUMBER OF SEQ ID NOS: 72
/ SEQ ID NO 39
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
US-10-487-634-39

Query Match 45.2%; Score 28; DB 16; Length 12;
Best Local Similarity 55.6%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9
||:|
Db 1 MPHSFANLP 9

RESULT 12
US-10-926-893-41
/ Sequence 41, Application US/10926893
/ Publication No. US20050074884A1
/ GENERAL INFORMATION:
/ APPLICANT: Robbins, Paul D.
/ APPLICANT: Mi, Zhibao
/ APPLICANT: Fritzel, Raymond
/ APPLICANT: Giorio, Joseph C.
/ APPLICANT: Gambotto, Andrea
/ TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT FACILITATE UPTAKE AND CYTOPLASMIC

```
/ TITLE OF INVENTION: NUCLEAR TRANSPORT
/ TITLE OF INVENTION: OF PROTEINS, DNA AND VIRUSES
/ FILE REFERENCE: AP32573-AAAB 072396, 0269
/ CURRENT APPLICATION NUMBER: US/10/926,893
/ CURRENT FILING DATE: 2004-08-26
/ PRIOR APPLICATION NUMBER: 60/151,980
/ PRIOR FILING DATE: 1999-09-01
/ PRIOR APPLICATION NUMBER: 60/188,944
/ PRIOR FILING DATE: 2000-03-13
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 41
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: random peptide library
US-10-926-893-41
```

```
Query Match          45.2%; Score 28; DB 17; Length 12;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 QNFYKLPQM 11
        |||:||||
DB      4 KNFPLPEL 12
```

RESULT 13

```
US-09-852-370-31
/ Sequence 31, Application US/09852370
/ Publication No. US20030126634A1
/ GENERAL INFORMATION:
/ APPLICANT: Pomerantz, Joel L.
/ APPLICANT: Sharp, Phillip A.
/ TITLE OF INVENTION: Chimeric DNA-binding proteins
/ FILE REFERENCE: APV-023, 02
/ CURRENT APPLICATION NUMBER: US/09/852,370
/ CURRENT FILING DATE: 2001-05-10
/ PRIOR APPLICATION NUMBER: 08/973,131
/ PRIOR FILING DATE: 1997-11-26
/ PRIOR APPLICATION NUMBER: PCT/US95/16982
/ PRIOR FILING DATE: 1995-12-29
/ PRIOR APPLICATION NUMBER: 08/366,083
/ PRIOR FILING DATE: 1994-12-29
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 31
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: human
US-09-852-370-31
```

```
Query Match          45.2%; Score 28; DB 10; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 NPYKLPQ 10
        |||:||||
DB      1 NPYLQPQ 7
```

RESULT 14

```
US-10-002-244-4
/ Sequence 4, Application US/10002244
/ Publication No. US20030143731A1
/ GENERAL INFORMATION:
/ APPLICANT: ARIAD Gene Therapeutics, Inc.
/ TITLE OF INVENTION: Use of Heterologous Transcription Factors in Gene Therapy
/ FILE REFERENCE: 346B USC1
/ CURRENT APPLICATION NUMBER: US/10/002,244
/ CURRENT FILING DATE: 2002-01-29
```

```
/ NUMBER OF SEQ ID NOS: 68
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 4
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: homo sapien
/ FEATURE:
/ NAME/KEY: DOMAIN
/ LOCATION: (1)..(18)
/ OTHER INFORMATION: glutamine rich region of Oct-2
US-10-002-244-4
```

```
Query Match          45.2%; Score 28; DB 14; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 NPYKLPQ 10
        |||:||||
DB      1 NPYLQPQ 7
```

RESULT 15

```
US-10-649-873-111
/ Sequence 111, Application US/10649873
/ Publication No. US20040171552A1
/ GENERAL INFORMATION:
/ APPLICANT: Biokine Therapeutics Ltd.
/ APPLICANT: Peled, Amnon
/ APPLICANT: Bizenberg, Orly
/ APPLICANT: Valzel-Obayon, Dalit
/ TITLE OF INVENTION: NOVEL CHEMOKINE BINDING PEPTIDES CAPABLE OF MODULATING THE
/ FILE REFERENCE: 26732
/ CURRENT APPLICATION NUMBER: US/10/649,873
/ CURRENT FILING DATE: 2003-08-28
/ NUMBER OF SEQ ID NOS: 157
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 111
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
US-10-649-873-111
```

```
Query Match          43.5%; Score 27; DB 16; Length 12;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 NPYKLPQ 10
        |||:||||
DB      4 NSYSLPQ 10
```

RESULT 16

```
US-10-014-340-803
/ Sequence 803, Application US/10014340
/ Publication No. US20030064411A1
/ GENERAL INFORMATION:
/ APPLICANT: Heratch, et al
/ TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
/ FILE REFERENCE: 9195-078
/ CURRENT APPLICATION NUMBER: US/10/014,340
/ CURRENT FILING DATE: 2001-12-10
/ NUMBER OF SEQ ID NOS: 823
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 803
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-014-340-803
```

Query Match 41.9%; Score 26; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PONEFKL 8
|:|:|:
DB 2 PENFFPL 9

RESULT 17

US-10-845-391-53
; Sequence 53, Application US/10845391
; Publication No. US2005003483A1
; GENERAL INFORMATION:
; APPLICANT: Hildebrand, William
; APPLICANT: Hickman, Heather
; TITLE OF INVENTION: COMPARATIVE LIGAND MAPPING FROM MHC CLASS I POSITIVE CELLS
; FILE REFERENCE: 6680.058
; CURRENT APPLICATION NUMBER: US/10/845,391
; CURRENT FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: 60/469,995
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: 60/518,132
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/240,143
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 60/299,452
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/327,907
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-845-391-53

Query Match 41.9%; Score 26; DB 17; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PONEFKL 8
|:|:|:
DB 3 PENFFPL 9

RESULT 18

US-09-920-174-3
; Sequence 3, Application US/09920174
; Patent No. US20020150590A1
; GENERAL INFORMATION:
; APPLICANT: KHANNA, RAJIV
; APPLICANT: KERR, BEVERLEY M.
; APPLICANT: MISKO, IHOR S.
; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FBRC:008USC2
; CURRENT APPLICATION NUMBER: US/09/920,174
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/920,175
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/194,450
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-920-174-3

Query Match 41.9%; Score 26; DB 9; Length 11;
Best Local Similarity 57.1%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 FYKLPQM 11
|:|:|:
DB 3 FYNIPPM 9

RESULT 19

US-09-920-195A-3
; Sequence 3, Application US/09920195A
; Publication No. US2003017530A1
; GENERAL INFORMATION:
; APPLICANT: KHANNA, RAJIV
; APPLICANT: KERR, BEVERLEY M.
; APPLICANT: MISKO, IHOR S.
; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FBRC:008USC1
; CURRENT APPLICATION NUMBER: US/09/920,195A
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/194,450
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-920-195A-3

Query Match 41.9%; Score 26; DB 10; Length 11;
Best Local Similarity 57.1%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 FYKLPQM 11
|:|:|:
DB 3 FYNIPPM 9

RESULT 20

US-10-752-380-3
; Sequence 3, Application US/10752380
; Publication No. US20050084498A1
; GENERAL INFORMATION:
; APPLICANT: KHANNA, RAJIV
; APPLICANT: KERR, BEVERLEY M.
; APPLICANT: MISKO, IHOR S.
; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FBRC:008
; CURRENT APPLICATION NUMBER: US/10/752,380
; CURRENT FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US/09/194,450
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3

```
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Peptide
US-10-752-380-3
```

```
Query Match 41.9%; Score 26; DB 17; Length 11;
Best Local Similarity 57.1%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 5 FYKLPQM 11
||:|
DB 3 FYNIRPM 9
```

```
RESULT 21
US-10-125-869A-43
; Sequence 43, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ranschoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-43
```

```
Query Match 41.9%; Score 26; DB 14; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 NPYKLP 9
||:|
DB 5 NFWQLP 10
```

```
RESULT 22
US-10-125-869A-119
; Sequence 119, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ranschoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 119
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-119
```

```
Query Match 41.9%; Score 26; DB 14; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 NPYKLP 9
||:|
DB 5 NFWQLP 10
```

```
RESULT 23
US-10-462-262-267
; Sequence 267, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin binding polypeptide
US-10-462-262-267
```

```
Query Match 41.9%; Score 26; DB 15; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 NPYKLP 9
||:|
DB 5 NFWQLP 10
```

```
RESULT 24
US-10-462-262-343
; Sequence 343, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin binding polypeptide
US-10-462-262-343
```

Query Match 41.9%; Score 26; DB 15; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFWKLP 9
|:|:|
Db 5 NFWKLP 10

RESULT 25

US-09-799-576A-22

; Sequence 22, Application US/09799576A
; Patent No. US20020034774A1
; GENERAL INFORMATION:

APPLICANT: HULTGREN, Scott

KUEHN, Meta

XU, Zheng

OGG, Derek

HARRIS, Mark

LEPISTO, Matti

KILBERG, Jan

JONES, Charles H.

TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,576A

FILING DATE: 07-Mar-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/640,877

FILING DATE: 10-OCT-1996

APPLICATION NUMBER: WO PCT/US94/13455

FILING DATE: 18-NOV-1994

ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek

REGISTRATION NUMBER: 30,427

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-09-799-576A-22

Query Match 41.9%; Score 26; DB 9; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFWKLP 9
|:|:|
Db 9 QNFWKLP 15

RESULT 26
US-09-799-540-22

; Sequence 22, Application US/09799540
; Patent No. US20020045199A1
; GENERAL INFORMATION:

APPLICANT: HULTGREN, Scott

KUEHN, Meta

XU, Zheng

OGG, Derek

HARRIS, Mark

LEPISTO, Matti

KILBERG, Jan

JONES, Charles H.

TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,540

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,877

FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek

REGISTRATION NUMBER: 30,427

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-799-540-22

Query Match 41.9%; Score 26; DB 9; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFWKLP 9
|:|:|
Db 9 QNFWKLP 15

RESULT 27
US-09-799-608-22

; Sequence 22, Application US/09799608
; Patent No. US20020146428A1
; GENERAL INFORMATION:

APPLICANT: HULTGREN, Scott

KUEHN, Meta

XU, Zheng

OGG, Derek

HARRIS, Mark

LEPISTO, Matti

KILBERG, Jan

JONES, Charles H.

TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,608
FILING DATE: 07-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,877
FILING DATE: <Unknown>
APPLICATION NUMBER: NO PCT/US94/13455
FILING DATE: 18-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 016921-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-799-608-22

Query Match 41.9%; Score 26; DB 9; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9
|:|:|:
DB 9 QDHYKMP 15

RESULT 28
US-09-798-932-22
Sequence 22, Application US/09798932
Publication No. US2003019892A1
GENERAL INFORMATION:
APPLICANT: HULTGREN, Scott
KUEHN, Meta
XU, Zheng
OGG, Derek
HARRIS, Mark
LEPISTO, Matti
KILBERG, Jan
JONES, Charles H.
TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/798,932
FILING DATE: 01-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/640,877
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: NO PCT/US94/13455
FILING DATE: 18-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 016921-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-798-932-22

Query Match 41.9%; Score 26; DB 10; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9
|:|:|:
DB 9 QDHYKMP 15

RESULT 29
US-09-799-680-22
Sequence 22, Application US/09799680
Publication No. US20030224468A1
GENERAL INFORMATION:
APPLICANT: HULTGREN, Scott
KUEHN, Meta
XU, Zheng
OGG, Derek
HARRIS, Mark
LEPISTO, Matti
KILBERG, Jan
JONES, Charles H.
TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,680
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/640,877

FILING DATE: 10-OCT-1996
APPLICATION NUMBER: WO PCT/US94/13455
FILING DATE: 18-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 016921-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-799-680-22

Query Match 41.9%; Score 26; DB 10; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 ONEFKLP 9
|:|:|
Db 9 ODHYKMP 15

RESULT 30
US-09-745-078A-21
Sequence 21, Application US/09745078A
Publication No. US20030050434A1
GENERAL INFORMATION:
APPLICANT: Garth J. S. COOPER
APPLICANT: Christina M. BUCHANAN
TITLE OF INVENTION: PEPTIDE
FILE REFERENCE: 441842000100
CURRENT APPLICATION NUMBER: US/09/745,078A
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: NZ336359
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: PCT/NZ00/00102
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Analog of human preptin
US-09-745-078A-21

Query Match 41.9%; Score 26; DB 10; Length 17;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 MPONFYKLP 9
|:|:|
Db 9 LPDNFPRYP 17

RESULT 31
US-09-962-756-1205
Sequence 1205, Application US/09962756
Publication No. US20030195147A1
GENERAL INFORMATION:
APPLICANT: PILIUTIA, RENUKA
APPLICANT: BRISSETTE, RENEE
APPLICANT: BLUME, ARTHUR J.
APPLICANT: SCHAEFER, LAUGE
APPLICANT: BRANDT, JAKOB
APPLICANT: GOLDSTEIN, NEIL I.

APPLICANT: SPETZLER, JANE
APPLICANT: OSTERGAARD, SOREN
APPLICANT: HANSEN, PER HERTZ
TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
FILE REFERENCE: 1878-4051US1
CURRENT APPLICATION NUMBER: US/09/962,756
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/538,038
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/146,127
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 2227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1205
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-962-756-1205

Query Match 41.9%; Score 26; DB 10; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PONFY 6
|:|:|
Db 3 PSNPF 7

RESULT 32
US-09-962-756-1757
Sequence 1757, Application US/09962756
Publication No. US20030195147A1
GENERAL INFORMATION:
APPLICANT: PILIUTIA, RENUKA
APPLICANT: BRISSETTE, RENEE
APPLICANT: BLUME, ARTHUR J.
APPLICANT: SCHAEFER, LAUGE
APPLICANT: BRANDT, JAKOB
APPLICANT: GOLDSTEIN, NEIL I.
APPLICANT: SPETZLER, JANE
APPLICANT: OSTERGAARD, SOREN
APPLICANT: HANSEN, PER HERTZ
TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
FILE REFERENCE: 1878-4051US1
CURRENT APPLICATION NUMBER: US/09/962,756
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/538,038
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/146,127
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 2227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1757
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-962-756-1757

Query Match 41.9%; Score 26; DB 10; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PONFY 6
|:|:|
Db 3 PSNPF 7


```
RESULT 33
US-09-962-756-1911
; Sequence 1911, Application US/09962756
; Publication No. US20030195147A1
; GENERAL INFORMATION:
; APPLICANT: PILLOTTA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUMS, ARTHUR J.
; APPLICANT: SCHAEFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1911
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-962-756-1911

Query Match      41.9%; Score 26; DB 10; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 PONFY 6
Db      3 PSNPFY 7

RESULT 34
US-10-374-624-21
; Sequence 21, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-21

Query Match      41.9%; Score 26; DB 14; Length 17;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 MPONFYKLP 9
Db      9 LPDNFPRYP 17

RESULT 35
US-10-253-471-1205
; Sequence 1205, Application US/10253471
; Publication No. US20030236190A1
; GENERAL INFORMATION:
; APPLICANT: PILLOTTA, RENUKA et al.
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4057
; CURRENT APPLICATION NUMBER: US/10/253,471
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1205
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-253-471-1205
```

```
Query Match      41.9%; Score 26; DB 15; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      2 PONFY 6
Db      3 PSNPFY 7

RESULT 36
US-10-253-471-1757
; Sequence 1757, Application US/10253471
; Publication No. US20030236190A1
; GENERAL INFORMATION:
; APPLICANT: PILLOTTA, RENUKA et al.
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4057
; CURRENT APPLICATION NUMBER: US/10/253,471
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1757
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-253-471-1757
```

```
Query Match      41.9%; Score 26; DB 15; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 3 PSNFI 7

RESULT 37
US-10-253-471-1911
; Sequence 1911, Application US/10253471
; Publication No. US20030236190A1
; GENERAL INFORMATION:
; APPLICANT: PILUITLA, RENUKA et al.
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4057
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1911
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-253-471-1911

Query Match 41.9%; Score 26; DB 15; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 POFNY 6
| | | |
Db 3 PSNFI 7

RESULT 38
US-10-253-493-1205
; Sequence 1205, Application US/10253493
; Publication No. US20040023887A1
; GENERAL INFORMATION:
; APPLICANT: PILUITLA, RENUKA et al.
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4056
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1205
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-253-493-1205

Query Match 41.9%; Score 26; DB 15; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 POFNY 6
| | | |

Db 3 PSNFI 7

RESULT 39
US-10-253-493-1757
; Sequence 1757, Application US/10253493
; Publication No. US20040023887A1
; GENERAL INFORMATION:
; APPLICANT: PILUITLA, RENUKA et al.
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4056
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1757
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-253-493-1757

Query Match 41.9%; Score 26; DB 15; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 POFNY 6
| | | |
Db 3 PSNFI 7

RESULT 40
US-10-253-493-1911
; Sequence 1911, Application US/10253493
; Publication No. US20040023887A1
; GENERAL INFORMATION:
; APPLICANT: PILUITLA, RENUKA et al.
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4056
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1911
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-253-493-1911

Query Match 41.9%; Score 26; DB 15; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 POFNY 6
| | | |
Db 3 PSNFI 7

Search completed: June 7, 2005, 23:31:38
Job time : 50.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:56:36 ; Search time 10.2 Seconds
(without alignment)
103.763 Million cell updates/sec

Title: US-10-691-157-6
Perfect score: 62
Sequence: 1 MPQNFYKLPQM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	40.3	17	2	hydroxyproline-ric
2	38.7	12	2	T-cell receptor al
3	38.7	13	2	T-cell receptor al
4	37.1	11	1	substance P - guin
5	37.1	11	1	substance P - hore
6	37.1	11	2	substance P - chic
7	35.5	11	2	phylalaemin - frog
8	35.5	11	2	ranatachytinin A -
9	35.5	11	2	benzo[1-COA ligase
10	35.5	15	2	benzo[1-COA ligase
11	33.9	8	2	benzo[1-COA ligase
12	33.9	9	2	benzo[1-COA ligase
13	33.9	12	2	benzo[1-COA ligase
14	32.3	7	2	benzo[1-COA ligase
15	32.3	11	4	benzo[1-COA ligase
16	32.3	11	4	benzo[1-COA ligase
17	32.3	12	2	benzo[1-COA ligase
18	32.3	12	2	benzo[1-COA ligase
19	32.3	12	2	benzo[1-COA ligase
20	32.3	12	2	benzo[1-COA ligase
21	32.3	12	2	benzo[1-COA ligase
22	32.3	12	2	benzo[1-COA ligase
23	32.3	12	2	benzo[1-COA ligase
24	32.3	12	2	benzo[1-COA ligase
25	32.3	12	2	benzo[1-COA ligase
26	32.3	12	2	benzo[1-COA ligase
27	32.3	12	2	benzo[1-COA ligase
28	32.3	12	2	benzo[1-COA ligase
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73	32.3	12	2	benzo[1-COA ligase
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75	32.3	12	2	benzo[1-COA ligase
76	32.3	12	2	benzo[1-COA ligase
77	32.3	12	2	benzo[1-COA ligase
78	32.3	12	2	benzo[1-COA ligase
79	32.3	12	2	benzo[1-COA ligase
80	32.3	12	2	benzo[1-COA ligase
81	32.3	12	2	benzo[1-COA ligase
82	32.3	12	2	benzo[1-COA ligase
83	32.3	12	2	benzo[1-COA ligase
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89	32.3	12	2	benzo[1-COA ligase
90	32.3	12	2	benzo[1-COA ligase
91	32.3	12	2	benzo[1-COA ligase
92	32.3	12	2	benzo[1-COA ligase
93	32.3	12	2	benzo[1-COA ligase
94	32.3	12	2	benzo[1-COA ligase
95	32.3	12	2	benzo[1-COA ligase
96	32.3	12	2	benzo[1-COA ligase
97	32.3	12	2	benzo[1-COA ligase
98	32.3	12	2	benzo[1-COA ligase
99	32.3	12	2	benzo[1-COA ligase
100	32.3	12	2	benzo[1-COA ligase

T cell receptor al
T-cell receptor be
T-cell receptor be
cob protein - comm
alpha-macroglobulin
hydrogensulfite re
prealbumin - weste
neuropeptide B - b
substance P-like p
substance P-like p
substance P - rain
photosystem II pro
glycophorin B/glyc
metal-binding prot
alpha-2-macroglobu
Ig heavy chain CRD
botulinum neurotox
S58862
hypothetical prote
hypothetical prote
urinary tract ston
hypothetical TBL/M
phospholipase A2 (b
beta-glucanase 13 -
neuropeptide A - b
cyclooligooligosac
hypothetical prote
neuropeptide GNFR
translation elonga
beta-D-galactosida
GRP-binding protei
hypothetical prote
protein QP200020 -
GRP-binding protei
protein QP200051 -
T-cell receptor be
T-cell receptor be
crystal protein, 2
mannose-specific 1
hemoglobin beta-x
gene Rhl protein -
ovohemerythrin - d
enkephalin-degradi
alkaline monooxygen
2S albumin small c
F7-I fibrinogen
hemoglobin alpha c
hypothetical prote
hutu protein - Kle
Ig heavy chain CRD
60k Ca binding pro
ranatachytinin B -
H+-transporting tw
214k exoantigen (v
transforming prote
probable minor cap
protein QH10045 -
VCM-1 5'UTR bindi
tryptophyl-in-reia
somatostatin I - B
somatostatin - ali
somatostatin I - c
somatostatin I - s
carbon-monoxide de
Ig heavy chain CRD
hypothetical 1.5K
dehydrin 4.5K poly
gene C-Ki-ras prot
T cell receptor al
corneal keratan su

ALIGNMENTS

RESULT 1

SS7991 hydroxyproline-rich protein - Sesbania rostrata (fragment)

C:Species: Sesbania rostrata

C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C:Accession: SS7991

R:Goomachig, S.; Valerio-Lepintec, M.; Szczyglowski, K.; van Montagu, M.; Holsters, M.

submitted to the EMBL Data Library, March 1995

A:Description: Use of differential display to identify novel Sesbania rostrata genes

A:Reference number: SS7991

A:Accession: SS7991

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-17 <GO>

A:Cross-references: UNIPROT:Q41400; EMBL:Z48673; NID:g899484; PID:g899485

C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 40.3%; Score 25; DB 2; Length 17;

Best Local Similarity 50.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PONYKLP 9

DB 3 PHYYKSP 10

RESULT 2

PH1454 T-cell receptor alpha chain (clone A3/72.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004

C:Accession: PH1454

R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Bannetier, C.; Regnault, A.; Ko

J. Exp. Med. 177, 811-820, 1993

A:Title: T cell receptor selection by and recognition of two class I major histocompatib

A:Reference number: PH1430; MUID:93171821; PMID:8436911

A:Accession: PH1454

A:Molecule type: mRNA

A:Residues: 1-12 <CAS>

A:Experimental source: cytolytic T-lymphocyte

C:Keywords: receptor; T-cell

Query Match 38.7%; Score 24; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ONFY 6

DB 7 ONFY 10

RESULT 3

PH0787 T-cell receptor alpha chain (F8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PH0787

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0787

A:Molecule type: mRNA

A:Residues: 1-13 <CAS>

A:Cross-references: EMBL:X60891

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 38.7%; Score 24; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ONFY 6

DB 8 ONFY 11

RESULT 4

A60654 substance P - guinea pig

C:Species: Cavia porcellus (guinea pig)

C:Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C:Accession: A60654

R:Murphy, R.

Neuropeptides 14, 105-110, 1989

A:Title: Primary amino acid sequence of guinea-pig substance P.

A:Reference number: A60654; MUID:90044685; PMID:2478925

A:Accession: A60654

A:Molecule type: protein

A:Residues: 1-11 <MUR>

A:Cross-references: UNIPROT:P01290

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; neuropeptide; tachykinin

F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.1%; Score 23; DB 1; Length 11;

Best Local Similarity 57.1%; Pred. No. 3.1e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PONYKLP 8

DB 4 PQQFRGL 10

RESULT 5

SPHO substance P - horse

C:Species: Equus caballus (domestic horse)

C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C:Accession: A01558

R:Studer, R.O.; Trzeciak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A:Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.

A:Reference number: A01558

A:Accession: A01558

A:Molecule type: protein

A:Residues: 1-11 <STU>

A:Cross-references: UNIPROT:P01290

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; hormone

F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.1%; Score 23; DB 1; Length 11;

Best Local Similarity 57.1%; Pred. No. 3.1e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PONYKLP 8

DB 4 PQQFRGL 10

RESULT 6

UN0023 substance P - chicken

C:Species: Gallus gallus (chicken)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C:Accession: UN0023

R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A:Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A:Reference number: UN0023; MUID:88204263; PMID:2452461

A:Accession: UN0023

A:Molecule type: protein
A:Residues: 1-11 <CON>

A:Cross-references: UNIPROT:P19850

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; tachykinin

F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 37.1%; Score 23; DB 2; Length 11;

Best Local Similarity 57.1%; Pred. No. 3.1e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PONFYKL 8

DB 4 PQDFYGL 10

RESULT 7

S07201 physalaemin - frog (Physalaemus fuscumaculatus)

C:Species: Physalaemus fuscumaculatus

C>Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-2004

C:Accession: S07201

R:Erspamer, V.; Anastasi, A.; Bertaccini, G.; Cei, J.M.

Experientia 20, 489-490, 1964

A:Title: Structure and pharmacological actions of physalaemin, the main active polypeptide

A:Reference number: S07201; PMID:66076612; PMID:5657249

A:Accession: S07201

A:Molecule type: protein

A:Residues: 1-11 <ERS>

A:Cross-references: UNIPROT:P08615

C:Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin

F:11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 35.5%; Score 22; DB 2; Length 11;

Best Local Similarity 57.1%; Pred. No. 4.8e+02; Mismatches 3; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PONFYKL 8

DB 4 PMKPYGL 10

RESULT 8

A61033 ranachykinin A - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: A61033; J00426

R:Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.

Regul. Pept. 42(Suppl.1), S12, 1992

A:Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and inte

A:Reference number: A61033

A:Accession: A61033

A:Molecule type: protein

A:Residues: 1-11 <KAN>

A:Cross-references: UNIPROT:P22688

R:Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 177, 588-595, 1991

A:Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and inte

A:Reference number: J00426; PMID:91254337; PMID:2043143

A:Accession: J00426

A:Molecule type: protein

A:Residues: 1-11 <KOZ>

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end; neuropeptide

F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 35.5%; Score 22; DB 2; Length 11;

Best Local Similarity 57.1%; Pred. No. 4.8e+02; Mismatches 3; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PONFYKL 8

DB 4 PDRFYGL 10

RESULT 9

D61033 ranachykinin D - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Aug-2004

C:Accession: D61033; J00429

R:Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.

Regul. Pept. 42(Suppl.1), S12, 1992

A:Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and inte

A:Reference number: A61033

A:Accession: D61033

A:Molecule type: protein

A:Residues: 1-11 <KAN>

A:Cross-references: UNIPROT:P22691

R:Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 177, 588-595, 1991

A:Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and inte

A:Reference number: J00429; PMID:91254337; PMID:2043143

A:Accession: J00429

A:Molecule type: protein

A:Residues: 1-11 <KOZ>

C:Keywords: amidated carboxyl end; neuropeptide

F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 35.5%; Score 22; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 4.8e+02; Mismatches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PONFY 6

DB 4 PERFY 8

RESULT 10

A48372 benzoyl-CoA ligase - Methanospirillum hungatei (fragment)

C:Species: Methanospirillum hungatei

C>Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A48372

R:Raburger, G.; Winter, J.

Appl. Microbiol. Biotechnol. 37, 789-795, 1992

A:Title: Purification and characterization of benzoyl-CoA ligase from a syntrophic, benz

A:Reference number: A48372; PMID:1369492

A:Accession: A48372

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <ADB>

A:Cross-references: UNIPROT:Q9UWM1

A:Note: sequence extracted from NCBI backbone (NCBI:118357)

Query Match 35.5%; Score 22; DB 2; Length 15;

Best Local Similarity 60.0%; Pred. No. 6.7e+02; Mismatches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PONFY 6

DB 5 PERFY 9

RESULT 11

A39892 P element, P cytotype-determining - fruit fly (Drosophila melanogaster) (fragment)

C:Species: Drosophila melanogaster

C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Feb-1997

C:Accession: A39892

R:Nitabaki, E.; Mukai, T.; Yamazaki, T.

Proc. Natl. Acad. Sci. U.S.A. 84, 7605-7608, 1987

A:Title: Repressor of P elements in Drosophila melanogaster: cytotype determination by a

A:Reference number: A39892

A:Accession: A39892
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <NT>
C:Genetics:
A:Gene: FlyBase:FBgn0003055
A:Cross-references: FlyBase:FBgn0003055

Query Match 33.9%; Score 21; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNF 5
:|:|
Db 1 IPKNF 5

RESULT 12

PT0270
Ig heavy chain CRD3 region (clone 3-100) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0270
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0270
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 33.9%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNFY 6
:|:|
Db 1 QNFY 4

RESULT 13

B60228
Fc mu (IgM) receptor surface complex beta chain - mouse (fragment)
N:Alternate names: membrane protein B29
C:Species: Mus musculus (house mouse)
C:Date: 08-Dec-1992 #sequence_revision 08-Dec-1992 #text_change 20-Mar-1998
C:Accession: B60228; B39398
R:Hombach, J.; Lottspeich, F.; Reith, M.
Eur. J. Immunol. 20, 2795-2799, 1990
A:Title: Identification of the genes encoding the IgM-alpha and Ig-beta components of th
A:Reference number: A60228; MUID:91099432; PMID:2269334
A:Accession: B60228
A:Molecule type: protein
A:Residues: 1-12 <HOM>
R:Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Gambier, J.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991
A:Title: IgM antigen receptor complex contains phosphoprotein products of B29 and mb-1 g
A:Accession: B39398
A:Reference number: A39398; MUID:91219496; PMID:2023945
A:Molecule type: protein
A:Residues: 'XX', 3-10 <CAM>
C:Keywords: membrane protein

Query Match 33.9%; Score 21; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 8.2e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9
:|:|
Db 4 LPLNFGSP 12

RESULT 14

B44787
Calliphoramide II - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: B44787
R:Duve, H.; Johnson, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thore
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A:Reference number: A41978; MUID:92196111; PMID:1549595
A:Accession: B44787
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <DUV>
A:Cross-references: UNIPROT:P41866
C:Keywords: amidated carboxyl end; neuropeptide
F:7/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 32.3%; Score 20; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PQNFYK 7
:|:|
Db 1 PDNFWR 6

RESULT 15

S07203
Uperolein - frog (Uperoleia marmorata)
C:Species: Uperoleia marmorata
C:Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-2004
C:Accession: S07203
R:Anastasi, A.; Erganer, V.; Eudean, R.
Experientia 31, 394-395, 1975
A:Title: Structure of uperolein, a physalamin-like endecapeptide occurring in the skin
A:Reference number: S07203; MUID:75131227; PMID:1120493
A:Accession: S07203
A:Molecule type: protein
A:Residues: 1-11 <ANA>
C:Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin
F:1/Modified site: pyroglutamic carboxyl end (Met) #status experimental
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 32.3%; Score 20; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PQNFYKL 8
:|:|
Db 4 PNAFYGL 10

RESULT 16

I52708
ELAV-like neuronal protein 1, truncated splice form - human
N:Alternate names: Drosophila ELAV(embryonic lethal, abnormal vision)-like 4; Hu antigen
C:Species: Homo sapiens (man)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: I52708
R:Seikido, Y.; Bader, S.A.; Cardone, D.P.; Johnson, B.E.; Minna, J.D.
Cancer Res. 54, 4988-4992, 1994
A:Title: Molecular analysis of the Hnd gene encoding a paraneoplastic encephalomyelitis
A:Reference number: I52708; MUID:94349312; PMID:8065866
A:Accession: I52708
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-11 <SEK>
A:Cross-references: UNIPROT:Q16234; GB:S73887; NID:9688242; PIDN:AA014142.1; PID:9426184
C:Comment: This abnormal peptide is expressed. For the long splice form, see PIR:I38726.
A:Gene: GDB:ELAVL4; HND; PNEW

Query Match 33.9%; Score 20; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

A/Cross-references: GDB:141875; OMIM:168360
 A/Map position: 1p36-1p36
 C/Keywords: alternative splicing

Query Match 32.3%; Score 20; DB 4; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPONFYKL 8
 |||
 Db 3 MPSRIKL 10

RESULT 17

A09985
 gamma-crystallin - haddock (fragments)
 C/Species: Melanogrammus aeglefinus (haddock)
 C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1993
 C/Accession: A09985
 R/Croft, L.R.
 Biochim. Biophys. Acta 295, 174-177, 1973
 A/Title: Amino and carboxy terminal sequence of gamma-crystallin, from haddock lens.
 A/Reference number: A09985; MUID:73088761; PMID:4685070
 A/Accession: A09985
 A/Molecule type: protein
 A/Residues: 1-12 <CRO>

Query Match 32.3%; Score 20; DB 2; Length 12;
 Best Local Similarity 42.9%; Pred. No. 1.3e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 FYKLPGM 11
 |||
 Db 5 FYITIDM 11

RESULT 18

S57570
 T cell receptor V-J junctional alpha chain region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
 C/Accession: S57570
 R/Burrows, S.R.; Salins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argact, V.P.
 submitted to the EMBL Data Library, June 1995
 A/Description: T cell receptor repertoire for a viral epitope in humans is diversified
 A/Reference number: S57494
 A/Accession: S57570
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-12 <BUR>
 A/Cross-references: EMBL:Z49954; NID:9887488; PIDN:CAA90225.1; PID:9887489
 C/Keywords: T-cell receptor

Query Match 32.3%; Score 20; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PONYF 6
 |||
 Db 6 PNOFY 10

RESULT 19

S74144
 aggrecan - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
 C/Accession: S74144
 R/Bonassar, L.U.; Stilm, J.L.; Peguio, C.G.; Frank, E.H.; Moore, V.L.; Lark, M.W.; Sandy
 Arch. Biochem. Biophys. 333, 359-367, 1996
 A/Title: Activation and inhibition of endogenous matrix metalloproteinases in articular
 A/Reference number: S74144; MUID:96404934; PMID:8809074
 A/Accession: S74144

A/Molecule type: mRNA
 A/Residues: 1-12 <BON>
 A/Experimental source: cartilage
 C/Keywords: cartilage; glycoprotein

Query Match 32.3%; Score 20; DB 2; Length 12;
 Best Local Similarity 33.3%; Pred. No. 1.3e+03;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFY 6
 |||
 Db 4 IPESFP 9

RESULT 20

S07436
 tachykinin - African tree frog (Kassina maculata)
 N/Alternate names: hylambatin
 C/Species: Kassina maculata
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
 C/Accession: S07436
 R/Yasunaka, T.; Nakajima, T.; Erepamer, G.F.; Erepamer, V.
 Biomed. Res. 2, 613-617, 1981
 A/Title: New tachykinins, Glu12, Pro5-kassinin (hylambates-kassinin) and hylambatin, in t
 A/Reference number: S07436
 A/Accession: S07436
 A/Molecule type: protein
 A/Residues: 1-12 <YAS>
 A/Cross-references: UNIPROT:P08614
 A/Experimental source: skin
 A/Note: the source is designated as Hylambates maculatus
 C/Keywords: amidated carboxyl end; neuropeptide; tachykinin
 P:12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 32.3%; Score 20; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PONYF 6
 |||
 Db 5 PDRFY 9

RESULT 21

T37075
 hypothetical protein SCU30.08 - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C/Accession: T37075
 R/Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, August 1999
 A/Reference number: Z21621
 A/Accession: T37075
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-16 <SAN>
 A/Cross-references: EMBL:AL109973; PIDN:CAM53303.1; GSPDB:GN00070; SCOEDB:SCU30.08
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Gene: SCOEDB:SCU30.08

Query Match 32.3%; Score 20; DB 2; Length 16;
 Best Local Similarity 44.4%; Pred. No. 1.7e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPONFYKLP 9
 |||
 Db 7 MPRSAIGLP 15

RESULT 22

C39398
 Fc mu (IgM) receptor surface complex gamma chain - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 20-Mar-1998
C:Accession: C39398
R:Campbell, K.S.; Hager, B.J.; Friedrich, R.J.; Gambler, J.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991
A:Title: IGM antigen receptor complex contains phosphoprotein products of B29 and mb-1 g
A:Reference number: A39398; MUID:91219496; PMID:2023945
A:Accession: C39398
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <CAM>

Query Match 30.6%; Score 19; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PQNPF 5
DB 4 LPNLF 8

RESULT 23

S23373
T-cell receptor alpha chain J region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S23373
R:Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichmar
Eur. J. Immunol. 21, 2749-2754, 1991
A:Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rhe
A:Reference number: S23364; MUID:92037820; PMID:1657615
A:Accession: S23373
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-11 <PLU>
A:Cross-references: EMBL:X58168
C:Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PQNFKL 8
DB 3 PSNYDKV 9

RESULT 24

S23306
Substance P - Atlantic cod
C:Species: Gadus morhua (Atlantic cod)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C:Accession: S23306
R:Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992

A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod
A:Reference number: S23186; MUID:92298992; PMID:1376687
A:Accession: S23306
A:Molecule type: protein
A:Residues: 1-11 <JEN>
A:Cross-references: UNIPROT:P28498
A:Experimental source: brain
C:Function:
A:Description: may play a physiological role in the regulation of cardiovascular and gas
A:Note: Substance P is derived by post-translational processing of preprotachykinin A
C:Keywords: neuropeptide; amidated carboxyl end; tachykinin
F11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 30.6%; Score 19; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PQNFKL 8

DB 4 PQQFYL 10

RESULT 25

S47358
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47358
R:Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47358
A:Accession: S47358
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35682; NID:9527453; PIDN:CAA84751.1; PID:9527454
C:Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQNPF 5
DB 10 PQHFL 13

RESULT 26

S51735
T-cell receptor beta-chain joining region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
C:Accession: S51735
R:Durinovic-Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.
submitted to the EMBL Data Library, November 1993
A:Reference number: S51732
A:Accession: S51735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <DUR>
A:Cross-references: EMBL:Z28344; NID:9607122; PIDN:CAA82198.1; PID:9607123
C:Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQNPF 5
DB 12 PQHFL 15

RESULT 27

B49655
T-cell-receptor beta chain variable region, TCR V beta (clone SF-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: B49655
R:Grom, A.A.; Thompson, S.D.; Luyrink, L.; Passo, M.; Choi, E.; Glass, D.N.
Proc. Natl. Acad. Sci. U.S.A. 90, 11104-11108, 1993
A:Title: Dominant T-cell-receptor beta chain variable region V beta 14+ clones in juveni
A:Reference number: B49655; MUID:94068553; PMID:8248215
A:Accession: B49655
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-15 <GRO>
A:Experimental source: knee joint, synovial fluid lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBI:P114046)
C:Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PGNF 5
||:|
Db 11 PQHF 14

RESULT 28

PA0008

Lectin B2 - Psophocarpus scandens (fragment)

C:Species: Psophocarpus scandens

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: PA0008

R:Kortt, A.A.

Phytochemistry 27, 2847-2855, 1988

A:Title: Isolation and characterization of the lectins from the seeds of Psophocarpus sc

A:Reference number: PA0005

A:Accession: PA0008

A:Molecule type: protein

A:Residues: 1-15 <KOR>

A:CROSS-references: UNIPROT:P22585

A:Experimental source: seed

C:Comment: The seeds of Psophocarpus contain two distinct groups of lectins which can be

C:Keywords: lectin

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NPYKLQ 10
||:|
Db 7 NPNKFEQ 13

RESULT 29

A36279

chemoattractant protein - earthworm (Lumbricus terrestris) (fragment)

C:Species: Lumbricus terrestris (common earthworm)

C:Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004

C:Accession: A36279

R:Jiang, X.C.; Inouchi, J.; Wang, D.; Halpern, M.

J. Biol. Chem. 265, 8736-8744, 1990

A:Title: Purification and characterization of a chemoattractant from electric shock-indu

snakes.

A:Reference number: A36279; MUID:90256800; PMID:2160465

A:Accession: A36279

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <DIA>

A:CROSS-references: UNIPROT:O44335

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 PGNFKLP 9
||:|
Db 5 PPGFTYLP 12

RESULT 30

PH1778

T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: PH1778

R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057

A:Accession: PH1778
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <POR>

Query Match 30.6%; Score 19; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NPYKL 8
||:|
Db 10 NDYKL 14

RESULT 31

E49255

T-cell receptor beta chain V-D-J-C region (V beta 17, J beta 1.5) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997

C:Accession: E49255

R:Rozenberg, W.M.; Moss, P.A.; Bell, J.I.

Eur. J. Immunol. 22, 541-549, 1992

A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using

A:Reference number: A49039; MUID:92164737; PMID:1311263

A:Accession: E49255

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-16 <ROS>

A:Note: sequence extracted from NCBI backbone (NCBI:P:90726)

C:Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PGNF 5
||:|
Db 12 PQHF 15

RESULT 32

F49039

T-cell receptor beta chain V-D-J-C region (V beta 2, J beta 1.5) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997

C:Accession: F49039

R:Rozenberg, W.M.; Moss, P.A.; Bell, J.I.

Eur. J. Immunol. 22, 541-549, 1992

A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using

A:Reference number: A49039; MUID:92164737; PMID:1311263

A:Accession: F49039

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-16 <ROS>

A:Note: sequence extracted from NCBI backbone (NCBI:P:90718)

C:Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PGNF 5
||:|
Db 12 PQHF 15

RESULT 33

S22040

cbb protein - common sunflower

C:Species: Helianthus annuus (common sunflower)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S22040

R:Koehler, R.H.

submitted to the EMBL Data Library, October 1991

A:Reference number: S22040
A:Accession: S22040
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <KOE>
A:Cross-references: UNIPROT:Q34699; EMBL:X62592; NID:g12990; PID:g12991

Query Match 30.6%; Score 19; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 NPY 6
|||
Db 3 NPY 5

RESULT 34

S23971
alpha-macroglobulin proteinase inhibitor - common octopus
C:Species: Octopus vulgaris (common octopus)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S23971
R:Hoegersen, I.B.; Salvesen, G.; Brucato, F.H.; Pizzo, S.V.; Enghild, J.J.
Biochem. J. 285, 521-527, 1992
A>Title: Purification and characterization of an alpha-macroglobulin proteinase inhibitor
A:Reference number: S23971; MUID:92344633; PMID:1379044
A:Accession: S23971
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <THO>
A:Cross-references: UNIPROT:E30800

Query Match 30.6%; Score 19; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 NPY 6
|||
Db 12 NPY 14

RESULT 35

S11556
hydrogenulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragment)
N:Alternate names: bisulfite reductase; desulfosulfid
C:Species: Desulfovibrio thermophilus
C:Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998
C:Accession: S11556
R:Faque, G.; Jino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.; I
Biochim. Biophys. Acta 1040, 112-118, 1990
A>Title: Purification and characterization of bisulfite reductase (desulfosulfid) from
A:Reference number: S11024; MUID:90335276; PMID:2165817
A:Accession: S11556
A:Molecule type: protein
A:Residues: 1-6 <FAU>
A:Keywords: oxidoreductase

Query Match 29.0%; Score 18; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PQNFK 7
|||
Db 1 PEEKY 6

RESULT 36

I49404
prealbumin - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49404

R:Ko, M.S.; Wang, X.; Horton, J.H.; Hegen, M.D.; Takahashi, N.; Maerzaki, Y.; Nadeau, J.H
Mamm. Genome 5, 349-355, 1994
A>Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49404
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <RES>
A:Cross-references: UNIPROT:Q62527; EMBL:U05689; NID:g497008; PID:AAB60461.1; PID:g6428

Query Match 29.0%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PQN 4
|||
Db 6 PQN 8

RESULT 37

B24749
neuropeptide B - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 09-Jul-2004
C:Accession: B24749
R:Yang, H.Y.T.; Fratka, W.; Majane, E.A.; Costa, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
A>Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b
A:Reference number: A94074; MUID:86067985; PMID:3865193
A:Accession: B24749
A:Molecule type: protein
A:Residues: 1-8 <YAN>
A:Cross-references: UNIPROT:P15507
C:Superfamily: unassigned animal peptides
C:Keywords: neuropeptide

Query Match 29.0%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PQNF 5
|||
Db 5 PQRF 8

RESULT 38

B60409
substance P-like peptide I - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004
C:Accession: B60409
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A>Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austra
A:Reference number: A60409; MUID:90287814; PMID:2356157
A:Accession: B60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
A:Cross-references: UNIPROT:P42989
C:Keywords: amidated carboxyl end; pyroglutamic acid
F11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 29.0%; Score 18; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 2.8e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PQNFKL 8
|||
Db 4 PDEFKGL 10

RESULT 39

F60409

Substance P-like peptide II - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri

C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004

C:Accession: F60409

R:Stimaco, M.; Severini, C.; De Blase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior

Peptides 11, 299-304, 1990

A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro

A:Reference number: A60409; MUID:90287814; PMID:2356157

A:Accession: F60409

A:Molecule type: protein

A:Residues: 1-11 <SIM>

C:Cross-references: UNIPROT:P42990

C:Keywords: amidated carboxyl end; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 29.0%; Score 18; DB 2; Length 11;

Best Local Similarity 42.9%; Pred. No. 2.8e+03;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PONTYKL 8

DB 4 PNEFFGL 10

RESULT 40

S23308

Substance P - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004

C:Accession: S23308

R:Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod

A:Reference number: S23186; MUID:92298992; PMID:1376687

A:Accession: S23308

A:Molecule type: protein

A:Residues: 1-11 <JEN>

A:Cross-references: UNIPROT:P28499

A:Experimental source: brain

C:Function:

A:Description: may play a physiological role in the regulation of cardiovascular and gas

A>Note: substance P is derived by post-translational processing of preprotachykinin A

C:Keywords: neuropeptide; amidated carboxyl end; tachykinin

F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 29.0%; Score 18; DB 2; Length 11;

Best Local Similarity 42.9%; Pred. No. 2.8e+03;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PONTYKL 8

DB 4 PNEFFGL 10

Search completed: June 7, 2005, 23:20:41

Job time : 11.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 48.4 Seconds

(without alignments)
116.382 Million cell updates/sec

Title: US-10-691-157-6

Perfect score: 62

Sequence: 1 MPQNFYKLPQM 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match length	ID	Description
1	26	41.9	15 1	SODM_ENTAB
2	25	40.3	17 2	O49225
3	25	40.3	17 2	O41400
4	24	38.7	11 1	TKNA_RANRI
5	24	38.7	13 2	O6LDM2
6	23	37.1	11 1	TKN2_UPERU
7	23	37.1	11 1	TKNA_CAVPO
8	23	37.1	11 1	TKNA_CHICK
9	23	37.1	11 1	TKNA_HORSE
10	23	37.1	13 1	SODM_ARTDA
11	22	35.5	11 1	TKNA_RANCA
12	22	35.5	11 1	TKND_RANCA
13	22	35.5	11 1	TKN_PHYFU
14	22	35.5	14 2	O9MIO3
15	22	35.5	15 1	GTEI_PSEVO
16	22	35.5	15 2	O9UWMI
17	22	35.5	17 2	O9UCM4
18	21	33.9	10 2	O6K6C9
19	21	33.9	10 2	O9XBH3
20	21	33.9	13 2	O9QVU4
21	21	33.9	15 2	O9TOX7
22	21	33.9	15 2	O9TGTO
23	21	33.9	16 1	BRB_BASAL
24	21	33.9	17 2	O6R9P0
25	21	33.9	17 2	O6R9P2
26	21	33.9	17 2	O6R9P2
27	21	33.9	17 2	O6R9P2
28	21	33.9	17 2	O6R9P4
29	21	33.9	17 2	O6R9P8
30	21	33.9	18 2	O9RGR1
31	21	33.9	18 2	O9RGR2

32	20	32.3	7 1	P41866 calliphora
33	20	32.3	9 1	P16223 locusta mty
34	20	32.3	1 1	P82026 uperoleia i
35	20	32.3	11 1	P08612 uperoleia r
36	20	32.3	11 2	O16234 homo sapien
37	20	32.3	11 2	O9RFZ2 mycoplasma
38	20	32.3	12 1	P08614 kaesina mac
39	20	32.3	12 2	O53579 rhodobacter
40	20	32.3	13 2	O9THR8 bryopsis sp
41	20	32.3	13 2	O9TKG6 lambda anta
42	20	32.3	13 2	O8J332 ficedula al
43	20	32.3	14 2	O7PE81 anophelis g
44	20	32.3	14 2	O7IGT8 andrena bro
45	20	32.3	15 2	O7IGX0 andrena ref
46	20	32.3	15 2	O9TCQ9 bos taurus
47	20	32.3	15 2	O9TR40 bos taurus
48	20	32.3	15 2	O7IGV0 andrena teg
49	20	32.3	15 2	O7IH02 andrena inc
50	20	32.3	15 2	O7IH38 andrena aur
51	20	32.3	15 2	O53580 rhodobacter
52	20	32.3	15 2	O9R4T2 bacillus in
53	20	32.3	16 2	O6Y662 mycoplasma
54	20	32.3	17 2	O7RY15 neurospora
55	20	32.3	17 2	O9QUY6 rattus sp.
56	20	32.3	18 2	O8SKY0 cuscuta ref
57	19	30.6	8 2	O9HC00 homo sapien
58	19	30.6	8 2	O45615 bacillus su
59	19	30.6	9 2	O67605 squash leaf
60	19	30.6	9 2	O67606 squash leaf
61	19	30.6	11 1	TKNA_GADMO
62	19	30.6	11 2	O9URG1
63	19	30.6	11 2	O80G99
64	19	30.6	13 1	UN02_PINDS
65	19	30.6	13 2	O7IA29 sus scrofa
66	19	30.6	13 2	O9T4K3 bryopsis sp
67	19	30.6	13 2	O9T4K4 bryopsis sp
68	19	30.6	13 2	O9T4K5 bryopsis sp
69	19	30.6	13 2	O9T4K6 bryopsis sp
70	19	30.6	13 2	O9THS2 bryopsis sp
71	19	30.6	13 2	O9THS3 bryopsis sp
72	19	30.6	14 2	O7IGY0 andrena ofe
73	19	30.6	15 1	LEC2_PSO5C
74	19	30.6	15 1	LG29_VIGUS
75	19	30.6	15 1	SODM_STRCR
76	19	30.6	15 2	O7RE88 plasmidium
77	19	30.6	15 2	O7RHB9 plasmidium
78	19	30.6	16 2	O7RHB9 plasmidium
79	19	30.6	16 2	O34699 helianthus
80	19	30.6	16 2	O38671 bacterioph
81	19	30.6	17 2	O13376 homo sapien
82	19	30.6	17 2	O7RM54 plasmidium
83	19	30.6	17 2	O9XSG1 bos taurus
84	19	30.6	17 2	O9PRU8 gallus galli
85	19	30.6	18 1	A2M_OCTVU
86	19	30.6	18 1	SODM_MYCHA
87	19	30.6	18 2	O97773 cercopithec
88	19	30.6	18 2	O7RH77 sus scrofa
89	19	30.6	18 2	O9ZG42 chlamydia t
90	19	30.6	18 2	O7TNW7 mus musculu
91	19	30.6	18 2	O7TNW8 rattus norv
92	18	29.0	8 1	NEMB_BOVIN
93	18	29.0	8 2	O6LDA7
94	18	29.0	8 2	O6Z527 mus epircus
95	18	29.0	9 2	O94VG2 varanus ind
96	18	29.0	9 2	O9S8J8 oryza sativ
97	18	29.0	10 2	O9H121 homo sapien
98	18	29.0	11 1	TKN4_PSEGU
99	18	29.0	11 1	TKN5_PSEGU
100	18	29.0	11 1	TKNA_ONCMY

ALIGNMENTS

```

RESULT 1
SODM_ENTAE STANDARD; PRT; 15 AA.
AC P22799;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
GN Name=soda;
OS Enterobacter aerogenes (Enterobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RP MEDLINE=91248479; PubMed=1368658;
RA Kim S.W., Lee S.O., Lee T.H.;
RT "Purification and characterization of superoxide dismutase from
RT Aerobacter aerogenes."
RL Agric. Biol. Chem. 55:101-108(1991).
CC -!- FUNCTION: Degrades radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR PIR: P06015; P06015.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; Sod_Fe_N; 1.
DR PROSITE: PS00088; SOD_NM; PARTIAL.
KW Direct protein sequencing; Iron; Metal-binding; Oxidoreductase.
FT NON TER 15
SQ SEQUENCE 15 AA; 1756 MW; 352F3D949202B642 CRC64;

Query Match 41.9%; Score 26; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKLPQM 11
DB 2 YELPOL 7

RESULT 2
049225 PRELIMINARY; PRT; 17 AA.
AC 049225;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hydroxyproline-rich glycoprotein (Fragment).
GN Name=hrgp;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Roots;
RX MEDLINE=94211912; PubMed=8159793; DOI=10.1104/pp.104.2.793;
RA Hong J.C., Chong Y.H., Nagao R.T., Bahk J.D., Cho M.J., Key J.L.;
RT "Isolation and characterization of three soybean extensin cDNAs."
RT Plant Physiol. 104:793-796(1994).
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE=Roots;
RA Mahalingam R., Knop H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF047052; AAC03558.1; -.
FT NON TER 1

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SQ SEQUENCE 17 AA; 2149 MW; 285E5B74515A2222 CRC64;

Query Match 40.3%; Score 25; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PONYKLP 9
DB 4 PHYYKSP 11

RESULT 3
041400 PRELIMINARY; PRT; 17 AA.
AC 041400;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hydroxyproline-rich protein (Fragment).
OS Sesbania rostrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.
OX NCBI_TaxID=3895;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Bacterial infected stem located root primordia;
RX MEDLINE=96112737; PubMed=8664492;
RA Geornachtig S., Valerio-Lepintec M., Szczylowski K., Van Montagu M.,
RA Holsters M., De Bruijn F.;
RT "Use of differential display to identify novel Sesbania rostrata genes
RT enhanced by Azorhizobium caulinodans infection."
RL Mol. Plant Microbe Interact. 8:816-824(1995).
DR EMBL: Z48673; CAA88592.1; -.
DR PIR: S57991; S57991.
FT NON TER 1
SQ SEQUENCE 17 AA; 2078 MW; 5060D2744515A22 CRC64;

Query Match 40.3%; Score 25; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PONYKLP 9
DB 3 PHYYKSP 10

RESULT 4
TKNA_RANRI STANDARD; PRT; 11 AA.
AC P29207;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ranakinin (Substance P-related peptide).
OS Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RP TISSUE=BRAIN;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Iovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda."
RL J. Neurochem. 57:2086-2091(1991).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.

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DR InterPro; IPR002040; Tachy Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
DR Amidaion; Direct protein sequencing; Neuropeptide; Tachykinin.
KW MOD RES 11
FT MOD RES 11 Methionine amide.
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match
Best Local Similarity 38.7%; Score 24; DB 1; Length 11;
Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PONTYKL 8
DB 4 PRTFYL 10

RESULT 5
O6LDM2 PRELIMINARY; PRT; 13 AA.
ID O6LDM2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAO;
RX MEDLINE=90036723; PubMed=2509433;
RA Hoshino T., Kose K.;
RT "Cloning and nucleotide sequence of brac, the structural gene for the
RT leucine-, isoleucine-, and valine-binding protein of Pseudomonas
RT aeruginosa PAO."
RL J. Bacteriol. 171:6300-6306(1989).
DR EMBL; M31071; AA08431.1; -.
KW Hypothetical protein.
FT NON TER 13
SQ SEQUENCE 13 AA; 1648 MW; F275BF6289EB3B51 CRC64;

Query Match
Best Local Similarity 38.7%; Score 24; DB 2; Length 13;
Pred. No. 1.6e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 MPONFYKLPOW 11
DB 1 MPEITHYLOQL 11

RESULT 6
TKN2 UPERU STANDARD; PRT; 11 AA.
ID TKN2 UPERU
AC P08616;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rugosauperolein II (lives, Thr6physalaemin).
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=80223080; PubMed=7389029;
RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;
RT "Physalaemin- and Bombesin-like peptides in the skin of the Australian
RT lepodactylid frog Uperoleia rugosa."

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RL Chem. Pharm. Bull. 28:689-695(1980).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amidaion; Amphibian defense peptide; Direct protein sequencing;
KW Neuropeptide; Pyroglutamate carboxylic acid; Tachykinin.
FT MOD RES 11
FT MOD RES 11 Methionine amide.
SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match
Best Local Similarity 37.1%; Score 23; DB 1; Length 11;
Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PONTYKL 8
DB 4 PRTFYL 10

RESULT 7
TKNA CAVPO STANDARD; PRT; 11 AA.
ID TKNA CAVPO
AC P67932; P01290;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Substance P.
GN Name=TAC1; Synonyms=NKA, NKNA, TAC2;
OS Bala porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Buthera; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RC TISSUE=Small intestine;
RX MEDLINE=90044685; PubMed=2478925; DOI=10.1016/0143-4179(89)90066-8;
RA Murphy R.;
RT "Primary amino acid sequence of guinea-pig substance P."
RL Neuropeptides 14:105-110(1989).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amidaion; Direct protein sequencing; Neuropeptide; Neurotransmitter;
KW Tachykinin.
FT MOD RES 11
FT MOD RES 11 Methionine amide.
SQ SEQUENCE 11 AA; 1349 MW; 3E75FE3C9D6C67 CRC64;

Query Match
Best Local Similarity 37.1%; Score 23; DB 1; Length 11;
Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PONTYKL 8
DB 4 PRTFYL 10

RESULT 8
TKNA CHICK STANDARD; PRT; 11 AA.
ID TKNA CHICK

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AC P19850;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Substance P. (Chicken).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;
RX MEDLINE=88204263; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "[Arg3] substance P and neurokinin A from chicken small intestine.";
RU Regul. Pept. 20:171-180(1988).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR InterPro: IPR002040; Tachy_Neurokinin.
DR Pfam: PF02202; Tachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Amide; Direct protein sequencing; Neuropeptide; Neurotransmitter;
KW Tachykinin.
FT MOD_RES 11 Methionine amide.
SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match
Best Local Similarity 37.1%; Score 23; DB 1; Length 11;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PQPFYKL 8
DB 4 PQPFYKL 10

RESULT 9
TKNA_HORSE STANDARD; PRT; 11 AA.
AC P67933; P01290;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Substance P.
OS Name=TA1; Synonyms=NKA, NKNA, TAC2;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RC Studer R.O., Trzeciak A., Lergier W.;
RT "Isolation and amino-acid sequence of substance P from horse
RT intestine.";
RU Helv. Chim. Acta 56:860-866(1973).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR InterPro: IPR002040; Tachy_Neurokinin.
DR Pfam: PF02202; Tachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Amide; Direct protein sequencing; Neuropeptide; Neurotransmitter;
KW Tachykinin.
FT MOD_RES 11 Methionine amide.
SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

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SQ SEQUENCE 11 AA; 1349 MW; 3E57FE3C9D6C6C7 CRC64;

Query Match
Best Local Similarity 37.1%; Score 23; DB 1; Length 11;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PQPFYKL 8
DB 4 PQPFYKL 10

RESULT 10
SODM_ARTDA STANDARD; PRT; 13 AA.
ID SODM_ARTDA
AC P83289;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Superoxide dismutase [Mn/Fe] (EC 1.15.1.1) (Fragment).
OS Arthropods; Arthropoda; Insecta; Diptera; Tephritidae; Tephritinae;
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Orbiliomycetes;
OC Orbiliales; Orbiliaceae; mitosporic Orbiliaceae; Arthropods;
OX NCBI_TaxID=74499;
RN [1]
RP SEQUENCE.
RC STRAIN=072;
RA Zhao M., Zhang K.;
RL Submitted (FEB-2002) to Swiss-Prot.
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese or iron ion per subunit (By
CC similarity).
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR InterPro: IPR001189; SODismutase.
DR PROSITE: PS00088; SOD_MN; PARTIAL.
KW Direct protein sequencing; Iron; Manganese; Metal-binding;
KW Oxidoreductase.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1515 MW; 69949202E642672B CRC64;

Query Match
Best Local Similarity 37.1%; Score 23; DB 1; Length 13;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKLPM 11
DB 2 YKLPM 7

RESULT 11
TKNA_RANCA STANDARD; PRT; 11 AA.
ID TKNA_RANCA
AC P22688;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ranataphykinin A (RTK A).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain, and Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo R.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RU Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
SQ SEQUENCE.

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RC TISSUE=Intestine;
 RX MEDLINE=94023216; PubMed=8210506; DOI=10.1016/0167-0115(93)90016-2;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (*Rana catesbeiana*) brain and
 RL intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR PIR: A61033; A61033.
 DR InterPro: IPR002040; Tachy_Neurokinin.
 DR InterPro: IPR008215; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 FT MOD_RES 11 Methionine amide.
 SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;
 Query Match 35.5%; Score 22; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 PONTYKL 8
 DB 4 PDRFYGL 10
 RESULT 12
 ID TKND_RANCA STANDARD; PRT; 11 AA.
 AC P22691;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ranachykinin D (RTK D).
 OS Rana catesbeiana (Bull. frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBT_TaxID=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (*Rana catesbeiana*)
 RT brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RL [2]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=94023216; PubMed=8210506; DOI=10.1016/0167-0115(93)90016-2;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (*Rana catesbeiana*) brain and
 RT intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR PIR: D61033; D61033.
 DR InterPro: IPR002040; Tachy_Neurokinin.
 DR PROSITE: PS00267; TACHYKININ; FALSE_NEG.
 KW Amphibia; Direct protein sequencing; Neuropeptide; Tachykinin.
 FT MOD_RES 11 Methionine amide.
 SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;
 Query Match 35.5%; Score 22; DB 1; Length 11;

Best Local Similarity 60.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PONTY 6
 DB 4 PERFY 8
 RESULT 13
 ID TKN_PHYFU STANDARD; PRT; 11 AA.
 AC P08615;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Physalaemin.
 OS Physalaemus fuscumaculatus (Neotropical frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Leptodactylidae;
 OC Leptodactylinae; Physalaemus.
 OX NCBT_TaxID=8378;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=66076612; PubMed=5857249;
 RA Erppamer V., Anastasi A., Bertaccini G., Col J.M.;
 RT "Structure and pharmacological actions of physalaemin, the main active
 RT polypeptide of the skin of *Physalaemus fuscumaculatus*.";
 RL Experientia 20:489-490(1964).
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR PIR: S07201; S07201.
 DR InterPro: IPR002040; Tachy_Neurokinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Amphibia; Amphibian defense peptide; Direct protein sequencing;
 KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
 FT MOD_RES 11 Pyroglutamic acid.
 FT MOD_RES 11 Methionine amide.
 SQ SEQUENCE 11 AA; 1283 MW; 329369359C3457 CRC64;
 Query Match 35.5%; Score 22; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 PONTYKL 8
 DB 4 PNTFYGL 10
 RESULT 14
 ID Q9MWQ3 PRELIMINARY; PRT; 14 AA.
 AC Q9MWQ3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Cytochrome b (Fragment).
 GN Name=Cytb;
 OS Podospora curvicolle.
 OS Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetiales; Sordariales; Lasiosphaeriaceae; Podospora.
 OX NCBT_TaxID=48157;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20150243; PubMed=10684923; DOI=10.1093/nar/28.6.1299;
 RA Saguez C., Lecellier G., Koll F.;

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RT "Intronic GIV-YIG endonuclease gene in the mitochondrial genome of
RT Padozpora curvicolli: evidence for mobility."
RL Nucleic Acids Res. 28:1299-1306 (2000).
DR EMBL: AJ249985; CAB72449.1; -.
DR GO: GO:0005739; C:mitochondrion; IEA.
DR InterPro: IPR005798; Cytb_b6_C.
DR PROSITE: PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 14 AA; 1603 MW; 2972D7731A723E43 CRC64;

Query Match 35.5%; Score 22; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FYKLPQM 11
Db 7 WTLPSM 13

RESULT 15
GREL_PSEUDO STANDARD; PRT; 15 AA.
AC P8299;
DT 05-JUL-2004 (rel. 44, Created)
DT 05-JUL-2004 (rel. 44, Last sequence update)
DT 05-JUL-2004 (rel. 44, Last annotation update)
DE Glutathione S-transferase (EC 2.5.1.18) (Fragment).
OS Pseudomonas sp. (strain M1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=95619;
RN [1]
RP LOCATION, FUNCTION, CATALYTIC ACTIVITY, SUBUNIT, AND SUBCELLULAR
RX MEDLINE=21896940; PubMed11900268; DOI=10.1016/S0923-2508(01)01293-1;
RA Santos P.M., Mignogna G., Heipieper H.J., Zennaro E.;
RT "Occurrence and properties of glutathione S-transferases in phenol-
RT degrading Pseudomonas strains".
RL Res. Microbiol. 153:89-98 (2002).
CC -1- FUNCTION: Conjugation of reduced glutathione to a wide number of
CC exogenous and endogenous hydrophobic electrophiles.
CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione..
CC -1- SUBUNIT: Monomer and homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GST superfamily.
DR GO: GO:0005737; C:cytoplasm; NAS.
DR GO: GO:0004364; F:glutathione transferase activity; NAS.
DR GO: GO:0008152; P:metabolism; IC.
KW Direct protein sequencing; Transferase.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1817 MW; 0E2A0FC555CBAC2 CRC64;

Query Match 35.5%; Score 22; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FYKLPQ 10
Db 7 FYHSPQ 12

RESULT 16
Q9UWM1 PRELIMINARY; PRT; 15 AA.
AC Q9UWM1;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Benzoyl-CoA ligase (Fragment).
OS Methanospirillum hungatei.
RL Archaea; Euryarchaeota; Methanomicrobia; Methanomicrobiales;

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OC Methanospirillaceae; Methanospirillum.
OX NCBI_TaxID=2203;
RN [1]
RP SEQUENCE.
RX MEDLINE=93040109; PubMed=1369492;
RA Auburger G., Winter J.;
RL Appl. Microbiol. Biotechnol. 37:789-795 (1992).
DR PIR: A48372; A48372.
SQ SEQUENCE 15 AA; 1880 MW; D2972EF3E690AC5C CRC64;

Query Match 35.5%; Score 22; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PONYFPY 6
Db 5 PEEFY 9

RESULT 17
Q9UCA4 PRELIMINARY; PRT; 17 AA.
AC Q9UCA4;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 25-OCT-2004 (TRENBLREL. 28, Last annotation update)
DE Tumor necrosis factor inhibitor I (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Suzuki J., Tomizawa S., Arai H., Seki Y., Maruyama K., Kurume T.;
RT "Purification of two types of TNF inhibitors in the urine of the
RT patient with chronic glomerulonephritis".
RL Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.
SQ SEQUENCE 17 AA; 1903 MW; D418485E691B28 CRC64;

Query Match 35.5%; Score 22; DB 2; Length 17;
Best Local Similarity 55.6%; Pred. No. 5e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PONYKLPQ 10
Db 5 PQGKYIHPQ 13

RESULT 18
Q6KC69 PRELIMINARY; PRT; 10 AA.
AC Q6KC69;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Putative glutamine synthetase (Fragment).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Eudicotyledons; core eudicots; rosids;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Eucalyptus.
OX NCBI_TaxID=71271;
RN [1]
RP SEQUENCE FROM N.A.
RA Pelosi A.;
RT "Molecular and genetic studies into the formation of lateral roots in
RT Eucalyptus and Arabidopsis".
RL Thesis (2002), Department of Biological Sciences, Monash University,
RL Melbourne, Australia.
RN [2]
RP SEQUENCE FROM N.A.
RA Hamill J.D.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ697760; CAG30778.1; -.

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FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1218 MW; CS19C76AA339C05D CRC64;

Query Match
 Best Local Similarity 33.9%; Score 21; DB 2; Length 10;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 POFYKLP 9
 DB 1 POFYKLP 8

RESULT 19

Q9XBH3 PRELIMINARY; PRT; 10 AA.

AC Q9XBH3;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Celf-like protein (Fragment).

OS Name=celf;
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1396;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10987;
 RX MEDLINE=99231848; PubMed=10217496;
 RA Oksaard O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;
 RT "Genome organization is not conserved between *Bacillus cereus* and
 RT *Bacillus subtilis*."
 RL Microbiology 145:621-631(1999).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10987;
 RA Hegna I.K.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ000394; CAB40625.1; -.

FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 1264 MW; D3757EC3339C9D6 CRC64;

Query Match
 Best Local Similarity 33.9%; Score 21; DB 2; Length 10;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPONFYKL 8
 DB 1 LPOFPCV 8

RESULT 20

Q9QVL4 PRELIMINARY; PRT; 13 AA.

AC Q9QVL4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 90 kDa advanced glycosylation ENDPRODUCT binding protein
 DE (Fragment).

OS Rattus sp.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OC NCBI_TaxID=10118;

RN [1]
 RP SEQUENCE.
 RX MEDLINE=91341412; PubMed=1651976;
 RA Yang Z., Makita Z., Horii Y., Brunelle S., Cerami A., Sehajpal P.,
 RA Suchanichiran M., Vlasara H.;
 RT "Two novel rat liver membrane proteins that bind advanced
 RT glycosylation endproducts: relationship to macrophage receptor for
 RT glucose-modified proteins."
 RL J. Exp. Med. 174:515-524(1991).

FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1466 MW; 349B02BEECFE9AB7 CRC64;

Query Match
 Best Local Similarity 33.9%; Score 21; DB 2; Length 13;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 KLPOM 11
 DB 4 KLPOM 8

RESULT 21

Q9TOX7 PRELIMINARY; PRT; 15 AA.

AC Q9TOX7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE Cartilage oligomeric matrix protein (Fragment).

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;

RN [1]
 RP SEQUENCE.
 RX MEDLINE=95046341; PubMed=7957930; DOI=10.1016/0014-5793(94)01134-6;
 RA Dicciare P., Hauser N., Lehman D., Pasumarti S., Paulsson M.;
 RT "Cartilage oligomeric matrix protein (COMP) is an abundant component
 RT of tendon."
 RL FEBS Lett. 354:237-240(1994).

SQ SEQUENCE 15 AA; 1689 MW; D709168394B5861C CRC64;
 Query Match
 Best Local Similarity 33.9%; Score 21; DB 2; Length 15;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 FYKLPOM 11
 DB 1 FYEGPCL 7

RESULT 22

Q71GTO PRELIMINARY; PRT; 15 AA.

AC Q71GTO;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Cytochrome oxidase subunit I.

OS Andrena aff. manifessta LLN-2002.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
 OC Andrenidae; Andreninae; Andrena.
 OC NCBI_TaxID=205242;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Larkin L.L., Neff J.L., Simpson B.B.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF504374; AA007719.1; -.
 DR GO:GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.

SQ SEQUENCE 15 AA; 1840 MW; 118B961922A39B59 CRC64;

Query Match
 Best Local Similarity 33.9%; Score 21; DB 2; Length 15;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPONFYKLPOM 11

Db 1 MNHSPNIPIM 11

RESULT 23

BRB_BASAL

ID BRB_BASAL STANDARD; PRT; 16 AA.

AC P83187;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE 05-JUL-2004 (Rel. 44, Last annotation update)

DE Beta-barubrin (Fragment).

OS Basella alba (Malabar spinach) (Ceylon spinach); Tracheophyta;

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllales; Basellaceae; Basella.

OC NCBI_TaxID=3589;

RN [1]

RP SEQUENCE, AND FUNCTION.

RC TISSUE=Seed; PubMed=11688973; DOI=10.1006/brc.2001.5822;

RX MEDLINE=21547763; PubMed=11688973; DOI=10.1006/brc.2001.5822;

RA Wang H., Ng T.B.;

RT "Novel antifungal peptides from ceylon spinach seeds.";

RL Biochem. Biophys. Res. Commun. 288:765-770(2001).

CC -1- FUNCTION: Possesses antifungal activity against B.cinerea,

CC M.arachidicola and F.oxysporum but not C.comatus and R.solani.

CC Inhibits HIV-1 reverse transcriptase and cell-free translation.

CC GO: GO:0050832; P:defense response to fungi; IDA.

DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IDA.

KW Direct protein sequencing; Fungicide.

FT NON TER 16 16 28FPPE4FC181682C CRC64;

SQ SEQUENCE 16 AA; 1952 MW; 28FPPE4FC181682C CRC64;

Query Match 33.9%; Score 21; DB 1; Length 16;

Best Local Similarity 50.0%; Pred. No. 7.1e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PONEFK 7

DB 6 PSKPYE 11

RESULT 24

Q6R9P0

ID Q6R9P0 PRELIMINARY; PRT; 17 AA.

AC Q6R9P0;

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Microcephalin (Fragment).

DE Name=McpH1;

OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;

OC Trachypithecus;

OC NCBI_TaxID=54180;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=15056608; DOI=10.1093/hmg/ddh127;

RA Wang Y.Q., Su B.;

RT "Molecular evolution of microcephalin, a gene determining human brain

RT size.";

RT Hum. Mol. Genet. 13:1131-1137(2004).

RN [2]

RP SEQUENCE FROM N.A.

RA Wang Y., Su B.;

RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY506356; AAS88719.1; -.

FT NON TER 1 1

SQ SEQUENCE 17 AA; 1931 MW; DC663AFLC7785E5B CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;

Best Local Similarity 80.0%; Pred. No. 7.6e+03; Mismatches 1; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 YKLPQ 10

DB 13 YKLPQ 17

RESULT 25

Q6R9P1

ID Q6R9P1 PRELIMINARY; PRT; 17 AA.

AC Q6R9P1;

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Microcephalin (Fragment).

DE Name=McpH1;

OS Trachypithecus phayrei (Phayre's leaf monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;

OC Trachypithecus.

OC NCBI_TaxID=61618;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=15056608; DOI=10.1093/hmg/ddh127;

RA Wang Y.Q., Su B.;

RT "Molecular evolution of microcephalin, a gene determining human brain

RT size.";

RT Hum. Mol. Genet. 13:1131-1137(2004).

RN [2]

RP SEQUENCE FROM N.A.

RA Wang Y., Su B.;

RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY506355; AAS88718.1; -.

FT NON TER 1 1

SQ SEQUENCE 17 AA; 1931 MW; DC663AFLC7785E5B CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;

Best Local Similarity 80.0%; Pred. No. 7.6e+03; Mismatches 1; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 YKLPQ 10

DB 13 YKLPQ 17

RESULT 26

Q6R9P2

ID Q6R9P2 PRELIMINARY; PRT; 17 AA.

AC Q6R9P2;

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Microcephalin (Fragment).

DE Name=McpH1;

OS Pygathrix nemaeus (Dove langur).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;

OC Pygathrix.

OC NCBI_TaxID=54133;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=15056608; DOI=10.1093/hmg/ddh127;

RA Wang Y.Q., Su B.;

RT "Molecular evolution of microcephalin, a gene determining human brain

RT size.";

RT Hum. Mol. Genet. 13:1131-1137(2004).

RN [2]

RP SEQUENCE FROM N.A.

RA Wang Y., Su B.;

RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY506354; AAS88717.1; -.

FT NON TER 1 1

SQ SEQUENCE 17 AA; 1931 MW; DC663AFLC7785E5B CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 YKLPQ 10
 |
 |
 |
 |
 Db 13 YLPPQ 17

RESULT 27

Q6R9P3 PRELIMINARY; PRT; 17 AA.

AC Q6R9P3; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 GN Name=McpH1;
 OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Pygathrix.
 OC NCBI_TaxID=61621;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
 RA Wang Y.Q., Su B.;
 RT "Molecular evolution of microcephalin, a gene determining human brain size."
 RT Hum. Mol. Genet. 13:1131-1137(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wang Y., Su B.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY506353; AAS88716.1; --
 FT NON TER 1
 SQ SEQUENCE 17 AA; 1931 MW; DC63AFLC7785B5B CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 YKLPQ 10
 |
 |
 |
 |
 Db 13 YLPPQ 17

RESULT 28

Q6R9P4 PRELIMINARY; PRT; 17 AA.

AC Q6R9P4; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 GN Name=McpH1 (Fragment).
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
 RA Wang Y.Q., Su B.;
 RT "Molecular evolution of microcephalin, a gene determining human brain size."
 RT Hum. Mol. Genet. 13:1131-1137(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wang Y., Su B.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY506352; AAS88715.1; --

FT NON TER 1
 SQ SEQUENCE 17 AA; 1931 MW; DC63AFLC7785B5B CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 YKLPQ 10
 |
 |
 |
 |
 Db 13 YLPPQ 17

RESULT 29

Q6R9P8 PRELIMINARY; PRT; 17 AA.

AC Q6R9P8; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 GN Name=McpH1.
 OS Erythrocebus patas (Red guenon) (Cercopithecus patas).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Erythrocebus.
 OC NCBI_TaxID=9538;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
 RA Wang Y.Q., Su B.;
 RT "Molecular evolution of microcephalin, a gene determining human brain size."
 RT Hum. Mol. Genet. 13:1131-1137(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wang Y., Su B.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY506348; AAS88711.1; --
 FT NON TER 1
 SQ SEQUENCE 17 AA; 1945 MW; DC63AFLC77F2B5B CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 YKLPQ 10
 |
 |
 |
 |
 Db 13 YLPPQ 17

RESULT 30

Q6R9R1 PRELIMINARY; PRT; 18 AA.

AC Q6R9R1; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 GN Name=fnaB;
 OS Bordetella parapertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OC NCBI_TaxID=519;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8234;
 RX MEDLINE=20290246; PubMed=10832649;
 RA Jacob-Dubuisson F., Kehoe B., Willery E., Reveneau N., Loch C.,
 Relman D.A.;
 RT "Molecular characterization of Bordetella bronchiseptica filamentous hemagglutinin and its secretion machinery."
 RT Microbiology 146:1211-1221(2000).
 DR EMBL; AF11798; AAF21948.1; --

FT NON TER 18 18
SQ SEQUENCE 18 AA; 2135 MW; F129A793B031E143 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 8e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPONFYKL 8
| | | | |
| | | | |
Db 1 MNTNLYRL 8

RESULT 31

Q9RGR2 PRELIMINARY; PRT; 18 AA.

ID Q9RGR2
AC Q9RGR2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Adhesin (Fragment).
GN Name=fhab;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OC NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50;
RX MEDLINE=20290246; PubMed=10832649;
RA Jacob-Dubuisson F., Kehoe B., Willery E., Reveneau N., Loch C.,
RA Relman D.A.;

RT "Molecular characterization of Bordetella bronchiseptica filamentous
hemagglutinin and its secretion machinery.";
RL Microbiology 146:1211-1221(2000).
DR EMBL, AF11797; AAF21947.1; -.

FT NON TER 18 18
SQ SEQUENCE 18 AA; 2151 MW; F139E793B031E143 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 8e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPONFYKL 8
| | | | |
| | | | |
Db 1 MNTNLYRL 8

RESULT 32

FARB CALVO STANDARD; PRT; 7 AA.

ID FARB CALVO
AC P41866;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calliphoridae 11.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OK NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;

RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliphoramides) from the blowfly Calliphora
vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.

DR PIR; B44787; B44787.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 7 Phenylalanine amide.
SQ SEQUENCE 7 AA; 926 MW; 69D40699C4AB700 CRC64;

Query Match 32.3%; Score 20; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PGNFYK 7
| | | | |
| | | | |
Db 1 PDNFRK 6

RESULT 33

TKL1 LOCOMI STANDARD; PRT; 9 AA.

ID TKL1 LOCOMI
AC P16223;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Locustatachykinin I (TK-I).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OC NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90184489; PubMed=2111766; DOI=10.1016/0014-5793(90)80601-E;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;

RT "Locustatachykinin I and II, two novel insect neuropeptides with
homology to peptides of the vertebrate tachykinin family.";
RL FEBS Lett. 261:397-401(1990).
CC -1- FUNCTION: Myoactive peptide. Stimulates the contraction of the
oviduct and foregut.

CC -1- SUBCELLULAR LOCATION: Secreted.
DR PIR; S08265; ECOLQ1M.
KW Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.
FT MOD RES 9 Arginine amide.
SQ SEQUENCE 9 AA; 939 MW; 2389C6B59C865A7 CRC64;

Query Match 32.3%; Score 20; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PGNFYK 6
| | | | |
| | | | |
Db 2 PSGFY 6

RESULT 34

TKN1 UPEIN STANDARD; PRT; 11 AA.

ID TKN1 UPEIN
AC P82026;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Uperin 1.1.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OK NCBI_TaxID=104953;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Raftery M.J., Bowle J.H., Tyler M.J., Wallace J.C.,
RA Adams G.W., Severini C.;

RT "Novel uperin peptides from the dorsal glands of the Australian
floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).

CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -1- MASS SPECTROMETRY: MW=1208; METHOD=FAH; RANGE=1-11, NOTE=Ref.1.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro: IPR002040; Tachy_Neurokinin.
 DR Pfam: PF02202; Tachykinin_1.
 DR PROSITE: PS00267; TACHYKININ, 1.
 KW Neuropeptide; Amphibian defense peptide; Direct protein sequencing;
 KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
 FT MOD RES 1 1 Methionine amide.
 FT MOD RES 11 11 Pyrrolidone carboxylic acid.
 SQ SEQUENCE 11 AA; 1226 MW; 329369359CDD457 CRC64;

Query Match 32.3%; Score 20; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 7.3e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PGNFYKL 8
 DB 4 PNAFYGL 10

RESULT 35
 TRK1_UPERU STANDARD; PRT; 11 AA.
 ID TKN1_UPERU
 AC P08612;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Uperolein.
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxId=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=75131227; PubMed=1120493;
 RA Anaestasi A., Exsperner V., Radean R.;
 RT "Structure of uperolein, a physalaemin-like endopeptide occurring in
 the skin of Uperoleia rugosa and Uperoleia marmorata.";
 RL Experientia 31:394-395(1975).
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro: IPR002040; Tachy_Neurokinin.
 DR InterPro: IPR008215; Tachykinin.
 DR Pfam: PF02202; Tachykinin_1.
 DR SMART: SM00203; TK, 1.
 DR PROSITE: PS00267; TACHYKININ, 1.
 KW Neuropeptide; Amphibian defense peptide; Direct protein sequencing;
 KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
 FT MOD RES 1 1 Methionine amide.
 FT MOD RES 11 11 Pyrrolidone carboxylic acid.
 SQ SEQUENCE 11 AA; 1252 MW; 328670359CDD457 CRC64;

Query Match 32.3%; Score 20; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 7.3e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PGNFYKL 8
 DB 4 PNAFYGL 10

RESULT 36
 Q16234 PRELIMINARY; PRT; 11 AA.
 ID Q16234
 AC Q16234;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hud protein.
 GN Name=Hud.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94349312; PubMed=8069866;
 RA Sekido Y., Bader S.A., Cardone D.P., Johnson B.E., Minna J.D.;
 RT "Molecular analysis of the Hud gene encoding a paraneoplastic
 RT encephalomyelitis antigen in human lung cancer cell lines.";
 RL Cancer Res 54:4988-4992(1994).
 DR EMBL: S73867; AAD14142.1; -.
 DR PIR: I52708; I52708.
 SQ SEQUENCE 11 AA; 1289 MW; 2EDCF20E204415A7 CRC64;

Query Match 32.3%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 7.3e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPQNFYKL 8
 DB 3 MPRRLKL 10

RESULT 37
 Q09RF22 PRELIMINARY; PRT; 11 AA.
 ID Q09RF22
 AC Q09RF22;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Fructose biphosphate aldolase (Fragment).
 GN Name=fba;
 OS Mycoplasma mycoides (subsp. capri).
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxId=40477;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PG3;
 RX MEDLINE=20193983; PubMed=10727835; DOI=10.1016/S0378-1135(99)00204-7;
 RA Thiencourt F., Lorenzon S., David A., Breard A.;
 RT "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing
 RT of a putative membrane protein gene.";
 RL Vet. Microbiol. 72:251-268(2000).
 DR EMBL: AF162998; AAF15255.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1371 MW; 50B0881A3331FB57 CRC64;

Query Match 32.3%; Score 20; DB 2; Length 11;
 Best Local Similarity 42.9%; Pred. No. 7.3e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPQNFYKL 7
 DB 1 MPKLTHK 7

RESULT 38
 TRK2_KASMA STANDARD; PRT; 12 AA.
 ID TKN2_KASMA
 AC P08614;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Hylambatin.
 OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Hylaroliidae;
 OX Kassina.
 RN NCBI_TaxID=8414;
 RM (1)
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Yasuhara T., Nakajima T., Erespamer G.F., Erespamer V.;
 RT "New tachykinins, Glu2, Pro5-kassinin (Hylambates-kassinin) and
 hylambatin, in the skin of the African rhacophorid frog Hylambates
 maculatus.";
 RL Biomed. Res. 2:613-617(1981).
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
 evoke behavioral responses, are potent vasodilators and
 secretagogues, and contract (directly or indirectly) many smooth
 muscles.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR PIR, S07436; S07436.
 DR InterPro, IPR002040; Tachy_Neurokinin.
 DR Pfam, PF02202; Tachykinin; 1.
 DR PROSITE, PS00267; TACHYKININ; 1.
 KW Amidation; Amphibian defense peptide; Direct protein sequencing;
 KM Neuropeptide; Tachykinin.
 FT MOD_RES 12 12 Methionine amide.
 SQ SEQUENCE 12 AA; 1441 MW; 3287CD2F0DD40AB7 CRC64;
 QY
 2 PONY 6
 1
 1
 1
 Db 5 PDRFY 9
 RESULT 39
 Q53579 PRELIMINARY; PRT; 12 AA.
 ID Q53579;
 AC Q53579;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE Light-harvesting complex I alpha polypeptide (Fragment).
 GN Name=puFA;
 OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Rhodobacter.
 OX NCBI_TaxID=1061;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92234963; PubMed=1569029;
 RA Richter P., Brand M., Drews G.;
 RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus puFA
 mutants.";
 RL J. Bacteriol. 174:3030-3041(1992).
 DR EMBL, S97551; AAC60405.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1627 MW; 0F92FEBA8A70532B CRC64;
 QY
 5 FYKL 8
 1
 1
 1
 Db 4 FYKI 7
 Query Match 32.3%; Score 20; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 8e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 40
 Q9THR8 PRELIMINARY; PRT; 13 AA.
 ID Q9THR8
 AC Q9THR8;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE PbsH (Fragment).
 GN Name=pbsH;
 OS Bryopsis sp. A.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;
 OC Bryopsidaceae; Bryopsis.
 OX NCBI_TaxID=103784;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Krellwitz E.C., Kowalik K.V., Manos P.S.;
 RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL, AF170413; AAD56858.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1785 MW; 3F9A1C3E247D0323 CRC64;
 QY
 1 MPQNYK 7
 1
 1
 1
 Db 1 MPXXYK 7
 Search completed: June 7, 2005, 23:19:02
 Job time : 51.4 secs
 Query Match 32.3%; Score 20; DB 2; Length 13;
 Best Local Similarity 42.9%; Pred. No. 8.7e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 80.7273 Seconds
(without alignments)
71.864 Million cell updates/sec

Title: US-10-691-157-7
Perfect score: 81
Sequence: 1.VLEMKPPPPQETVT 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	4	AAW72506 Colostrin
2	81	100.0	15	4	AAW59312 Ewe colos
3	81	100.0	15	4	AAW72252 Colostrin
4	81	100.0	15	4	AAW72538 Colostrin
5	81	100.0	15	5	AAO14583 Neural ce
6	81	100.0	15	5	AAW51042 Colostrin
7	81	100.0	15	5	AAW20234 Colostrin
8	81	100.0	15	5	AAW60301 Constitute
9	81	100.0	15	8	AAW74388 Ewe colos
10	81	100.0	16	4	AAW59343 Ewe colos
11	38	46.9	14	4	AAW06249 Antigenic
12	38	46.9	15	8	AAW38585 HSV-4 lat
13	38	46.9	18	2	AAW47567 Extendin a
14	38	46.9	18	2	AAW47571 Extendin a
15	38	46.9	18	2	AAW47577 Extendin a
16	38	46.9	18	2	AAW47550 Extendin a
17	38	46.9	18	2	AAW03738 Extendin a
18	38	46.9	18	2	AAW03721 Extendin a
19	38	46.9	18	3	AAW52880 Extendin
20	38	46.9	18	3	AAW52886 Extendin
21	38	46.9	18	3	AAW52876 Extendin
22	38	46.9	18	3	AAW52885 Extendin
23	37	45.7	15	5	AAW52860 Human rib
24	37	45.7	18	2	AAW05469 SH3-bind
25	37	45.7	18	2	AAW37677 PPPY mot

26	37	45.7	18	2	AAW38909 Peptide r
27	37	45.7	18	2	AAW47562 Extendin a
28	37	45.7	18	2	AAW03733 Extendin a
29	37	45.7	18	7	AAW49303 Novel KW
30	36	44.4	10	2	AAW07284 Smooth mu
31	36	44.4	14	4	AAW79174 Peptide d
32	36	44.4	15	4	AAW79166 Synthetic
33	36	44.4	18	2	AAW47569 Extendin a
34	36	44.4	18	2	AAW47552 Extendin a
35	36	44.4	18	2	AAW47564 Extendin a
36	36	44.4	18	2	AAW03740 Extendin a
37	36	44.4	18	2	AAW03723 Extendin a
38	36	44.4	18	2	AAW03742 Extendin a
39	36	44.4	18	2	AAW03735 Extendin a
40	36	44.4	18	3	AAW52878 Extendin
41	36	44.4	18	3	AAW52873 Extendin
42	36	44.4	18	8	AAW50264 Human car
43	36	44.4	18	8	AAW49142 Human car
44	35	43.2	10	2	AAW47943 AE101 ana
45	35	43.2	10	4	AAW09138 Ema/VASP
46	35	43.2	12	2	AAW48084 AE101 ser
47	35	43.2	13	2	AAW38053 Peptide r
48	35	43.2	13	7	AAW49201 Biocitinyl
49	35	43.2	15	1	AAW10189 Sequence
50	35	43.2	15	1	AAW70999 Sequence
51	35	43.2	15	1	AAW80033 Beta-huma
52	35	43.2	15	1	AAW91840 Analogue
53	35	43.2	15	2	AAW39024 Peptide r
54	35	43.2	15	2	AAW38952 Peptide r
55	35	43.2	15	2	AAW37268 Peptide d
56	35	43.2	15	2	AAW69452 HCG anti
57	35	43.2	15	2	AAW93437 Human hCG
58	35	43.2	15	3	AAW87482 Human cho
59	35	43.2	15	3	AAW20559 Human cho
60	35	43.2	15	4	AAW01142 Structure
61	35	43.2	15	4	AAW48388 Human cho
62	35	43.2	15	4	AAW02840 Human cho
63	35	43.2	15	4	AAW04124 Peptide f
64	35	43.2	16	2	AAW47923 Mammalian
65	35	43.2	16	4	AAW73469 Mammalian
66	35	43.2	16	8	AAW12046 Mammalian
67	35	43.2	16	8	AAW038264 Mammalian
68	35	43.2	17	6	AAW83411 G protein
69	34	42.0	5	2	AAW37157 EVH1 lig
70	34	42.0	5	4	AAW79177 Amino aci
71	34	42.0	5	4	AAW09140 Ema/VASP
72	34	42.0	5	5	AAW01762 Zyxine VA
73	34	42.0	6	2	AAW31441 Transcrip
74	34	42.0	9	2	AAW47926 Human MHC
75	34	42.0	9	4	AAW09144 Ema/VASP
76	34	42.0	10	2	AAW47942 AE101 ana
77	34	42.0	13	2	AAW38008 WW domain
78	34	42.0	14	4	AAW83035 Human Sma
79	34	42.0	15	2	AAW02172 Peptide w
80	34	42.0	15	2	AAW38059 PPPY mot
81	34	42.0	15	2	AAW39006 Peptide r
82	34	42.0	15	2	AAW38942 Peptide r
83	34	42.0	15	5	AAW25358 Abi SH3 d
84	34	42.0	15	5	AAW59535 Human rib
85	34	42.0	15	7	AAW49249 Biocitinyl
86	34	42.0	16	2	AAW78284 GAr7884 GRH immu
87	34	42.0	16	2	AAW82834 Mutated P
88	34	42.0	16	2	AAW82832 PY motif
89	34	42.0	16	2	AAW82832 MUC1 muta
90	34	42.0	16	3	AAW65944 Amino aci
91	34	42.0	17	5	AAW66086 LRP5 prot
92	33	40.7	7	4	AAW83313 LRP5 prot
93	33	40.7	7	4	AAW72512 Colostrin
94	33	40.7	7	4	AAW59315 Ewe colos
95	33	40.7	7	4	AAW72259 Colostrin
96	33	40.7	7	4	AAW72544 Colostrin
97	33	40.7	7	5	AAW14590 Neural ce
98	33	40.7	7	5	AAW51048 Colostrin
99	33	40.7	7	5	AAW20241 Colostrin

99 33 40.7 7 8 ADN60308
100 33 40.7 7 8 ADS74391

Adn60308 Constitue
Ad874391 Ovine col

ALIGNMENTS

RESULT 1
AAB72506
ID AAB72506 standard; peptide; 15 AA.

XX AAB72506;

XX 09-MAY-2001 (first entry)

XX Colostrinin peptide #7.

XX Dermatological; oxidative stress regulator; colostrinin.

XX Unidentified.

XX WO200112650-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US022665.

XX 17-AUG-1999; 99US-0149310P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

PT Modulating oxidative stress level in a cell, involves contacting the cell
PT with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations.

XX Claim 6; Page 25; 48pp; English.

CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidizing species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEMKFPPPPQETVT 15
DB 1 VLEMKFPPPPQETVT 15

RESULT 2
AAB59312
ID AAB59312 standard; peptide; 15 AA.

XX AAB59312;

XX 21-MAR-2001 (first entry)

XX Ewe colostrinin peptide fragment A-3.

KM Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KM central nervous system disorder; dietary supplement; beta-amyloid plaque.

OS Ovis sp.
XX WO200075173-A2.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-GB002128.

XX 02-JUN-1999; 99GB-00012852.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-071058/08.

PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.

XX Claim 7; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEMKFPPPPQETVT 15
DB 1 VLEMKFPPPPQETVT 15

RESULT 3
AAB72252
ID AAB72252 standard; peptide; 15 AA.

XX AAB72252;

XX 14-MAY-2001 (first entry)

XX Colostrinin derived cytokine inducing peptide SEQ ID 7.

KM Colostrinin; immune response; cytokine; blood cell proliferation;
KM central nervous system disorder; neurological disorder; mental disorder;
KM dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KM neurosis; infection.

XX Synthetic.

XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US022818.

XX 17-AUG-1999; 99US-0149311P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2001-202804/20.
 XX Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrin as an immunological
 PT regulator.
 XX
 XX Claim 1; Page 34; 50pp; English.
 PS
 XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrin,
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides
 CC have immune response modulatory activity, and are capable of inducing
 CC cytokines. Colostrin and its derived peptides are useful for inducing
 CC cytokine production, for modulating an immunological response and for
 CC inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 81; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEMKFPPPPQETVT 15
 DB 1 VLEMKFPPPPQETVT 15
 RESULT 4
 AAB72538
 ID AAB72538 standard; peptide; 15 AA.
 XX
 AC AAB72538;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DB Colostrin peptide #7.
 XX
 KW Neuroprotective; neural cell differentiation regulator; colostrin;
 KW colostrum.
 XX
 OS Unidentified.
 XX
 MO200112651-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US022774.
 XX
 PR 17-AUG-1999; 99US-0149633P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I;
 PT
 DR WPI; 2001-226545/23.
 XX
 PT Use of colostrin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating damaged
 PT neural cells in a patient.
 XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrin and
 CC colostrin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrin is a polypeptide complex found in colostrum
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEMKFPPPPQETVT 15
 DB 1 VLEMKFPPPPQETVT 15
 RESULT 5
 AAO14583
 ID AAO14583 standard; peptide; 15 AA.
 XX
 AC AAO14583;
 XX
 DT 27-MAY-2002 (first entry)
 XX
 DE Neural cell regulatory colostrin peptide 7.
 XX
 KW Neural cell differentiation; neural cell regulator; colostrin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 15 /note="Optional C-terminal amide"
 FT
 MO200213851-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022777.
 XX
 PR 17-AUG-2000; 2000WO-US022777.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I, Stanton JG, Hughes TK;
 PT
 DR WPI; 2002-269152/31.
 XX
 PT Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 7; Page 21; 37pp; English.
 XX
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrin peptide used in
 CC the method of the invention
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 81; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEMKFPPPPQETVT 15
 DB 1 VLEMKFPPPPQETVT 15
 RESULT 6
 AAM51042

ID AAM51042 standard; peptide; 15 AA.
 XX AAM51042;
 AC
 XX 30-MAY-2002 (first entry)
 DT
 XX Colostrinin constituent peptide.
 DE
 XX Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; human.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 15 /note="optional C-terminal amidation"
 FT
 XX WO200213849-A1.
 PN
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US022775.
 PF
 XX 17-AUG-2000; 2000WO-US022775.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX (REGE-) REGEN THERAPEUTICS PLC.
 PA
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 PI WPI: 2002-269150/31.
 DR
 XX Modulation of blood cell proliferation in a patient involves use of blood
 PT cell regulator selected from colostrinin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 1; Page 34; 54pp; English.
 XX
 CC The present sequence is that of a colostrinin constituent peptide that is
 CC preferred for use as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. Methods are claimed for:
 CC inducing a cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ or an
 CC organism, and the cell is mammalian, including human; modulating an
 CC immune response in a cell by contact with the immunological regulator
 CC under conditions effective to induce a cytokine; modulating an immune
 CC response in a patient by administering an immunological regulator under
 CC conditions effective to induce a cytokine, where the immunological
 CC regulator is administered topically or as part of a dietary supplement,
 CC and where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation by
 CC contacting blood cells with a blood cell regulator, where the blood cells
 CC are present in a cell culture or an organism, are mammalian or human, and
 CC where the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patient. A claimed
 CC cytokine-inducing composition comprises a pharmaceutical carrier and an
 CC active agent such as the present peptide. Cytokines induced by this
 CC peptide in human leucocyte cultures include interferon-gamma, tumour
 CC necrosis factor-alpha, interleukin-4, interleukin-6 and interleukin-10
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 81; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEMKFPPPPQETVT 15
 |||||
 DB 1 VLEMKFPPPPQETVT 15

RESULT 7
 AAE20234

ID AAE20234 standard; peptide; 15 AA.
 XX AAE20234;
 AC
 XX 18-JUN-2002 (first entry)
 DT
 XX Colostrinin constituent peptide #7.
 DE
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnerrary.
 KW
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 15 /note="Optionally C-terminal amide"
 FT
 XX WO200213850-A1.
 PN
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US022776.
 PF
 XX 17-AUG-2000; 2000WO-US022776.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Stanton GJ, Hughes TK, Boldogh I;
 PI WPI: 2002-269151/31.
 DR
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog.
 XX
 PS Claim 6; Page 25; 51pp; English.
 XX
 CC The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress level
 CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
 CC organ, or organism; or for treating oxidative damage to the skin of a
 CC patient e.g. animal or human; to modulate oxidative stress during/ after
 CC a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 81; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEMKFPPPPQETVT 15
 |||||
 DB 1 VLEMKFPPPPQETVT 15

RESULT 8
 ADN60301
 ID ADN60301 standard; peptide; 15 AA.
 XX

AC ADN60301;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Constituent peptide of colostrinin SEQ ID NO:7.
 XX
 KW modulator; colostrinin; intracellular signaling molecule modulator;
 KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibitor;
 KW DNA damage; beta-amyloid; retinoic acid; cyclostatic; 4HNE inhibitor;
 KW 4HNE-protein adduct formation reduction;
 KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;
 KW c-Jun NH2-terminal kinase inhibition.
 XX
 OS Synthetic.
 XX
 PN WO2004037851-A2.
 XX
 PD 06-MAY-2004.
 XX
 PF 22-OCT-2003; 2003WO-US033423.
 XX
 PR 22-OCT-2002; 2002US-0420369P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (BOLD/) BOLDOGH I.
 PA (STAN/) STANTON J G.
 PA (GEOR/) GEORGIADIS J A.
 PA (HUGH/) HUGHES T K.
 PA (KRUZ/) KRUZEL M.
 XX
 PI Bolldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;
 XX
 DR WPI; 2004-365494/34.
 XX
 PT Use of colostrinin for e.g. modulating an intracellular signaling
 PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a
 PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
 PT a cell.
 XX
 PS Claim 6; SEQ ID NO 7; 46pp; English.
 XX
 CC The present invention describes the use of a modulator selected from
 CC colostrinin, its constituent peptide, its active analogue, and a
 CC combination of these, for modulating an intracellular signaling molecule
 CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
 CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
 CC The modulator has cyclostatic activity, and can be used as a 4HNE
 CC inhibitor. The modulator is useful in the manufacture of a medicament for
 CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated
 CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,
 CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.
 CC Colostrinin, or its constituent peptide or active analogue is useful for
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
 CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
 CC The present sequence represents a synthetic constituent peptide of
 CC colostrinin, which can be used as a modulator in the present invention.
 XX
 SQ Sequence 15 AA;
 XX

AC ADS74388;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Ovine colostrinin peptide.
 XX
 KW Colostrum; colostrinin; sheep; peptide purification.
 XX
 OS Ovis aries.
 XX
 PN WO2004081038-A1.
 XX
 PD 23-SEP-2004.
 XX
 PF 10-MAR-2004; 2004WO-GB001014.
 XX
 PR 11-MAR-2003; 2003GB-00005552.
 XX
 PR 08-MAR-2004; 2004GB-00005190.
 XX
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;
 XX
 DR WPI; 2004-677519/66.
 XX
 PT Recovering peptides such as colostrinin from mammalian colostrum, by
 PT mixing colostrum with alcohol to form alcohol phase containing peptides
 PT and precipitate, separating alcohol phase from precipitate, and
 PT recovering alcohol phase.
 XX
 PS Example; SEQ ID NO 3; 41pp; English.
 XX
 CC The present sequence is that of a peptide that can be recovered from
 CC ovine colostrum using the method of the invention. The invention
 CC provides a method for the recovery of peptides (especially colostrinin)
 CC from colostrum in substantially pure, biologically active form and in
 CC high yield. The method involves mixing the colostrum with an alcohol to
 CC form an alcohol phase containing the colostrinin and a precipitate
 CC containing higher molecular weight caseins and other proteins. Best
 CC results are obtained using methanol or ethanol of at least 80%, and
 CC preferably up to 100%, purity. The alcohol phase is then separated from
 CC the precipitate, and the colostrinin is separated from the alcohol,
 CC preferably by evaporation, to form a colostrinin-rich phase, which is
 CC recovered. A precipitation agent, such as ammonium sulfate, may be added
 CC either to the alcohol phase or, preferably, to the colostrinin-rich phase
 CC to induce precipitation of the colostrinin peptides. The method is
 CC generally applicable to the separation of peptides from fluids containing
 CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic
 CC acids. In an example from the invention, the antigenic profile of
 CC peptides recovered from sheep colostrum using the alcohol precipitation
 CC methods was determined by ELISA using antibodies prepared against 9
 CC synthetic peptides, including a peptide having the present sequence
 CC (denoted antigen class A-3).
 XX
 SQ Sequence 15 AA;
 XX

Query Match 100.0%; Score 81; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. NO. 9.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

QY 1 VLEMKFPPPPPTV 15
 |||||
 DB 1 VLEMKFPPPPPTV 15

RESULT 10
 AAB59343
 ID AAB59343 standard; peptide; 16 AA.
 XX
 AC AAB59343;
 XX
 DT 21-MAR-2001 (first entry)
 XX

DE Ewe colostrinin peptide fragment derived sequence #3.
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 OS Ovis sp.
 XX WO200075173-A2.
 XX
 XX 14-DEC-2000.
 XX
 XX 02-JUN-2000; 2000WO-GB002128.
 XX
 XX 02-JUN-1999; 99GB-00012852.
 XX
 XX (REGG-) REGEN THERAPEUTICS PLC.
 XX
 XX Georgiades JA;
 XX
 XX WPI; 2001-071058/08.
 XX
 XX Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system and
 PT immune system, viral and bacterial infections, and diseases characterized
 PT by amyloid plaques.
 XX
 XX Claim 8; Page 27; 63pp; English.
 XX
 XX The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques
 CC
 XX Sequence 16 AA;
 SQ
 Query Match 100.0%; Score 81; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0001;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEMKPPPPPPPTVT 15
 DB 2 VLEMKPPPPPPPTVT 16
 RESULT 11
 AAR06249
 ID AAR06249 standard; protein; 14 AA.
 XX
 XX AAR06249;
 XX
 XX 09-JAN-2003 (revised)
 DT 07-DEC-1990 (first entry)
 DT
 XX Antigenic peptide fragment selected from the 12 N-terminal AAs of
 DE heptadecagastrin (G17).
 DE
 XX Gastrin; tumours; peptic ulcers; diphtheria toxoid; tetanus toxin.
 KW
 XX Unidentified.
 OS
 XX EP380230-A.
 PN
 XX 01-AUG-1990.
 PD
 XX 17-JAN-1990; 90EP-00300456.
 PF
 XX 24-JAN-1989; 89US-00301353.
 PR
 XX 12-MAY-1989; 89US-00351193.
 PR
 XX

PA (APHT-) APHTON CORP.
 XX
 XX Gevas PC, Grimes S, Karr SL, Littenberg RL;
 PI
 XX WPI; 1990-233029/31.
 XX
 XX Immunogens against gastrin peptide(s) - used to induce antibodies that
 PT specifically neutralise single form of gastrin, G17 or G34.
 PT
 XX Claim 8; Page 19; 32pp; English.
 XX
 XX Antigenic fragments may be attached to an immunogenic carrier and used to
 CC raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide
 CC fragments capable of binding to these Abs are useful in neutralising anti
 CC -gastrin Abs in vivo. (Updated on 09-JAN-2003 to add missing OS field.)
 CC
 XX Sequence 14 AA;
 SQ
 Query Match 46.9%; Score 38; DB 2; Length 14;
 Best Local Similarity 70.0%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 LEMKPPPPQ 11
 DB 5 LEMKPPPPK 14
 RESULT 12
 ADJ38585
 ID ADJ38585 standard; peptide; 15 AA.
 XX
 XX ADJ38585;
 AC
 XX 06-MAY-2004 (first entry)
 DT
 XX HSV-4 latent membrane protein 2A late domain motif mutant peptide #4.
 DE
 XX Virucide; HSV infection; antiviral; late domain motif; mutant.
 KW
 XX Human herpesvirus 4.
 OS
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 9 /note= "Wild-type residue replaced with Gln"
 FT
 XX MO200409027-A2.
 PN
 XX 29-JAN-2004.
 PD
 XX 21-JUL-2003; 2003WO-US022828.
 PF
 XX 19-JUL-2002; 2002US-0397265P.
 PR
 XX 19-JUL-2002; 2002US-0397477P.
 PR
 XX 03-MAR-2003; 2003US-0451903P.
 XX
 XX (MYRI-) MYRIAD GENETICS INC.
 PA
 XX Morham S, Zavitz K, Hobden A;
 PI
 XX WPI; 2004-123282/12.
 DR
 XX Use of cells displaying herpes simplex virus (HSV) altered budding
 PT phenotype for the manufacture of a medicament for treating HSV infection.
 PT
 XX Example 12; Page 63; 74pp; English.
 PS
 XX The present invention relates to cells displaying herpes simplex virus
 CC (HSV) altered budding phenotype which are useful for the manufacture of a
 CC medicament for treating HSV infection. The medicament further comprises
 CC an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL
 CC -4, IL-12, IL-18 or gamma-interferon. The cells are human cells and

CC contain a nucleic acid encoding a mutant HSV protein or a nucleic acid
 CC encoding the polypeptide sufficient for virus-like particle assembly but
 CC devoid of late-domain motifs. The nucleic acid is within an HSV genome.
 CC The genome is devoid of late domain motifs capable of effecting viral
 CC budding. The composition also comprises a compound capable of interfering
 CC with the protein-protein interaction between a host cell protein capable
 CC of binding a late domain motif and a HSV protein containing a late domain
 CC motif. The composition further comprises another HSV protein or its
 CC immunogenic fragment, and/or a nucleic acid encoding the other HSV
 CC protein or the immunogenic fragment. The present sequence is a mutant HSV
 CC peptide, derived from the wild-type peptide ADJ3858L, used to illustrate
 CC the invention.

SQ Sequence 15 AA;

Query Match 46.9%; Score 38; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PPPQG 12
 |||||
 Db 5 PPPQG 10

RESULT 13
 AAM47567
 ID AAM47567 standard; peptide; 18 AA.

AC AAM47567;
 DT 03-JUL-1998 (first entry)

DE Exendin agonist (18).

KW Exendin agonist; gastric motility; gastric emptying; treatment; spasm;
 KW postprandial dumping syndrome; postprandial hyperglycaemia;
 KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;
 KW Gila monster venom.

OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 18
 FT /note= "amidated"

PN W09805351-A1.

PD 12-FEB-1998.

PF 08-AUG-1997; 97WO-US014199.

PR 08-AUG-1996; 96US-00694954.

PA (AMYL-) AMYLIN PHARM INC.

PI Young AA, Gedulin B, Beeley NRA, Prickett KS;

DR WPI; 1998-145351/13.

PT Regulating gastrointestinal motility using exendins or their agonists -
 PT for treating spasm, diabetic postprandial hyperglycaemia, impaired
 PT glucose tolerance etc., also in diagnostic investigations.

PS Example 21; Fig 8; 70pp; English.

CC The present sequence is an exendin agonist, which reduces gastric
 CC motility and delays gastric emptying. It can be used to treat spasm
 CC (where associated with acute diverticulitis or disorders of the biliary
 CC tract or sphincter of Oddi), postprandial dumping syndrome and
 CC hyperglycaemia (particularly associated with type 2 diabetes), type 1
 CC diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist
 CC is administered to prevent stomach contents passing into the intestines,
 CC then the stomach pumped) and obesity. It can also be administered to

CC subjects undergoing gastrointestinal diagnostic investigation,
 CC particularly radiological or by magnetic resonance imaging. Exendins,
 CC components of Gila monster venom, have some sequence similarity to
 CC glucagon-like peptides (GLP). They are GLP agonists and have been
 CC suggested (US5424286) for treatment of diabetes and prevention of
 CC hyperglycaemia

SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 2; Length 18;
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLEMKPPPP 10
 .|::|||
 Db 8 LLFVPPPP 17

RESULT 14
 AAM47571
 ID AAM47571 standard; peptide; 18 AA.

AC AAM47571;

DT 03-JUL-1998 (first entry)

DE Exendin agonist (22).

KW Exendin agonist; gastric motility; gastric emptying; treatment; spasm;
 KW postprandial dumping syndrome; postprandial hyperglycaemia;
 KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;
 KW Gila monster venom.

OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 18
 FT /note= "amidated"

PN W09805351-A1.

PD 12-FEB-1998.

PF 08-AUG-1997; 97WO-US014199.

PR 08-AUG-1996; 96US-00694954.

PA (AMYL-) AMYLIN PHARM INC.

PI Young AA, Gedulin B, Beeley NRA, Prickett KS;

DR WPI; 1998-145351/13.

PT Regulating gastrointestinal motility using exendins or their agonists -
 PT for treating spasm, diabetic postprandial hyperglycaemia, impaired
 PT glucose tolerance etc., also in diagnostic investigations.

PS Example 25; Fig 8; 70pp; English.

CC The present sequence is an exendin agonist, which reduces gastric
 CC motility and delays gastric emptying. It can be used to treat spasm
 CC (where associated with acute diverticulitis or disorders of the biliary
 CC tract or sphincter of Oddi), postprandial dumping syndrome and
 CC hyperglycaemia (particularly associated with type 2 diabetes), type 1
 CC diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist
 CC is administered to prevent stomach contents passing into the intestines,
 CC then the stomach pumped) and obesity. It can also be administered to
 CC subjects undergoing gastrointestinal diagnostic investigation,
 CC particularly radiological or by magnetic resonance imaging. Exendins,
 CC components of Gila monster venom, have some sequence similarity to
 CC glucagon-like peptides (GLP). They are GLP agonists and have been
 CC suggested (US5424286) for treatment of diabetes and prevention of
 CC hyperglycaemia

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XX SQ Sequence 18 AA;
Query Match 46.9%; Score 38; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLEMKFPPPP 10
   :|::|
   8 LLEFIFPPPP 17

RESULT 15
AAM47577
ID AAM47577 standard; peptide; 18 AA.
AC AAM47577;
DT 03-JUL-1998 (first entry)
DE Extendin agonist (28).
XX Extendin agonist; gastric motility; gastric emptying; treatment; spasm;
KW postprandial dumping syndrome; postprandial hyperglycaemia;
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;
KW Gila monster venom.
XX Synthetic.
OS Synthetic.
XX Key Location/Qualifiers
FH Modified-site 14
FT /label= Hyp
FT Modified-site 15
FT /label= Hyp
FT Modified-site 16
FT /label= Hyp
FT Modified-site 17
FT /label= Hyp
FT Modified-site 18
FT /note= "amidated"
XX W09805351-A1.
XX 12-FEB-1998.
XX 08-AUG-1997; 97WO-US014199.
XX 08-AUG-1996; 96US-00694954.
XX (AMYL-) AMYLIN PHARM INC.
XX Young AA, Gedulin B, Beeley NRA, Prickett KS;
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their agonists -
XX for treating spasm, diabetic postprandial hyperglycaemia, impaired
XX glucose tolerance etc., also in diagnostic investigations.
XX
XX Example 31; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm
XX (where associated with acute diverticulitis or disorders of the biliary
XX tract or sphincter of Oddi), postprandial dumping syndrome and
XX hyperglycaemia (particularly associated with type 2 diabetes), type 1
XX diabetes, impaired glucose tolerance, toxin ingestion (an extendin agonist
XX is administered to prevent stomach contents passing into the intestines,
XX then the stomach pumped) and obesity. It can also be administered to
XX subjects undergoing gastrointestinal diagnostic investigation,
XX particularly radiological or by magnetic resonance imaging. Extendin,
XX components of Gila monster venom, have some sequence similarity to
XX glucagon-like peptides (GLP). They are GLP agonists and have been

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CC suggested (US5424286) for treatment of diabetes and prevention of
CC hyperglycaemia
XX SQ Sequence 18 AA;
Query Match 46.9%; Score 38; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLEMKFPPPP 10
   :|::|
   8 LLEFIFPPPP 17

RESULT 16
AAM47550
ID AAM47550 standard; peptide; 18 AA.
AC AAM47550;
DT 03-JUL-1998 (first entry)
DE Extendin agonist (1).
XX Extendin agonist; gastric motility; gastric emptying; treatment; spasm;
KW postprandial dumping syndrome; postprandial hyperglycaemia;
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;
KW Gila monster venom.
XX Synthetic.
OS Synthetic.
XX Key Location/Qualifiers
FH Modified-site 18
FT /note= "amidated"
XX W09805351-A1.
XX 12-FEB-1998.
XX 08-AUG-1997; 97WO-US014199.
XX 08-AUG-1996; 96US-00694954.
XX (AMYL-) AMYLIN PHARM INC.
XX Young AA, Gedulin B, Beeley NRA, Prickett KS;
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their agonists -
XX for treating spasm, diabetic postprandial hyperglycaemia, impaired
XX glucose tolerance etc., also in diagnostic investigations.
XX
XX Example 4; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm
XX (where associated with acute diverticulitis or disorders of the biliary
XX tract or sphincter of Oddi), postprandial dumping syndrome and
XX hyperglycaemia (particularly associated with type 2 diabetes), type 1
XX diabetes, impaired glucose tolerance, toxin ingestion (an extendin agonist
XX is administered to prevent stomach contents passing into the intestines,
XX then the stomach pumped) and obesity. It can also be administered to
XX subjects undergoing gastrointestinal diagnostic investigation,
XX particularly radiological or by magnetic resonance imaging. Extendins,
XX components of Gila monster venom, have some sequence similarity to
XX glucagon-like peptides (GLP). They are GLP agonists and have been
XX suggested (US5424286) for treatment of diabetes and prevention of
XX hyperglycaemia
XX SQ Sequence 18 AA;
Query Match 46.9%; Score 38; DB 2; Length 18;

```

Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEMKPPPP 10
:|::|
Db 8 LLFIEPPPP 17

RESULT 17

AAV03738
ID AAV03738 standard; peptide; 18 AA.

AC AAY03738;

DT 08-JUN-1999 (first entry)

DE Extendin agonist compound 18.

KW Extendin; agonist; diabetes; disorder; plasma glucose; gastric;
diagnostic; gastro-intestinal; radiological.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 18
/note= "C-terminal amide"

PN WO9907404-A1.

PD 18-FEB-1999.

PF 06-AUG-1998; 98WO-US016387.

PR 08-AUG-1997; 97US-0055404P.

PA (AMYL-) AMYLIN PHARM INC.

PI Beley NRA, Prickett KS;

DR WPI, 1999-180403/15.

PT New extendin agonists - useful in the treatment of Type I and II diabetes.

PS Claim 17; Fig 1D-B; 70pp; English.

CC The invention relates to extendin agonists which slow gastric emptying and
lower plasma glucose levels. The extendin agonists are used to treat Type
I and II diabetes, disorders which would be benefited by agents which
lower plasma glucose levels, and disorders which would be benefited by
agents useful in delaying and/or slowing gastric emptying. Delayed
gastric emptying is a useful diagnostic aid in gastro-intestinal
radiological examinations. Sequences AAV03721-51 represent specifically
claimed examples of the extendin agonist compounds of the invention. (Also
see AAV03720 for extendin generic peptide formula and description)

SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEMKPPPP 10
:|::|
Db 8 LLFIEPPPP 17

RESULT 18

AAV03721
ID AAV03721 standard; peptide; 18 AA.

AC AAY03721;

DT 08-JUN-1999 (first entry)

XX Extendin agonist compound 1.

DE Extendin; agonist; diabetes; disorder; plasma glucose; gastric;
diagnostic; gastro-intestinal; radiological.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 18
/note= "C-terminal amide"

PN WO9907404-A1.

PD 18-FEB-1999.

PF 06-AUG-1998; 98WO-US016387.

PR 08-AUG-1997; 97US-0055404P.

PA (AMYL-) AMYLIN PHARM INC.

PI Beley NRA, Prickett KS;

DR WPI, 1999-180403/15.

PT New extendin agonists - useful in the treatment of Type I and II diabetes.

PS Claim 17; Fig 1A-B; 70pp; English.

CC The invention relates to extendin agonists which slow gastric emptying and
lower plasma glucose levels. The extendin agonists are used to treat Type
I and II diabetes, disorders which would be benefited by agents which
lower plasma glucose levels, and disorders which would be benefited by
agents useful in delaying and/or slowing gastric emptying. Delayed
gastric emptying is a useful diagnostic aid in gastro-intestinal
radiological examinations. Sequences AAV03721-51 represent specifically
claimed examples of the extendin agonist compounds of the invention. (Also
see AAV03720 for extendin generic peptide formula and description)

SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEMKPPPP 10
:|::|
Db 8 LLFIEPPPP 17

RESULT 19

AAB52880
ID AAB52880 standard; peptide; 18 AA.

AC AAB52880;

DT 28-FEB-2001 (first entry)

DE Extendin agonist compound #8.

KW Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;
insulin-resistance syndrome; food intake.

OS Heloderma sp.

PN WO20006629-A1.

PD 09-NOV-2000.

PF 28-APR-2000; 2000WO-US011814.

PR 30-APR-1999; 99US-0132018P.

XX (AMYL-) AMYLIN PHARM INC.
PA Young A, Prickett K;
XX WPI, 2000-672834/65.
XX
XX Modified extendin or an extendin agonist linked to one or more polyethylene
PT glycol (PEG) polymers, modulate plasma glucose levels, useful for
PT treating disorders such as diabetes and obesity.
XX
XX Disclosure; Fig 3; 11pp; English.
XX
XX The present invention relates to extendins and their agonists which have
CC been modified with molecular weight increasing agents such as
CC polyethylene glycol (PEG). These can be used in the treatment of
CC diabetes, obesity, impaired glucose tolerance, postprandial dumping
CC syndrome, postprandial hyperglycaemia, eating disorders, insulin
CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion
XX
SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 3; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEMKFPPPP 10
:|::|
Db 8 LLFVFPPPP 17

RESULT 20
AAB52886
ID AAB52886 standard; peptide; 18 AA.
XX AAB52886;
XX
XX 28-FEB-2001 (first entry)
XX
XX Extendin agonist compound #14.
XX
XX Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;
XX insulin-resistance syndrome; food intake.
XX
XX Heloderma sp.
XX
XX WO200066629-A1.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US011814.
XX
XX 30-APR-1999; 99US-0132018P.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Young A, Prickett K;
XX
XX WPI, 2000-672834/65.
XX
XX Modified extendin or an extendin agonist linked to one or more polyethylene
PT glycol (PEG) polymers, modulate plasma glucose levels, useful for
PT treating disorders such as diabetes and obesity.
XX
XX Disclosure; Fig 3; 11pp; English.
XX
XX The present invention relates to extendins and their agonists which have
CC been modified with molecular weight increasing agents such as
CC polyethylene glycol (PEG). These can be used in the treatment of
CC diabetes, obesity, impaired glucose tolerance, postprandial dumping
CC syndrome, postprandial hyperglycaemia, eating disorders, insulin
CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion
XX

SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 3; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEMKFPPPP 10
:|::|
Db 8 LLFVFPPPP 17

RESULT 21
AAB52876
ID AAB52876 standard; peptide; 18 AA.
XX AAB52876;
XX
XX 28-FEB-2001 (first entry)
XX
XX Extendin agonist compound #4.
XX
XX Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;
XX insulin-resistance syndrome; food intake.
XX
XX Heloderma sp.
XX
XX WO200066629-A1.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US011814.
XX
XX 30-APR-1999; 99US-0132018P.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Young A, Prickett K;
XX
XX WPI, 2000-672834/65.
XX
XX Modified extendin or an extendin agonist linked to one or more polyethylene
PT glycol (PEG) polymers, modulate plasma glucose levels, useful for
PT treating disorders such as diabetes and obesity.
XX
XX Disclosure; Fig 3; 11pp; English.
XX
XX The present invention relates to extendins and their agonists which have
CC been modified with molecular weight increasing agents such as
CC polyethylene glycol (PEG). These can be used in the treatment of
CC diabetes, obesity, impaired glucose tolerance, postprandial dumping
CC syndrome, postprandial hyperglycaemia, eating disorders, insulin
CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion
XX
SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 3; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEMKFPPPP 10
:|::|
Db 8 LLFVFPPPP 17

RESULT 22
AAB52885
ID AAB52885 standard; peptide; 18 AA.
XX AAB52885;
XX
XX 28-FEB-2001 (first entry)
XX
XX Extendin agonist compound #13.
XX

XX Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;
 KW insulin-resistance syndrome; food intake.
 XX Heloderma sp.
 XX WO20066629-A1.
 XX 09-NOV-2000.
 XX 28-APR-2000; 2000WO-US011814.
 XX 30-APR-1999; 99US-0132018P.
 XX (AMYL-) AMYLIN PHARM INC.
 XX Young A, Prickett K;
 XX WPI; 2000-672834/65.
 XX Modified extendin or an extendin agonist linked to one or more polyethylene
 PT glycol (PEG) polymers, modulate plasma glucose levels, useful for
 PT treating disorders such as diabetes and obesity.
 XX Disclosure; Fig 3; 119pp; English.
 XX The present invention relates to extendins and their agonists which have
 CC been modified with molecular weight increasing agents such as
 CC polyethylene glycol (PEG). These can be used in the treatment of
 CC diabetes, obesity, impaired glucose tolerance, postprandial dumping
 CC syndrome, postprandial hyperglycaemia, eating disorders, insulin
 CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion
 SQ Sequence 18 AA;
 SQ
 Query Match 46.9%; Score 38; DB 3; Length 18;
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VLEMKPPPP 10
 : : : : :
 Db 8 LRFIFPPPP 17
 RESULT 23
 ABG72860
 ID ABG72860 standard; peptide; 15 AA.
 XX
 AC ABG72860;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 DE Human ribosomal protein 17.05 N-terminal.
 XX
 KW Human; ribosomal protein 17.05; malignant tumour; haemopathy;
 KW human immunodeficiency virus; HIV; immunological disease; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN CN1352106-A.
 XX
 PD 05-JUN-2002.
 XX
 PF 06-NOV-2000; 2000CN-00127235.
 XX
 PR 06-NOV-2000; 2000CN-00127235.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-683308/74.
 XX

PT New human ribosomal protein 17.05 polypeptide for treating malignant
 PT tumors, hemopathy, human immunodeficiency virus infection, immunological
 PT diseases and various inflammations.
 XX
 XX Example 5; Page 18 (Disclosure); 33pp; Chinese.
 XX
 CC The present invention discloses a new kind of polypeptide, human
 CC ribosomal protein 17.05, polynucleotides encoding the polypeptide and a
 CC DNA recombination process to produce the polypeptide. The present
 CC invention also describes applying the polypeptide in treating various
 CC diseases, such as malignant tumours, haemopathy, human immunodeficiency
 CC virus (HIV) infection, immunological diseases and various inflammations.
 CC Also discloses is the antagonist resisting the polypeptide and its
 CC treatment effect, and the application of the polynucleotides encoding
 CC human ribosomal protein 17.05. This is the amino acid sequence of the
 CC novel human ribosomal protein 17.05 N-terminal
 XX
 SQ Sequence 15 AA;
 SQ
 Query Match 45.7%; Score 37; DB 5; Length 15;
 Best Local Similarity 54.5%; Pred. No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 4 MKPPPPQETV 14
 : : : : :
 Db 3 VSFPPPPKQGV 13
 RESULT 24
 AAW05469
 ID AAW05469 standard; peptide; 18 AA.
 XX
 AC AAW05469;
 XX
 DT 24-FEB-1998 (first entry)
 XX
 DE SH3-binding peptide bSH3020.
 XX
 KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
 KW cellular signalling element; cellular structural element; malignancy;
 KW protein identification; functional domain; protein screening;
 KW cellular signal transduction process; binding peptide.
 XX
 OS Synthetic.
 XX
 PN WO9631625-A1.
 XX
 PD 10-OCT-1996.
 XX
 PF 04-APR-1996; 96WO-US004454.
 XX
 PR 07-APR-1995; 95US-00417872.
 XX
 PR 03-APR-1996; 96US-00630915.
 XX
 PA (CYTO-) CYTOGEN CORP.
 PA (UNNC-) UNIV NORTH CAROLINA.
 XX
 PI Sparks AB, Hoffman N, Kay BK, Fowlkes DM, McConnell SJ;
 XX
 DR WPI; 1996-465045/46.
 XX
 PT Identifying polypeptide(s) having specific functional domain (esp. SH3
 PT domain) - comprises detecting selective binding to recognition unit.
 PT regardless of sequence homology.
 XX
 PS Example; Fig 12B; 174pp; English.
 XX
 CC AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding
 CC peptides. These sequences were used as pairs of multivalent recognition
 CC unit complexes used in the method of the invention. The method of the
 CC invention is for identifying polypeptides containing functional domains
 CC of interest (especially SH3 domains). It comprises contacting a
 CC multivalent recognition unit (RU) complex with a number of peptides and

CC identifying polypeptides having a selective binding affinity for the RU
 CC complex. The method is based on functional similarities and does not rely
 CC on sequence similarities. Prior methods only gave limited success for
 CC identifying proteins containing an SH3 domain due to the minimal sequence
 CC homology among known SH3 proteins. Multivalent RU complexes are
 CC particularly suited to screening for polypeptides containing functional
 CC domains that are similar to, but not identical in sequence to, the
 CC original target functional domain. The new method enables proteins having
 CC a common function to be identified. Identification of novel SH3 proteins
 CC will be useful for a better understanding of cell growth, malignancy,
 CC signal transduction processes, etc. New candidate drugs can be
 CC identified, and their specificities (e.g. pharmacological activities) can
 CC be assessed using the method of the invention

XX SQ Sequence 18 AA;

Query Match 45.7%; Score 37; DB 2; Length 18;
 Best Local Similarity 60.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 EMKPPPPPOE 12
 | ||||| :
 Db 7 EPDFPPPPPD 16

RESULT 25

AAW37677
 ID AAW37677 standard; peptide; 18 AA.

XX AAW37677;

DT 23-APR-1998 (first entry)

XX PPPY motif containing peptide bSH3020 used to bind WW domains.

XX Peptide recognition unit; WW domain; cell signalling; growth regulation;

KM cytoskeleton organisation; targeted drug screening; modulator;

KW WW domain interaction; YAP protein; dystrophin.

XX Synthetic.

OS WO9737223-A1.

XX PD 09-OCT-1997.

XX PF 03-APR-1997; 97WO-US005547.

XX PR 03-APR-1996; 96US-00630916.

XX PA (CYTO-) CYTOGEN CORP.

XX PI (UWNC-) UNIV NORTH CAROLINA.

XX PI Pirozzi G, Kay BK, Fowlkes DM;

XX WPI; 1997-503234/46.

XX Identifying cell signalling and growth regulatory polypeptides by

XX reaction with multivalent recognition complex - polypeptides are useful

XX in targeted drug selection.

XX Example 6.3; Fig 7; 220pp; English.

XX Peptides AAW37653-77 contain PPPPY-like motifs. The PPPY motif is found

XX in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides

XX containing this residue have been shown to bind the YAP WW domain, but

XX not the WW domain from dystrophin or to a panel of SH3 domains. Peptides

XX AAW37653-77 were biotinylated and complexed with alkaline streptavidin,

XX and used in a cross affinity mapping experiment. They were tested for

XX their ability to bind to the 12 individual novel WW domains of WPI

XX (AAW36794), WWP2 (AAW36795), WWP3 (AAW37696) and WWP4 (AAW36797), which

XX were expressed as glutathione-S-transferase expression proteins. The

XX present peptide, derived from a vinculin protein, does not bind to WW

XX domains of the novel proteins. The WW domain is a small functional

CC domain. Its name is derived from the observation that two tryptophan
 CC residues, one in the amino terminal portion of the WW domain and one in
 CC the carboxyl terminal portion, are conserved. Most proteins containing WW
 CC domain have a function involving cell signalling and growth regulation
 CC or the organisation of the cytoskeleton. Polypeptides containing a WW
 CC domain are identified by treating a multivalent recognition unit complex
 CC that has selective binding affinity for a WW domain, with many
 CC polypeptides and identifying those with selective affinity for the
 CC complex. Proteins containing WW domains are used for targeted drug
 CC screening, i.e. to identify potential modulators of specific WW domain
 CC interactions

XX SQ Sequence 18 AA;

Query Match 45.7%; Score 37; DB 2; Length 18;
 Best Local Similarity 60.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 EMKPPPPPOE 12
 | ||||| :
 Db 7 EPDFPPPPPD 16

RESULT 26

AAW38909
 ID AAW38909 standard; peptide; 18 AA.

XX AAW38909;

DT 27-MAR-1998 (first entry)

XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:305.

KM Cortactin; SH3 domain; binding peptide; Src homology region 3;

KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;

KW PLCgamma; p53bp2; Ctk; Yes; Grb2.

XX Synthetic.

OS WO9730074-A1.

XX PD 21-AUG-1997.

XX PF 14-FEB-1997; 97WO-US002298.

XX PR 16-FEB-1996; 96US-00602999.

XX PA (CYTO-) CYTOGEN CORP.

XX PI (UWNC-) UNIV NORTH CAROLINA.

XX PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ, Fowlkes DM;

XX Rider JB;

XX WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src tyrosine

XX kinase(s) and to stimulate immune response by increasing production of

XX certain lymphokine(s), e.g. interleukin-1.

XX Claim 22; Page 90; 131pp; English.

XX The present sequence represents a peptide which resembles a Src homology

XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:

XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which

XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain

XX of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which

XX bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain

XX of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Ctk;

XX (h) peptides which bind the SH3 domain of Yes; and (i) peptides which

XX bind the amino-terminal SH3 domain of Grb2. The purified binding peptides

XX can be used in the method to identify inhibitors of their binding to

XX their respective SH3 domains, which could be used to modulate the

XX pharmacological activity of proteins or polypeptide containing the SH3

CC domain. The peptides can also be used to activate Src or Src-related
 CC protein tyrosine kinases, to stimulate the immune response by increasing
 CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha
 CC and interleukin-1, or to deliver a conjugated molecule to certain
 CC cellular compartments containing Src or Src related proteins
 CC
 SQ Sequence 18 AA;

Query Match 45.7%; Score 37; DB 2; Length 18;
 Best Local Similarity 55.6%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FPPPEQETV 14
 ||||| : :
 Db 7 FPPPEYQPI 15

RESULT 27
 AAM47562
 ID AAM47562 standard; peptide; 18 AA.
 XX
 AC AAM47562;

DT 03-JUN-1998 (first entry)
 XX
 XX

DE Exendin agonist (13).
 XX

KM Exendin agonist; gastric motility; gastric emptying; treatment; spasm;
 KM postprandial dumping syndrome; postprandial hyperglycaemia;
 KM type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;
 KM Gila monster venom.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FH Modified-site 8
 FT /note= "pentylglycine"
 FT Modified-site 18
 FT /note= "amidated"

PN WO9805351-A1.
 XX
 PD 12-FEB-1998.

PR 08-AUG-1997; 97MO-US014199.
 XX
 PR 08-AUG-1996; 96US-00694954.

PA (AMYL-) AMYLIN PHARM INC.
 XX
 PI Young AA, Gedulin B, Beeley NRA, Prickett KS;

DR WPI; 1998-145351/13.
 XX
 CC

PT Regulating gastrointestinal motility using exendins or their agonists -
 PT for treating spasm, diabetic postprandial hyperglycaemia, impaired
 PT glucose tolerance etc., also in diagnostic investigations.
 XX
 PS Example 16; Fig 8; 70pp; English.

CC The present sequence is an exendin agonist, which reduces gastric
 CC motility and delays gastric emptying. It can be used to treat spasm
 CC (where associated with acute diverticulitis or disorders of the biliary
 CC tract or sphincter of Oddi), postprandial dumping syndrome and
 CC hyperglycaemia (particularly associated with type 2 diabetes), type 1
 CC diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist
 CC is administered to prevent stomach contents passing into the intestines,
 CC then the stomach pumped) and obesity. It can also be administered to
 CC subjects undergoing gastrointestinal diagnostic investigation,
 CC particularly radiological or by magnetic resonance imaging. Exendins,
 CC components of Gila monster venom, have some sequence similarity to
 CC glucagon-like peptides (GLP). They are GLP agonists and have been
 CC suggested (US5424286) for treatment of diabetes and prevention of

CC hyperglycaemia
 XX
 SQ Sequence 18 AA;

Query Match 45.7%; Score 37; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEMKEPPP 10
 | : |||||
 Db 9 LFIEPPPP 17

RESULT 28
 AAY03733
 ID AAY03733 standard; peptide; 18 AA.
 XX
 AC AAY03733;

DT 08-JUN-1999 (first entry)
 XX
 XX

DE Exendin agonist compound 13.
 XX

KM Exendin; agonist; diabetes; disorder; plasma glucose; gastric;
 KM diagnostic; gastro-intestinal; radiological.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FH Modified-site 8
 FT /note= "pentylglycine"
 FT Modified-site 18
 FT /note= "C-terminal amide"

PN WO9907404-A1.
 XX
 PD 18-FEB-1999.

PR 06-AUG-1998; 98MO-US016387.
 XX
 PR 08-AUG-1997; 97US-0055404P.

PA (AMYL-) AMYLIN PHARM INC.
 XX
 PI Beeley NRA, Prickett KS;

DR WPI; 1999-180403/15.
 XX
 CC

PT New exendin agonists - useful in the treatment of Type I and II diabetes.
 PT Claim 17; Fig 1A-B; 70pp; English.
 XX
 PS

CC The invention relates to exendin agonists which slow gastric emptying and
 CC lower plasma glucose levels. The exendin agonists are used to treat Type
 CC I and II diabetes, disorders which would be benefited by agents which
 CC lower plasma glucose levels, and disorders which would be benefited by
 CC agents useful in delaying and/or slowing gastric emptying. Delayed
 CC gastric emptying is a useful diagnostic aid in gastro-intestinal
 CC radiological examinations. Sequences AAY03721-51 represent specifically
 CC claimed examples of the exendin agonist compounds of the invention. (Also
 CC see AAY03720 for exendin generic peptide formula and description)
 XX
 SQ Sequence 18 AA;

Query Match 45.7%; Score 37; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEMKEPPP 10
 | : |||||
 Db 9 LFIEPPPP 17

```

RESULT 29
ADB49303
ID ADB49303 standard; peptide; 18 AA.
XX
XX ADB49303;
AC
XX 04-DEC-2003 (first entry)
DT
XX
XX Novel WW domain binding peptide #25.
DE
XX
XX MW domain; drug candidate screening; drug discovery; drug modification;
KW drug refinement; immunogen; WW binding protein; WW domain.
XX
XX Unidentified.
OS
XX
XX US200307577-A1.
PN
XX
XX 24-APR-2003.
PD
XX
XX 28-JUN-2002; 2002US-00185050.
PF
XX
XX 03-APR-1996; 96US-00630916.
PR
XX 03-APR-1997; 97US-00826516.
PA
XX (PIRO/) PIROZZI G.
PA (KAYB/) KAY B K.
PA (FOWL/) FOWLKES D M.
XX
XX Pirozzi G, Kay BK, Fowlkes DM;
PI
XX
XX WPI; 2003-635075/60.
DR
XX
XX Novel purified polypeptide comprising WW domain, useful for drug
PT discovery, modification and refinement, for discovering polypeptides
PT involved in pharmacological activities, or as an immunogen to generate
XX antibodies.
XX
XX Example; Fig 7; 133pp; English.
XX
XX The invention describes a purified polypeptide (I) comprising a WW domain
CC which has a sequence (S1) selected from 11 sequences fully defined in the
CC specification, a sequence (S2) selected from 48 sequences fully defined
CC in the specification or a sequence (S3) comprising 683, 906, 224 or 725
CC amino acids fully defined in the specification. (I) is useful for
CC screening a potential drug candidate, by allowing (I) to come into
CC contact with at least one recognition unit having a selective affinity
CC for the WW domain in (I), in the presence of an amount of a potential
CC drug candidate, such that (I) and the recognition unit are capable of
CC interacting when brought into contact with one another in the absence of
CC the drug candidate, and determining the effect, if any, of the presence
CC of the amount of the drug candidate on the interaction of (I) with the
CC recognition unit. (I) is useful for drug discovery, modification and
CC refinement, for discovering polypeptides involved in pharmacological
CC activities, or as an immunogen to generate antibodies. This is the amino
CC acid sequence of a peptide that binds the novel WW domains of the
CC invention
XX
XX
XX Sequence 18 AA;
SQ

```

```

Query Match 45.7%; Score 37; DB 7; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 3 EMKPPPPPOE 12
   | | | | | :
Db 7 EPPPPPPPPD 16

```

```

RESULT 30
AAR07284
ID AAR07284 standard; protein; 10 AA.
XX
XX AAR07284;
AC

```

```

XX
XX 31-JAN-1991 (first entry)
DT
XX
XX Smooth muscle myosin-2 immunogen for antibody prodn.
DE
XX
XX Smooth muscle myosin isoform 2; monoclonal antibody; immunogen;
KW diagnosis; arteriosclerosis.
XX
XX Homo sapiens.
OS
XX
XX WO9011520-A.
PN
XX
XX 04-OCT-1990.
PD
XX
XX 28-MAR-1989; 89JP-00075884.
PF
XX
XX 28-MAR-1989; 89JP-00075884.
PR
XX 28-MAR-1989; 89JP-00075884.
PA
XX (YAMS ) YAMASA SHOYU KK.
PA
XX
XX Nagai R, Kuroo M, Kato H;
PI
XX
XX WPI; 1990-320366/42.
DR
XX
XX Antibody against heavy chain of smooth muscle myosin - as reagent for
PT histological staining of smooth muscle or diagnosis of blood vessel
PT disorders.
XX
XX Claim 7; Page 42; 61pp; Japanese.
XX
XX The oligopeptide is used as immunogen for the prodn. of monoclonal
CC antibodies recognising isoform SM-2 of the heavy chain of smooth muscle
CC myosin, pref. from heart or skeletal muscle, esp. human. The peptide
CC contains the part which differs between isoforms SM1-3. The antibodies
CC may be obtained by immunisation with the immunogen, followed by cell
CC fusion to produce a hybridoma, cloning and culturing the chosen hybridoma
CC clone. The Ab is a reagent for the histological staining of smooth
CC muscle, and is useful in the diagnosis of arteriosclerosis, blood vessel
CC disorders etc. See also AAR07283-5
XX
XX
XX Sequence 10 AA;
SQ

```

```

Query Match 44.4%; Score 36; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 8 PPOQET 13
   | | | | |
Db 3 PPOQET 8

```

```

RESULT 31
AAG79174
ID AAG79174 standard; peptide; 14 AA.
XX
XX AAG79174;
AC
XX
XX 03-JAN-2002 (first entry)
DT
XX
XX
XX Peptide derived from ActA, and containing EVH1-binding site.
DE
XX
XX ActA; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;
KW enabled/vasodilator-stimulated phosphoprotein protein; T cell;
KW T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;
KW infectious disease; cancer; autoimmune disease; inflammation;
KW platelet aggregation; wound healing; clotting.
XX
XX
XX Listeria monocytogenes.
OS
XX
XX
XX WO200174858-A2.
PN
XX
XX 11-OCT-2001.
PD
XX

```



```

PF 03-APR-2001; 2001WO-US010753.
XX
XX 03-APR-2000; 2000US-0194215P.
PR
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX (GBPB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
PA
XX Krause M, Sechi AS, Gertler FB, Wehland J;
XX MPI; 2001-616686/71.
XX
XX Modulating cytoskeletal rearrangement to regulate T cell and macrophage
XX activation for treating cancer, autoimmune disease, and infectious
XX disease, comprises contacting with a Fyb/SLAP complex modulator.
XX
XX Example 5; Page 43; 79pp; English.
XX
XX The specification describes Fyb/SLAP proteins. Fyb/SLAP proteins are
XX ligands for the EVH1 domains of Ena(enabled)/vasodilator-stimulated
XX phosphoprotein (VASP) proteins. The specification describes a method for
XX modulating cytoskeletal rearrangement in a cell, or T cell response to T
XX cell receptor stimulation. The method comprises contacting the cell or T
XX cell with a Fyb/SLAP complex modulator sufficient to modulate the
XX formation of a complex of an Ena/VASP protein and a Fyb/SLAP protein. The
XX method is useful for modulating cytoskeletal rearrangement in a cell such
XX as a lymphocyte, preferably a T cell, a macrophage or a cell fragment
XX such as a platelet and for modulating T cell response to a T cell
XX receptor stimulation. T cell response is increased in a subject having or
XX at risk of developing infectious disease or cancer and T cell response is
XX inhibited in a subject having or is at risk of developing an autoimmune
XX disease or a condition characterized by inflammation. A composition
XX comprising a Fyb/SLAP complex inhibitor is useful for increasing platelet
XX aggregation for promoting wound healing or clotting. The present sequence
XX represents a peptide derived from Acta, which is used in the course of
XX the invention
XX
XX Sequence 14 AA;
XX
XX Query Match 44.4%; Score 36; DB 4; Length 14;
XX Best Local Similarity 62.5%; Pred. No. 1.9e+02;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 5 KPPPPQQR 12
XX :|||||:
XX 2 EPPPPPTD 9
XX
XX Db
XX
XX RESULT 32
XX AAG79166
XX ID AAG79166 standard; peptide; 15 AA.
XX AC AAG79166;
XX
XX DT 03-JAN-2002 (first entry)
XX
XX DE Synthetic antigenic peptide derived from Acta.
XX
XX Acta; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;
XX enabled/vasodilator-stimulated phosphoprotein protein; T cell;
XX T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;
XX infectious disease; cancer; autoimmune disease; inflammation;
XX platelet aggregation; wound healing; clotting.
XX
XX OS Synthetic.
XX OS Liberaia monocytogenes.
XX
XX PN WO200174858-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 03-APR-2001; 2001WO-US010753.
XX
XX PR 03-APR-2000; 2000US-0194215P.
XX

```

```

XX
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX (GBPB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
PA
XX Krause M, Sechi AS, Gertler FB, Wehland J;
XX MPI; 2001-616686/71.
XX
XX Modulating cytoskeletal rearrangement to regulate T cell and macrophage
XX activation for treating cancer, autoimmune disease, and infectious
XX disease, comprises contacting with a Fyb/SLAP complex modulator.
XX
XX Example 1; Page 36; 79pp; English.
XX
XX The present sequence represents an antigenic peptide derived from Acta.
XX polyclonal antibodies raised against this peptide were used to screen
XX mouse embryo expression library to isolate Fyb/SLAP clones. Fyb/SLAP
XX proteins are ligands for the EVH1 domains of Ena(enabled)/vasodilator-
XX stimulated phosphoprotein (VASP) proteins. The specification describes a
XX method for modulating cytoskeletal rearrangement in a cell, or T cell
XX response to T cell receptor stimulation. The method comprises contacting
XX the cell or T cell with a Fyb/SLAP complex modulator sufficient to
XX modulate the formation of a complex of an Ena/VASP protein and a Fyb/SLAP
XX protein. The method is useful for modulating cytoskeletal rearrangement
XX in a cell such as a lymphocyte, preferably a T cell, a macrophage or a
XX cell fragment such as a platelet and for modulating T cell response to a
XX T cell receptor stimulation. T cell response is increased in a subject
XX having or at risk of developing infectious disease or cancer and T cell
XX response is inhibited in a subject having or is at risk of developing an
XX autoimmune disease or a condition characterized by inflammation. A
XX composition comprising a Fyb/SLAP complex inhibitor is useful for
XX increasing platelet aggregation for promoting wound healing or clotting
XX
XX Sequence 15 AA;
XX
XX Query Match 44.4%; Score 36; DB 4; Length 15;
XX Best Local Similarity 62.5%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 5 KPPPPQQR 12
XX :|||||:
XX Db 3 EPPPPPTD 10
XX
XX RESULT 33
XX AAW47569
XX ID AAW47569 standard; peptide; 18 AA.
XX AC AAW47569;
XX
XX DT 03-JUL-1998 (first entry)
XX
XX DE Exendin agonist (20).
XX
XX Exendin agonist; gastric motility; gastric emptying; treatment; spasm;
XX postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;
XX Gila monster venom.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 11 /note= "tert-butylglycine"
XX FT Modified-site 18 /note= "amidated"
XX
XX PN WO9805351-A1.
XX
XX PD 12-FEB-1998.
XX
XX PF 08-AUG-1997; 97WO-US014199.
XX
XX

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PR 08-AUG-1996; 96US-00694954.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Young AA, Gedulin B, Beeley NRA, Prickett KS;
XX
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using exendins or their agonists -
PT for treating spasm, diabetic postprandial hyperglycaemia, impaired
PT glucose tolerance etc., also in diagnostic investigations.
XX
XX Example 23; Fig 8; 70pp; English.
XX
XX The present sequence is an exendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm
XX (where associated with acute diverticulitis or disorders of the biliary
XX tract or sphincter of Oddi), postprandial dumping syndrome and
XX hyperglycaemia (particularly associated with type 2 diabetes), type 1
XX diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist
XX is administered to prevent stomach contents passing into the intestines,
XX then the stomach pumped) and obesity. It can also be administered to
XX subjects undergoing gastrointestinal diagnostic investigation,
XX particularly radiological or by magnetic resonance imaging. Exendins,
XX components of Gila monster venom, have some sequence similarity to
XX glucagon-like peptides (GLP). They are GLP agonists and have been
XX suggested (US5424286) for treatment of diabetes and prevention of
XX hyperglycaemia
XX
XX Sequence 18 AA:
SQ
XX
XX Query Match 44.4%; Score 36; DB 2; Length 18;
XX Best Local Similarity 60.0%; Pred. No. 2.5e+02;
XX Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 VLEMKRPPPP 10
XX : |||||
XX 8 ILFXEPPPP 17
XX
XX Db
XX
XX RESULT 34
XX AAM47552
XX ID AAM47552 standard; peptide; 18 AA.
XX
XX AC AAM47552;
XX
XX DT 03-JUL-1998 (first entry)
XX
XX DE Exendin agonist (3).
XX
XX KW Exendin agonist; gastric motility; gastric emptying; treatment; spasm;
XX postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;
XX Gila monster venom.
XX
XX OS Synthetic.
XX
XX FT Key Location/Qualifiers
XX Modified-site 18 /note= "amidated"
XX
XX PN WO9805351-A1.
XX
XX PD 12-FEB-1998.
XX
XX PF 08-AUG-1997; 97WO-US014199.
XX
XX PR 08-AUG-1996; 96US-00694954.
XX
XX PA (AMYL-) AMYLIN PHARM INC.
XX
XX PI Young AA, Gedulin B, Beeley NRA, Prickett KS;
XX
XX PT

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```

DR WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using exendins or their agonists -
PT for treating spasm, diabetic postprandial hyperglycaemia, impaired
PT glucose tolerance etc., also in diagnostic investigations.
XX
XX Example 6; Fig 8; 70pp; English.
XX
XX The present sequence is an exendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm
XX (where associated with acute diverticulitis or disorders of the biliary
XX tract or sphincter of Oddi), postprandial dumping syndrome and
XX hyperglycaemia (particularly associated with type 2 diabetes), type 1
XX diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist
XX is administered to prevent stomach contents passing into the intestines,
XX then the stomach pumped) and obesity. It can also be administered to
XX subjects undergoing gastrointestinal diagnostic investigation,
XX particularly radiological or by magnetic resonance imaging. Exendins,
XX components of Gila monster venom, have some sequence similarity to
XX glucagon-like peptides (GLP). They are GLP agonists and have been
XX suggested (US5424286) for treatment of diabetes and prevention of
XX hyperglycaemia
XX
XX Sequence 18 AA:
SQ
XX
XX Query Match 44.4%; Score 36; DB 2; Length 18;
XX Best Local Similarity 71.4%; Pred. No. 2.5e+02;
XX Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 MKRPPPP 10
XX : |||||
XX 11 IEFPPPP 17
XX
XX Db
XX
XX RESULT 35
XX AAM47564
XX ID AAM47564 standard; peptide; 18 AA.
XX
XX AC AAM47564;
XX
XX DT 03-JUL-1998 (first entry)
XX
XX DE Exendin agonist (15).
XX
XX KW Exendin agonist; gastric motility; gastric emptying; treatment; spasm;
XX postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;
XX Gila monster venom.
XX
XX OS Synthetic.
XX
XX FT Key Location/Qualifiers
XX Modified-site 9 /note= "pentylglycine"
XX Modified-site 18 /note= "amidated"
XX
XX PN WO9805351-A1.
XX
XX PD 12-FEB-1998.
XX
XX PF 08-AUG-1997; 97WO-US014199.
XX
XX PR 08-AUG-1996; 96US-00694954.
XX
XX PA (AMYL-) AMYLIN PHARM INC.
XX
XX PI Young AA, Gedulin B, Beeley NRA, Prickett KS;
XX
XX DR WPI; 1998-145351/13.
XX
XX PT Regulating gastrointestinal motility using exendins or their agonists -
XX for treating spasm, diabetic postprandial hyperglycaemia, impaired
XX
XX PT

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RESULT 38
AA03742
ID AAY03742 standard; peptide; 18 AA.
XX
AC AAY03742;
XX
DT 08-JUN-1999 (first entry)
XX
DE Extendin agonist compound 22.
XX
KM Extendin; agonist; diabetes; disorder; plasma glucose; gastric;
KW diagnostic; gastro-intestinal; radiological.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 18
FT /note= "C-terminal amide"
XX
PN MO9907404-A1.
XX
PD 18-FEB-1999.
XX
PF 06-AUG-1998; 98WO-US016387.
XX
PR 08-AUG-1997; 97US-0055404P.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beley NRA, Prickett KS;
XX
DR WPI; 1999-180403/15.
XX
PT New extendin agonists - useful in the treatment of Type I and II diabetes.
XX
PS Claim 17; Fig 1D-E; 70pp; English.
XX
CC The invention relates to extendin agonists which slow gastric emptying and
CC lower plasma glucose levels. The extendin agonists are used to treat Type
CC I and II diabetes, disorders which would be benefited by agents which
CC lower plasma glucose levels, and disorders which would be benefited by
CC agents useful in delaying and/or slowing gastric emptying. Delayed
CC gastric emptying is a useful diagnostic aid in gastro-intestinal
CC radiological examinations. Sequences AAY03721-51 represent specifically
CC claimed examples of the extendin agonist compounds of the invention. (Also
CC see AAY03720 for extendin generic peptide formula and description)
XX
SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKFPPPP 10
DB 11 IEFPPPP 17

RESULT 39
AA03735
ID AAY03735 standard; peptide; 18 AA.
XX
AC AAY03735;
XX
DT 08-JUN-1999 (first entry)
XX
DE Extendin agonist compound 15.
XX
KM Extendin; agonist; diabetes; disorder; plasma glucose; gastric;
KW diagnostic; gastro-intestinal; radiological.
XX

```

```

OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9
FT /note= "pentyglycine"
FT Modified-site 18
FT /note= "C-terminal amide"
XX
PN MO9907404-A1.
XX
PD 18-FEB-1999.
XX
PF 06-AUG-1998; 98WO-US016387.
XX
PR 08-AUG-1997; 97US-0055404P.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beley NRA, Prickett KS;
XX
DR WPI; 1999-180403/15.
XX
PT New extendin agonists - useful in the treatment of Type I and II diabetes.
XX
PS Claim 17; Fig 1D-E; 70pp; English.
XX
CC The invention relates to extendin agonists which slow gastric emptying and
CC lower plasma glucose levels. The extendin agonists are used to treat Type
CC I and II diabetes, disorders which would be benefited by agents which
CC lower plasma glucose levels, and disorders which would be benefited by
CC agents useful in delaying and/or slowing gastric emptying. Delayed
CC gastric emptying is a useful diagnostic aid in gastro-intestinal
CC radiological examinations. Sequences AAY03721-51 represent specifically
CC claimed examples of the extendin agonist compounds of the invention. (Also
CC see AAY03720 for extendin generic peptide formula and description)
XX
SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKFPPPP 10
DB 11 IEFPPPP 17

RESULT 40
AAB52878
ID AAB52878 standard; peptide; 18 AA.
XX
AC AAB52878;
XX
DT 28-FEB-2001 (first entry)
XX
DE Extendin agonist compound #6.
XX
KM Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;
KW insulin-resistance syndrome; food intake.
XX
OS Heloderma sp.
XX
PN WO20006629-A1.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011814.
XX
PR 30-APR-1999; 99US-0132018P.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Young A, Prickett K;

```

XX WPI: 2000-672834/65.

DR Modified extendin or an extendin agonist linked to one or more polyethylene
XX glycol (PEG) polymers, modulate plasma glucose levels, useful for
PT treating disorders such as diabetes and obesity.
PT

XX Disclosure: Fig 3; 119pp; English.

XX The present invention relates to extendins and their agonists which have
CC been modified with molecular weight increasing agents such as
CC polyethylene glycol (PEG). These can be used in the treatment of
CC diabetes, obesity, impaired glucose tolerance, postprandial dumping
CC syndrome, postprandial hyperglycaemia, eating disorders, insulin
CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion
XX

SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 3; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLEMKRPPPP 10
: |||||
Db 8 LIFXEPFPPPP 17

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Job time : 83.7273 secs

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OM protein - protein search, using sw model

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54.743 Million cell updates/sec

Title: US-10-691-157-7
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Sequence: 1 VLEMKFPPPPQETVT 15

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Post-processing: Minimum Match 0%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	4	US-09-641-803-7
2	37	45.7	18	3	US-08-630-916A-109
3	37	45.7	18	3	US-08-602-999A-305
4	37	45.7	18	4	US-08-630-915A-165
5	37	45.7	18	4	US-09-500-124-305
6	37	45.7	18	4	US-09-879-957-165
7	35	43.2	10	2	US-08-968-676-19
8	35	43.2	10	4	US-09-823-240A-1
9	35	43.2	12	4	US-09-261-894A-19
10	35	43.2	12	2	US-08-968-676-161
11	35	43.2	12	4	US-09-261-894A-161
12	35	43.2	13	3	US-08-630-916A-7
13	35	43.2	15	3	US-08-602-999A-349
14	35	43.2	15	3	US-08-602-999A-423
15	35	43.2	15	4	US-09-500-124-349
16	35	43.2	15	4	US-09-500-124-423
17	35	43.2	15	4	US-09-413-564C-4
18	35	43.2	16	2	US-08-968-676-1
19	35	43.2	16	4	US-09-396-813-1
20	35	43.2	16	4	US-09-261-894A-1
21	34	42.0	5	4	US-09-823-240A-3
22	34	42.0	5	4	US-09-377-285B-47
23	34	42.0	6	4	US-09-823-240A-12
24	34	42.0	6	4	US-09-823-240A-14
25	34	42.0	9	2	US-08-968-676-160
26	34	42.0	9	4	US-09-823-240A-7
27	34	42.0	9	4	US-09-261-894A-160

28	34	42.0	10	2	US-08-968-676-18	Sequence 18, Appl
29	34	42.0	10	4	US-09-261-894A-18	Sequence 18, Appl
30	34	42.0	10	6	5252466-18	Patent No. 5252466
31	34	42.0	10	6	5252466-18	Patent No. 5252466
32	34	42.0	15	3	US-08-630-916A-55	Sequence 55, Appl
33	34	42.0	15	3	US-08-602-999A-339	Sequence 339, Appl
34	34	42.0	15	3	US-08-602-999A-405	Sequence 405, Appl
35	34	42.0	15	4	US-09-500-124-339	Sequence 339, Appl
36	34	42.0	15	4	US-09-500-124-405	Sequence 405, Appl
37	34	42.0	16	1	US-08-188-223-7	Sequence 7, Appl
38	34	42.0	16	2	US-08-844-312-8	Sequence 8, Appl
39	34	42.0	16	2	US-08-844-312-10	Sequence 10, Appl
40	34	42.0	16	3	US-08-968-466-7	Sequence 7, Appl
41	34	42.0	16	3	US-08-478-546B-7	Sequence 7, Appl
42	34	42.0	16	4	US-09-674-973A-261	Sequence 261, Appl
43	34	42.0	17	4	US-09-060-299-403	Sequence 403, Appl
44	34	42.0	17	4	US-09-641-803-14	Sequence 14, Appl
45	34	42.0	17	4	US-09-641-803-14	Sequence 14, Appl
46	33	40.7	11	4	US-09-547-693-135	Sequence 135, Appl
47	33	40.7	11	4	US-09-547-693-199	Sequence 199, Appl
48	33	40.7	12	3	US-08-630-916A-52	Sequence 52, Appl
49	33	40.7	12	3	US-08-630-916A-88	Sequence 88, Appl
50	33	40.7	12	3	US-08-630-915A-144	Sequence 144, Appl
51	33	40.7	12	4	US-09-879-957-144	Sequence 144, Appl
52	33	40.7	15	1	US-08-302-771-1	Sequence 1, Appl
53	33	40.7	15	3	US-08-602-999A-367	Sequence 367, Appl
54	33	40.7	15	3	US-08-602-999A-373	Sequence 373, Appl
55	33	40.7	15	3	US-08-602-999A-439	Sequence 439, Appl
56	33	40.7	15	4	US-09-500-124-367	Sequence 367, Appl
57	33	40.7	15	4	US-09-500-124-373	Sequence 373, Appl
58	33	40.7	15	4	US-09-500-124-439	Sequence 439, Appl
59	33	40.7	16	3	US-08-630-916A-11	Sequence 11, Appl
60	33	40.7	17	3	US-08-602-999A-336	Sequence 336, Appl
61	33	40.7	17	4	US-09-500-124-336	Sequence 336, Appl
62	32	39.5	15	3	US-08-976-255-20	Sequence 20, Appl
63	32	39.5	18	1	US-08-279-058B-20	Sequence 20, Appl
64	32	39.5	18	4	US-08-828-323-20	Sequence 20, Appl
65	31	38.3	8	3	US-09-343-011B-9	Sequence 9, Appl
66	31	38.3	9	4	US-09-295-996B-29	Sequence 29, Appl
67	31	38.3	9	4	US-09-295-846B-32	Sequence 32, Appl
68	31	38.3	9	4	US-09-551-737C-32	Sequence 32, Appl
69	31	38.3	9	4	US-09-551-738B-29	Sequence 29, Appl
70	31	38.3	10	1	US-08-230-047-11	Sequence 11, Appl
71	31	38.3	10	2	US-08-968-676-162	Sequence 162, Appl
72	31	38.3	10	4	US-09-261-894A-162	Sequence 162, Appl
73	31	38.3	11	1	US-08-336-343A-26	Sequence 26, Appl
74	31	38.3	11	3	US-08-652-877-23	Sequence 23, Appl
75	31	38.3	11	4	US-08-476-515A-23	Sequence 23, Appl
76	31	38.3	12	3	US-09-700-993A-24	Sequence 24, Appl
77	31	38.3	12	3	US-09-602-999A-168	Sequence 168, Appl
78	31	38.3	12	4	US-09-460-384-25	Sequence 25, Appl
79	31	38.3	12	4	US-09-500-124-268	Sequence 268, Appl
80	31	38.3	12	4	US-09-428-082B-312	Sequence 312, Appl
81	31	38.3	12	4	US-09-428-082B-313	Sequence 313, Appl
82	31	38.3	13	3	US-09-460-384-26	Sequence 26, Appl
83	31	38.3	14	3	US-08-630-916A-56	Sequence 56, Appl
84	31	38.3	15	3	US-08-602-999A-298	Sequence 298, Appl
85	31	38.3	15	3	US-08-602-999A-352	Sequence 352, Appl
86	31	38.3	15	3	US-08-602-999A-354	Sequence 354, Appl
87	31	38.3	15	4	US-08-602-999A-377	Sequence 377, Appl
88	31	38.3	15	4	US-09-500-124-298	Sequence 298, Appl
89	31	38.3	15	4	US-09-500-124-352	Sequence 352, Appl
90	31	38.3	15	4	US-09-500-124-354	Sequence 354, Appl
91	31	38.3	15	4	US-09-500-124-377	Sequence 377, Appl
92	31	38.3	16	1	US-08-064-400B-1	Sequence 1, Appl
93	31	38.3	16	1	US-08-477-509B-17	Sequence 17, Appl
94	31	38.3	16	2	US-08-844-312-11	Sequence 11, Appl
95	31	38.3	16	3	US-08-630-916A-107	Sequence 107, Appl
96	31	38.3	16	3	US-08-482-085B-17	Sequence 17, Appl
97	31	38.3	16	3	US-08-602-999A-344	Sequence 344, Appl
98	31	38.3	16	3	US-08-602-999A-422	Sequence 422, Appl
99	31	38.3	16	3	US-08-630-915A-163	Sequence 163, Appl
100	31	38.3	16	3	US-08-630-915A-163	Sequence 163, Appl

ALIGNMENTS

RESULT 1
US-09-641-803-7
; Sequence 7, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDGOH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-7

Query Match 100.0%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKPPPPQETVT 15
| | | | | | | | | | | | | | | | |
Db 1 VLEMKPPPPQETVT 15

RESULT 2
US-08-630-916A-109
; Sequence 109, Application US/08630916A
; Patent No. 6011137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-916A-109

Query Match 45.7%; Score 37; DB 3; Length 18;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 EKKPPPPQEQE 12
| | | | | | | | | | | | | | | | |
Db 7 EPDPFPPPPD 16

RESULT 3
US-08-602-999A-305
; Sequence 305, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: RAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-305

Query Match 45.7%; Score 37; DB 3; Length 18;
Best Local Similarity 55.6%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FPPPPQETV 14
| | | | | | | | | | | | | | | | |
Db 7 FPPPPQETV 15

RESULT 4
US-08-630-915A-165
; Sequence 165, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNTE
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-165

Query Match 45.7%; Score 37; DB 3; Length 18;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EKKFPPEPQE 12
| | | | | :
Db 7 EPPDFPPPPD 16

RESULT 5
US-09-500-124-305
; Sequence 305, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: OULILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 305:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-305

Query Match 45.7%; Score 37; DB 4; Length 18;
Best Local Similarity 55.6%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FPPPEQETV 14
| | | | | :
Db 7 FPPPEYQPI 15

RESULT 6
US-09-879-957-165
; Sequence 165, Application US/09879957
; Patent No. 6709821
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6709821h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8664/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 165:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-09-879-957-165

Query Match 45.7%; Score 37; DB 4; Length 18;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKFPFPPQ 12
| | | | | :
DB 7 EPDFPPPPD 16

RESULT 7
US-08-968-676-19
Sequence 19, Application US/08968676
Patent No. 5919639
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Sharlene
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,676
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-968-676-19

Query Match 43.2%; Score 35; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKFPFPPQ 11
| | | | | :
DB 1 LMKLPKPPK 10

RESULT 8
US-09-823-240A-1
Sequence 1, Application US/09823240A
Patent No. 6716597
GENERAL INFORMATION:
APPLICANT: Frank B. Gertler
APPLICANT: James E. Bear
APPLICANT: Jürgen Weiland
APPLICANT: Joseph Loureiro
TITLE OF INVENTION: Methods and Products for Regulating Cell
FILE REFERENCE: M00656.70064.US
CURRENT APPLICATION NUMBER: US/09/823,240A
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 60/194,564
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 1
LENGTH: 10
TYPE: PRT
ORGANISM: Listeria monocytogenes
FEATURE:
NAME/KEY: Misc.feature
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa is Asp or Glu
NAME/KEY: Misc.feature
LOCATION: (7)...(7)
OTHER INFORMATION: Xaa is any amino acid
US-09-823-240A-1

Query Match 43.2%; Score 35; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FPPFPPQ 12
| | | | | :
DB 2 FPPFPPD 8

RESULT 9
US-09-261-894A-19
Sequence 19, Application US/09261894A
Patent No. 6835382
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT E.
APPLICANT: ADAMS, SHARLENE
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION
FILE REFERENCE: REH-2006
CURRENT APPLICATION NUMBER: US/09/261,894A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO: 19
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-261-894A-19

Query Match 43.2%; Score 35; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKEPPPO 11
| | | | |
| | | | |
DB 1 LMKLPPKPPK 10

RESULT 10
US-08-968-676-161
; Sequence 161, Application US/08968676
; Patent No. 5919639

GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Sharlene
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,676
FILING DATE:
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 161:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-968-676-161

Query Match 43.2%; Score 35; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKEPPPO 11
| | | | |
| | | | |
DB 1 LMKLPPKPPK 10

RESULT 11
US-09-261-894A-161
; Sequence 161, Application US/09261894A
; Patent No. 6835382

GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT E.
APPLICANT: ADAMS, SHARLENE
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION
FILE REFERENCE: REH-2006
CURRENT APPLICATION NUMBER: US/09/261,894A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 167

SOFTWARE: Patent Ver. 3.2
SEQ ID NO 161
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-261-894A-161

Query Match 43.2%; Score 35; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKEPPPO 11
| | | | |
| | | | |
DB 1 LMKLPPKPPK 10

RESULT 12
US-08-630-916A-7
; Sequence 7, Application US/08630916A
; Patent No. 6011137

GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: Kay, Brian K.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-916A-7

Query Match 43.2%; Score 35; DB 3; Length 13;
Best Local Similarity 71.4%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PEPPOE 12
| | | | |
| | | | |
DB 5 YPPPPPE 11

RESULT 13
US-09-602-999A-349

; Sequence 349, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18, 872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 349:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-349

Query Match 43.2%; Score 35; DB 3; Length 15;
Best Local Similarity 54.5%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPPPQK 12
| : |||||
Db 1 LPSREPPPPQK 11

RESULT 14
US-08-602-999A-423
; Sequence 423, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York

STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18, 872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 423:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-423

Query Match 43.2%; Score 35; DB 3; Length 15;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPPK 12
|||:|
Db 8 PPPPK 13

RESULT 15
US-09-500-124-349
; Sequence 349, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18, 872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 349:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPR: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-349

Query Match 43.2%; Score 35; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPPPQOE 12
| : |||| :
Db 1 LPSRPPPPQK 11

RESULT 16
US-09-500-124-423

Sequence 423, Application US/09500124
Patent No. 6432920

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian X.
APPLICANT: THORN, Judith M.
APPLICANT: OUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18, 872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 423:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPR: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-423

Query Match 43.2%; Score 35; DB 4; Length 15;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQOE 12
| : |||| :
Db 8 PPPPPE 13

RESULT 17
US-09-413-564C-4

Sequence 4, Application US/09413564C
Patent No. 6716428

GENERAL INFORMATION:
APPLICANT: The Ohio State University Research Foundation
APPLICANT: Stevens, Vernon
TITLE OF INVENTION: Antigenic modification of polypeptides
FILE REFERENCE: URF 2-056 AVI
CURRENT APPLICATION NUMBER: US/09/413,564C
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: 09/413,564
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patent in version 3.0
SEQ ID NO 4
LENGTH: 15
TYPR: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(15)
US-09-413-564C-4

Query Match 43.2%; Score 35; DB 4; Length 15;
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQET 13
| : |||| :
Db 4 PPPPSDT 10

RESULT 18
US-08-968-676-1

Sequence 1, Application US/08968676
Patent No. 5919639

GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Sharlene
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,676
FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:

TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-968-676-1

Query Match 43.2%; Score 35; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKEPPPPQ 11
| | | | |
Db 1 LRMKLKPKPK 10

RESULT 19
US-09-396-813-1
; Sequence 1, Application US/09396813
; Patent No. 6432409
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E.
; APPLICANT: Xu, Minzhen
; TITLE OF INVENTION: HYBRID PEPTIDES MODULATE THE IMMUNE RESPONSE
; FILE REFERENCE: REH2007
; CURRENT APPLICATION NUMBER: US/09/396,813
; CURRENT FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mouse
US-09-396-813-1

Query Match 43.2%; Score 35; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKEPPPPQ 11
| | | | |
Db 1 LRMKLKPKPK 10

RESULT 20
US-09-261-894A-1
; Sequence 1, Application US/09261894A
; Patent No. 6835382
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT E.
; APPLICANT: ADAMS, SHARLENE
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION
; FILE REFERENCE: REH-2006
; CURRENT APPLICATION NUMBER: US/09/261,894A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-261-894A-1

Query Match 43.2%; Score 35; DB 4; Length 16;

Best Local Similarity 60.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 LEMKEPPPPQ 11
| | | | |
Db 1 LRMKLKPKPK 10

RESULT 21
US-09-823-240A-3
; Sequence 3, Application US/09823240A
; Patent No. 6716597
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jurgen Wehlend
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; FILE REFERENCE: M00656.70064.US
; CURRENT APPLICATION NUMBER: US/09/823,240A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-09-823-240A-3

Query Match 42.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4; 1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPPPP 10
| | | | |
Db 1 PPPPP 5

RESULT 22
US-09-377-285B-47
; Sequence 47, Application US/09377285B
; Patent No. 6720175
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: WORLEY, Paul
; APPLICANT: TU, Jian
; APPLICANT: XIAO, Bo
; APPLICANT: LEAHY, Daniel
; APPLICANT: BENKEN, Jutta
; APPLICANT: LANAHAN, Anthony
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1B PROTEIN (AS AMENDED)
; FILE REFERENCE: JH01580-4
; CURRENT APPLICATION NUMBER: US/09/377,285B
; CURRENT FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/138,426
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,493
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,494
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/097,334
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: optimal ligand

US-09-377-285B-47

Query Match 42.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPPPP 10
|||
Db 1 PPPPP 5

RESULT 23

US-09-823-240A-12
; Sequence 12, Application US/09823240A
; Patent No. 6716597
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jurgen Weiland
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; FILE REFERENCE: M00656.70064.US
; CURRENT APPLICATION NUMBER: US/09/823,240A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-09-823-240A-12

Query Match 42.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPPPP 10
|||
Db 2 PPPPP 6

RESULT 24

US-09-823-240A-14
; Sequence 14, Application US/09823240A
; Patent No. 6716597
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jurgen Weiland
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; FILE REFERENCE: M00656.70064.US
; CURRENT APPLICATION NUMBER: US/09/823,240A
; CURRENT FILING DATE: 2001-03-30
; PRIOR FILING DATE: 60/194,564
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
; FEATURES:
; NAME/KEY: Misc feature
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa is Asp or Glu
US-09-823-240A-14

Query Match 42.0%; Score 34; DB 4; Length 6;

Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPPPP 10
|||
Db 2 PPPPP 6

RESULT 25

US-08-968-676-160
; Sequence 160, Application US/08968676
; Patent No. 5919639
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E
; APPLICANT: Adams, Sharlene
; APPLICANT: Xu, Minzhen
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P. O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,676
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-968-676-160

Query Match 42.0%; Score 34; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LMKPPPP 10
|||
Db 1 LMKLPKPP 9

RESULT 26

US-09-823-240A-7
; Sequence 7, Application US/09823240A
; Patent No. 6716597
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jurgen Weiland
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; FILE REFERENCE: M00656.70064.US
; CURRENT APPLICATION NUMBER: US/09/823,240A
; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO: 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: Misc feature
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa is any amino acid
US-09-823-240A-7

Query Match 42.0%; Score 34; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 FPPPP 10
|||
Db 1 FPPPP 5

RESULT 27
US-09-261-894A-160
; Sequence 160, Application US/09261894A
; Patent No. 6835382
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT E.
; APPLICANT: ADAMS, SHARLENE
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION
; FILE REFERENCE: REH-2006
; CURRENT APPLICATION NUMBER: US/09/261,894A
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 160
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-261-894A-160

Query Match 42.0%; Score 34; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 LEMKPPPP 10
|||
Db 1 LEMKLPKPP 9

RESULT 28
US-08-968-676-18
; Sequence 18, Application US/08968676
; Patent No. 5919639
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT E.
; APPLICANT: ADAMS, SHARLENE
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,676
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-968-676-18

Query Match 42.0%; Score 34; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 LEMKPPPP 10
|||
Db 1 LEMKLPKPP 9

RESULT 29
US-09-261-894A-18
; Sequence 18, Application US/09261894A
; Patent No. 6835382
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT E.
; APPLICANT: ADAMS, SHARLENE
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION
; FILE REFERENCE: REH-2006
; CURRENT APPLICATION NUMBER: US/09/261,894A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-261-894A-18

Query Match 42.0%; Score 34; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 LEMKPPPP 10
|||
Db 1 LEMKLPKPP 9

RESULT 30
5252466-18
; Patent No. 5252466
; APPLICANT: CRONAN, JOHN E.
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
; PURIFYING THEM
; NUMBER OF SEQUENCES: 24


```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/525,568
; FILING DATE: 18-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 354,266
; FILING DATE: 19-MAY-1989
; SEQ ID NO:18:
; LENGTH: 10
5252466-18

Query Match          42.0%; Score 34; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PPPQETV 14
DB 3 PPPPGTV 10

RESULT 31
5252466-18
; Patent No. 5252466
; APPLICANT: CROMAN, JOHN E.
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
; PURIFYING THEM
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/525,568
; FILING DATE: 18-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 354,266
; FILING DATE: 19-MAY-1989
; SEQ ID NO:18:
; LENGTH: 10
5252466-18

Query Match          42.0%; Score 34; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PPPQETV 14
DB 3 PPPPGTV 10

RESULT 32
US-08-630-916A-55
; Sequence 55, Application US/08630916A
; Patent No. 6011137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-916A-55

Query Match          42.0%; Score 34; DB 3; Length 15;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PPPQETV 14
DB 4 PPPPYTV 11

RESULT 33
US-08-602-999A-339
; Sequence 339, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLEY, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-339

Query Match          42.0%; Score 34; DB 3; Length 15;
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Best Local Similarity 83.3%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPOE 12
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Db 6 PPPPOK 11

RESULT 34

US-08-602-999A-405
; Sequence 405, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18, 872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 405:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-405

Query Match 42.0%; Score 34; DB 3; Length 15;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KPPPPQ 11
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Db 4 KPPPPQ 10

RESULT 35

US-09-500-124-339
; Sequence 339, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.

APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18, 872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-339

Query Match 42.0%; Score 34; DB 4; Length 15;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPOE 12
|||||:
Db 6 PPPPOK 11

RESULT 36

US-09-500-124-405
; Sequence 405, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 405:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-405

Query Match 42.0%; Score 34; DB 4; Length 15;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KPPEPPQ 11
Db 4 KPPEPPQ 10

RESULT 37
US-08-188-223-7
Sequence 7, Application US/08188223
Patent No. 5688506
GENERAL INFORMATION:
APPLICANT: Grimes, Stephen
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: Immungene Against Gonadotropin
TITLE OF INVENTION: Releasing Hormone
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, Esq.
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,223
FILING DATE: 27-JAN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Drivas Esq., Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8286
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: YES
FEATURE:
NAME/KEY: Region
LOCATION: 1..6
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FEATURE:
NAME/KEY: Region
LOCATION: 7..16
OTHER INFORMATION: /note= "immunomimic"
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LOCATION: 16
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US-08-188-223-7

Query Match 42.0%; Score 34; DB 1; Length 16;
Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 12
Db 2 PPPPQ 7

RESULT 38
US-08-844-312-8
Sequence 8, Application US/08844312
Patent No. 5948639
GENERAL INFORMATION:
APPLICANT: Carlos J. Gimeno and Dean A. Falb
TITLE OF INVENTION: No. 5948639el TGF-(SYMBOL 98 \f "Symbol") Pathway Genes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,312
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-844-312-8

Query Match 42.0%; Score 34; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 EMKPPPP 10
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DB 4 ELESPPPP 11

RESULT 39

US-08-844-312-10
; Sequence 10, Application US/08844312
; Patent No. 5948639
; GENERAL INFORMATION:
; APPLICANT: Carlos J. Gimeno and Dean A. Faib
; TITLE OF INVENTION: No. 5948639e1 TGF-(SYMBOL 98 \f "Symbol") Pathway Genes
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,312
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MN1-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-844-312-10

Query Match 42.0%; Score 34; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 EMKPPPP 10
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DB 4 ELESPPPP 11

RESULT 40
US-08-968-466-7
; Sequence 7, Application US/08968466
; Patent No. 6132720
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immungens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA

ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,466
; FILING DATE: 27-JAN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 7..16
; OTHER INFORMATION: /note= "immunomimic"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /label= GLYNH2
; OTHER INFORMATION: /note= "glycinamide"
US-08-968-466-7

Query Match 42.0%; Score 34; DB 3; Length 16;
Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 PPPPP 12
|:|:|
DB 2 PPPPP 7

Search completed: June 7, 2005, 23:23:18
Job time : 21.4545 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 23:00:52 ; Search time 67.5 Seconds
(without alignments)
85.185 Million cell updates/sec

Title: US-10-691-157-7

Perfect score: 81
Sequence: 1 VLEMKFPPEPQETVT 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 38334425 residues

Total number of hits satisfying chosen parameters: 309695

Minimum DB seq length: 0
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Listing first 100 summaries

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Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	38	46.9	9	US-09-825-144-10	Sequence 10, Appli
5	38	46.9	14	US-10-762-236-2	Sequence 2, Appli
6	38	46.9	17	US-10-981-434-4	Sequence 4, Appli
7	37	45.7	18	US-09-879-957-165	Sequence 165, App
8	37	45.7	18	US-10-185-050-109	Sequence 109, App
9	37	45.7	18	US-10-161-791-305	Sequence 105, App
10	37	45.7	18	US-10-807-856-165	Sequence 165, App
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14	35	43.2	10	US-09-261-894-19	Sequence 19, Appli
15	35	43.2	12	US-09-261-894-161	Sequence 161, App
16	35	43.2	13	US-10-185-050-7	Sequence 7, Appli
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18	35	43.2	15	US-10-161-791-423	Sequence 423, App
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27	34	42.0	5	US-10-192-381-47	Sequence 47, Appli
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29	34	42.0	9	US-09-823-240-7	Sequence 7, Appli
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82	32	39.5	11	US-10-226-007-741	Sequence 741, App
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85	32	39.5	11	14	US-10-226-007-780	Sequence 780, App
86	32	39.5	11	14	US-10-226-007-792	Sequence 792, App
87	32	39.5	11	14	US-10-226-007-803	Sequence 803, App
88	32	39.5	11	14	US-10-226-007-1027	Sequence 1027, App
89	32	39.5	11	14	US-10-226-007-1040	Sequence 1040, App
90	32	39.5	11	14	US-10-226-007-1053	Sequence 1053, App
91	32	39.5	11	14	US-10-226-007-1500	Sequence 1500, App
92	32	39.5	11	14	US-10-226-007-1502	Sequence 1502, App
93	32	39.5	12	10	US-09-990-832C-96	Sequence 96, Appl
94	32	39.5	12	14	US-10-226-007-742	Sequence 742, App
95	32	39.5	12	14	US-10-226-007-755	Sequence 755, App
96	32	39.5	12	14	US-10-226-007-768	Sequence 768, App
97	32	39.5	12	14	US-10-226-007-781	Sequence 781, App
98	32	39.5	12	14	US-10-226-007-793	Sequence 793, App
99	32	39.5	12	14	US-10-226-007-804	Sequence 804, App
100	32	39.5	12	14	US-10-226-007-814	Sequence 814, App

ALIGNMENTS

```

RESULT 1
US-10-281-652-7
; Sequence 7, Application US/10281652
; Publication No. US20030091606a1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/1149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-10-281-652-7

```

Query Match	100.0%;	Score 81;	DB 14;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 0.00027;		
Matches 15; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 VLEMKFPPPPQETVT 15
|||
Db 1 VLEMKFPPPPQETVT 15

```

RESULT 2
US-10-691-157-7
; Sequence 7, Application US/10691157
; Publication No. US20040266681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADES, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUEHL, Malian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265, 00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; CURRENT FILING DATE: 2003-10-22

```

```

: Prior Application Number: 10/281,652
: Prior Filing Date: 2002-10-28
: Prior Application Number: 09/641,803
: Prior Filing Date: 2000-08-17
: Prior Application Number: 60/149,310
: Prior Filing Date: 1999-08-17
: Prior Application Number: 60/420,369
: Prior Filing Date: 2002-10-22
: Number of SEQ ID NOS: 34
: Software: PatentIn version 3.2
: SEQ ID NO 7
: Length: 15
: Type: PRT
: Organism: artificial
: Feature:
: Other Information: Synthetic Peptides
US-10-691-157-7

Query Match          100.0%;   Score 81;   DB 16;   Length 15;
Best Local Similarity 100.0%;   Pred. No. 0.00027;
Matches    15;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0,

```

QY 1 VLEMKFPDPQETVT 15
|||
Db 1 VLEMKFPDPQETVT 15

RESULT 3
US-10-691-330-7

```

Sequence 7, Application US/10691330
Publication No. US20050042300A1
GENERAL INFORMATION:
APPLICANT: Boldogh, Istvan
APPLICANT: Stanton, G. John
APPLICANT: Georgiades, Jerry A.
APPLICANT: Hughes, Thomas K., Jr.
APPLICANT: Krugel, Marian
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
FILE REFERENCE: 265.00390101
CURRENT FILING DATE: US/10/691,330
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: US 60/420,369
PRIOR FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 15
TYPE: PRT
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: Synthetic Peptides
US-10-691-330-7

```

Query Match	100.0%;	Score 81;	DB 17;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 0.00027;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 VLEMKFPPPPQETVT 15
|||
Db 1 VLEMKFPPPPQETVT 15

RESULT 4
US-09-825-144-10

```

; Sequence 10 Application US/99825144
; Patent No. US20020037286A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Matthias Krause
; APPLICANT: Antonio S. Sechi
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Wehlard
;
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation

```

FILE REFERENCE: M0656/7065
CURRENT APPLICATION NUMBER: US/09/825,144
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/194,215
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-825-144-10

Query Match 46.9%; Score 38; DB 9; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.5e+06;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FPPPPQETV 14
| | | | | : :
| | | | | : :
Db 1 FPPPPDDDI 9

RESULT 5
US-10-762-226-2
Sequence 2, Application US/10762226
Publication No. US20050025770A1
GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Kair, Stephen L.
APPLICANT: Grimes, Stephen
APPLICANT: Michaeli, Dov
APPLICANT: Watson, Susan A.
TITLE OF INVENTION: Immunological Methods for the Treatment of
FILE REFERENCE: 1102865-0031
CURRENT APPLICATION NUMBER: US/10/762,226
CURRENT FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: 60/011,411
PRIOR FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Pyroglutamic acid residue
US-10-762-226-2

Query Match 46.9%; Score 38; DB 17; Length 14;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LEMKPPPPQ 11
| | | | | : :
| | | | | : :
Db 5 LEMKPPPPK 14

RESULT 6
US-10-981-434-4
Sequence 4, Application US/10981434
Publication No. US20050112742A1
GENERAL INFORMATION:
APPLICANT: Thompson, Vicki S.
APPLICANT: Apel, William A.
APPLICANT: Schaller, Kasli D.
TITLE OF INVENTION: HIGH TEMPERATURE AND ALKALINE STABLE CATALASE
FILE REFERENCE: B-372
CURRENT APPLICATION NUMBER: US/10/981,434
CURRENT FILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patent In version 3.2
SEQ ID NO 4
LENGTH: 17
TYPE: PRT
ORGANISM: Thermus brockianus
US-10-981-434-4

Query Match 46.9%; Score 38; DB 17; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEMKPPPPQ 11
| | | | | : :
| | | | | : :
Db 8 LQIRLPPE 17

RESULT 7
US-09-879-957-165
Sequence 165, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
HOFMAN, No. US20020034755A1
KAY, Brian K.
FOWLES, Dana M.
MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mastrok, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 165:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-09-879-957-165
Query Match 45.7%; Score 37; DB 9; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 7 EPDPPEPPPD 16

RESULT 8
US-10-185-050-109
; Sequence 109, Application US/10185050
; Publication No. US20030077577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 28-Jun-2002
; APPLICATION NUMBER: US/10/185,050
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8664/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-10-185-050-109

Query Match 45.7%; Score 37; DB 14; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKPEPPPE 12
| | | | | :
Db 7 EPDPPEPPPD 16

RESULT 9
US-10-161-791-305
; Sequence 305, Application US/10161791
; Publication No. US2003018663A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: OUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/10/161,791
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8664
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-305

Query Match 45.7%; Score 37; DB 14; Length 18;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 PPPPEQETV 14
| | | | | :
Db 7 PPPPEYQPI 15

RESULT 10
US-10-807-856-165
; Sequence 165, Application US/10807856
; Publication No. US20040157216A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, Noah
; KAY, Brian K.
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

1 APPLICATION NUMBER: US/10/807, 8566
 2 FILING DATE: 23-Mar-2004
 3 CLASSIFICATION: 536
 4
 5 PRIOR APPLICATION DATA:
 6 APPLICATION NUMBER: US/08/630, 915
 7 FILING DATE: 03-APR-1996
 8
 9 ATTORNEY/AGENT INFORMATION:
 10 NAME: Misticok, S. Leslie
 11 REGISTRATION NUMBER: 18,872
 12 REFERENCE/DOCKET NUMBER: 1101-174
 13
 14 TELECOMMUNICATION INFORMATION:
 15 TELEPHONE: (212) 790-8090
 16
 17 TELEFAX: (212) 869-8864/9741
 18
 19 TELEX: 66141 PENNIE
 20
 21 INFORMATION FOR SEQ ID NO: 165:
 22 SEQUENCE CHARACTERISTICS:
 23 LENGTH: 18 amino acids
 24 TYPE: amino acid
 25 STRANDEDNESS: <unknown>
 26
 27 TOPOLOGY: unknown
 28
 29 MOLECULE TYPE: peptide
 30 SEQUENCE DESCRIPTION: SEQ ID NO: 165:
 31 US-10-807-856-165

Query Match	45.7%	Score 37/	DB 16/	Length 18/
Best Local Similarity	60.0%	Pred. No. 2.5e+02/		
Matches	6/	Conservative	1/	Mismatches 3/
			Indels	0/
			Gaps	0/
QY	3	EMKPPPPQZ	12	
db	7	BPDPPEPPPD	16	

```

RESULT 11
US-09-825-144-12
; Sequence 12, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Matthias Krause
; APPLICANT: Antonio S. Sechl
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Wehlard
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-09-825-144-12

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Query Match	44.4%	Score 36;	DB 9;	length 14;
Best Local Similarity	62.5%	Pred. No. 2.6e+02;		
Matches	5;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0;
QY	5	KPPPPQQ	12	
	:		:	
ob	2	RPPPPTD	9	

```

RESULT12
US-09-825-144-1
; Sequence 1, Application US/09625144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Matthias Krause
; APPLICANT: Antonio S. Sechi
; APPLICANT: Frank B. Gertler

```

```

APPLICANT: Jorgen Wehland
TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
FILE REFERENCE: M0656/7065
CURRENT APPLICATION NUMBER: US/09/825,144
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/194,215
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
/
/
LENGTH: 15
/
TYPE: PRT
/
ORGANISM: Listeria monocytogenes
US-09-825-144-1

```

```

Query Match      44.4%; Score 36; DB 9; Length 15;
Best Local Similarity 62.5%;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 5 KPPPPPP 12
   :|||||
Db 3 EPPPPPTD 10

```

```

RESULT 13
US-09-823-240-1
; Sequence 1, Application US/09823240
; Patent No. US20020048813A1
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James B. Gear
; APPLICANT: Jürgen Wehlend
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; TITLE OF INVENTION: Moxility
; FILE REFERENCE: M0656/7064 (HCL)
; CURRENT APPLICATION NUMBER: US/09/823,240
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PR1
; ORGANISM: Listeria monocytogenes
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa is Asp or Glu
; NAME/KEY: UNSURE
; LOCATION: (7)...(7)
; OTHER INFORMATION: Xaa is any amino acid
US-09-823-240-1

```

Query Match	43.2%	Score 35;	DB 9;	Length 10;
Best Local Similarity	71.4%	Pred. No. 2.5e+02;		
Matches	5;	Conservative	1;	Indels 0;
				Gaps 0;
Oy	6	FPFPPQ	12	
db	2	FPFPPXD	8	

```

RESULT 14
US-09-261-894-19
: Sequence 19, Application US/09261894
: Publication No. US20030207324A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Humphreys, Robert E
:
: APPLICANT: Adams, Shariene
:
: APPLICANT: Xu, Minzhen
:
: TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN

```

NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/261,894
FILING DATE: March 3, 1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-261-894-19

Query Match 43.2%; Score 35; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPPPQ 11
Db 1 LMKLPPKPK 10

RESULT 15
US-09-261-894-161
Sequence 161, Application US/09261894
Publication No. US20030207324A1
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Shariene
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/261,894
FILING DATE: March 3, 1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:

TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 161:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-261-894-161

Query Match 43.2%; Score 35; DB 10; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPPPQ 11
Db 1 LMKLPPKPK 10

RESULT 16
US-10-185-050-7
Sequence 7; Application US/10185050
Publication No. US2003007577A1
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 233
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 28-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-185-050-7

Query Match 43.2%; Score 35; DB 14; Length 13;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PPPPPE 12

Db 5 YPPPPPE 11

RESULT 17

US-10-161-791-349
; Sequence 349, Application US/10161791
; Publication No. US2003018683A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: OULLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 349:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-349

Query Match 43.2%; Score 35; DB 14; Length 15;
Best Local Similarity 54.5%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPPPPOE 12
| : ||||| :
Db 1 LPSREPPPPQK 11

RESULT 18

US-10-161-791-423
; Sequence 423, Application US/10161791
; Publication No. US2003018683A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: OULLIAM, Lawrence A.
; APPLICANT: DER, Channing J.

APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10161,791
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 423:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-423

Query Match 43.2%; Score 35; DB 14; Length 15;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPP 12
| : ||||| :
Db 8 PPPPP 13

RESULT 19
US-09-261-894-1
; Sequence 1, Application US/09261894
; Publication No. US20030207324A1
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert B
; APPLICANT: Adams, Sparlene
; APPLICANT: XU, Minzhen
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/261,894

FILING DATE: March 3, 1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fairrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-261-894-1

Query Match 43.2%; Score 35; DB 10; Length 16;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKPPPPQ 11
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 1 LRMKLPKPPK 10

RESULT 20
US-10-197-000-1
Sequence 1, Application US/10197000
Publication No. US20030091582A1
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E.
APPLICANT: Adams, Sharlene
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: HYBRID PEPTIDES MODULATE THE IMMUNE RESPONSE
FILE REFERENCE: REH2007
CURRENT APPLICATION NUMBER: US/10/197,000
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 16
TYPE: PRT
ORGANISM: Mouse
US-10-197-000-1

Query Match 43.2%; Score 35; DB 14; Length 16;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKPPPPQ 11
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 1 LRMKLPKPPK 10

RESULT 21
US-10-245-871-1
Sequence 1, Application US/10245871
Publication No. US20030235594A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1
LENGTH: 16
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Mammalian Ii-key
US-10-245-871-1

Query Match 43.2%; Score 35; DB 15; Length 16;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKPPPPQ 11
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 1 LRMKLPKPPK 10

RESULT 22
US-10-253-286-1
Sequence 1, Application US/10253286
Publication No. US20040058881A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 16
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Mammalian Ii-key
US-10-253-286-1

Query Match 43.2%; Score 35; DB 15; Length 16;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKPPPPQ 11
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 1 LRMKLPKPPK 10

RESULT 23
US-10-225-567A-2084
Sequence 2084, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burnet, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2084
LENGTH: 17
TYPE: PRT

; ORGANISM: Homo sapiens
US-10-225-567A-2084

Query Match 43.2%; Score 35; DB 14; Length 17;
Best Local Similarity 70.0%; Pred. No. 4.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKPPPPQ 11
DB 2 LEAKAPPPQ 11

RESULT 24
US-09-825-144-15
; Sequence 15, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Matthias Krause
; APPLICANT: Antonio S. Secchi
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Wehlend
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-144-15

Query Match 42.0%; Score 34; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPPPP 10
DB 1 PPPPP 5

RESULT 25
US-09-823-240-3
; Sequence 3, Application US/09823240
; Patent No. US20020048813A1
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jorgen Wehlend
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; TITLE OF INVENTION: Motility
; FILE REFERENCE: M0656/7064 (HCL)
; CURRENT APPLICATION NUMBER: US/09/823,240
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-09-823-240-3

Query Match 42.0%; Score 34; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPPPP 10

DB 1 PPPPP 5

RESULT 26
US-09-989-188-1
; Sequence 1, Application US/09989188
; Publication No. US20020136717A1
; GENERAL INFORMATION:
; APPLICANT: JORDAN, BIRGIT
; APPLICANT: DRUCKES, PETER
; APPLICANT: JARCHAU, THOMAS
; APPLICANT: WALTER, ULRICH
; TITLE OF INVENTION: PROCESS FOR SCREENING CHEMICAL COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: THE INTERACTION OF AN EVH1 DOMAIN OR A PROTEIN HAVING
; TITLE OF INVENTION: HAVING AN EVH1 BINDING DOMAIN, AND A PROCESS FOR DETECTING
; FILE REFERENCE: 02481.1761-00000
; CURRENT APPLICATION NUMBER: US/09/989,188
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: DE 10058596.5
; PRIOR FILING DATE: 2000-11-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-989-188-1

Query Match 42.0%; Score 34; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPPPP 10
DB 1 PPPPP 5

RESULT 27
US-10-192-381-47
; Sequence 47, Application US/10192381
; Publication No. US20030170807A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: MORLEY, PAUL
; APPLICANT: TU, JIAN
; APPLICANT: XIAO, BO
; APPLICANT: LEAHY, DANIEL
; APPLICANT: BENKEN, JUTTA
; APPLICANT: LANAHAN, ANTHONY
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS
; TITLE OF INVENTION: AMENDED)
; FILE REFERENCE: JHU1580-4
; CURRENT APPLICATION NUMBER: US/10/192,381
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US/09/377,285
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/138,426
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,493
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,494
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/097,334
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47

LENGTH: 5
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: optimal ligand
US-10-192-381-47

Query Match 42.0%; Score 34; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
|||
Db 1 FPPPP 5

RESULT 28
US-09-943-944E-69
Sequence 69, Application US/09943944E
Publication No. US20040014036A1
GENERAL INFORMATION:
APPLICANT: Peasbne, et al.
TITLE OF INVENTION: Transcriptional Activation System, Activators, and Uses
FILE REFERENCE: 0342941-0065
CURRENT APPLICATION NUMBER: US/09/943,944E
CURRENT FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 69
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Random peptide
US-09-943-944E-69

Query Match 42.0%; Score 34; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
|||
Db 1 FPPPP 5

RESULT 29
US-09-823-240-7
Sequence 7, Application US/09823240
Patent No. US20020048813A1
GENERAL INFORMATION:
APPLICANT: Frank B. Gertler
APPLICANT: James E. Bear
APPLICANT: Jurgen Weiland
APPLICANT: Joseph Loureiro
TITLE OF INVENTION: Methods and Products for Regulating Cell
FILE REFERENCE: M0656/7064 (HCL)
CURRENT APPLICATION NUMBER: US/09/823,240
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 60/194,564
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: UNSURE
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa is any amino acid

US-09-823-240-7

Query Match 42.0%; Score 34; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
|||
Db 1 FPPPP 5

RESULT 30
US-09-261-894-160
Sequence 160, Application US/09261894
Publication No. US20030207324A1
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Shariene
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/261,894
FILING DATE: March 3, 1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0528
TELEFAX: (207) 363-0558
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-09-261-894-160

Query Match 42.0%; Score 34; DB 10; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LMKFPPPP 10
|||
Db 1 LMKLPKPP 9

RESULT 31
US-09-261-894-18
Sequence 18, Application US/09261894
Publication No. US20030207324A1
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Shariene
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:

ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/261,894
FILING DATE: March 3, 1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-261-894-18

Query Match 42.0%; Score 34; DB 10; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKPPPP 10
| | | | |
DB 1 LMKLPKPP 9

RESULT 32
US-10-307-956-20
; Sequence 20, Application US/10307956
; Publication No. US20030119072A1
; GENERAL INFORMATION:
; APPLICANT: Hoekestra, Merl F.
; APPLICANT: Xie, Weilin
; APPLICANT: Murray, Brian
; APPLICANT: Mercutio, Frank
; TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
; TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
; FILE REFERENCE: 860098.433
; CURRENT APPLICATION NUMBER: US/10/307,956
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US/09/385,918
; PRIOR FILING DATE: 1998-08-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FASTSEQ For Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-307-956-20

Query Match 42.0%; Score 34; DB 14; Length 14;
Best Local Similarity 62.5%; Pred. No. 4.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EMKPPPP 10
| | | | |
DB 1 ELESPPP 8

RESULT 33
US-10-185-050-55
; Sequence 55, Application US/10185050
; Publication No. US2003007577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.
; Fowler, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-185-050-55

Query Match 42.0%; Score 34; DB 14; Length 15;
Best Local Similarity 75.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PPPQETV 14
| | | | |
DB 4 PPPPYTV 11

RESULT 34
US-10-161-791-339
; Sequence 339, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: POWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
CLASSIFICATION:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-339

Query Match 42.0%; Score 34; DB 14; Length 15;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 12
| | | | |
| | | | |
Db 6 PPPPQ 11

RESULT 35
US-10-161-791-405
Sequence 405, Application US/10161791
Publication No. US2003018663A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OULLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 405:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-405

Query Match 42.0%; Score 34; DB 14; Length 15;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KPPPPQ 11
| | | | |
| | | | |
Db 4 KPPPPQ 10

RESULT 36
US-10-776-224-261
Sequence 261, Application US/10776224
Publication No. US20050074849A1
GENERAL INFORMATION:
APPLICANT: Bricksen, Jon Amund
APPLICANT: Moller, Mona
APPLICANT: Gjertsen, Marianne Klemp
APPLICANT: Saeterdal, Ingvil
TITLE OF INVENTION: Peptides
FILE REFERENCE: 01702.401510
CURRENT APPLICATION NUMBER: US/10/776,224
CURRENT FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: US 09/674,973
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 459
SOFTWARE: PatentIn version 3.0
SEQ ID NO 261
LENGTH: 16
TYPE: PPT
ORGANISM: Homo sapiens
US-10-776-224-261

Query Match 42.0%; Score 34; DB 17; Length 16;
Best Local Similarity 66.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PPPQETVT 15
| | | | |
| | | | |
Db 5 PPPPAHGT 13

RESULT 37
US-10-331-907-403
Sequence 403, Application US/10331907
Publication No. US20030181660A1
GENERAL INFORMATION:
APPLICANT: Todd, John A
APPLICANT: Hees, John W
APPLICANT: Caskey, Charles T
APPLICANT: Cox, Roger D
APPLICANT: Gerhold, David
APPLICANT: Hammond, Holly


```

; Hey, Patricia
; Kawaguchi, Yoshiniko
; Merriam, Tony R
; Metzker, Michael L
; TITLE OF INVENTION: No. US20030181660A1e1 LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. US20030181660A1e1 Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/331,907
; FILING DATE: 31-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-Apr-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-Apr-1997
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J.Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 403:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 403:
US-10-331-907-403

Query Match      42.0%; Score 34; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PPPP 10
DB      6 PPPP 10

RESULT 38
US-10-281-652-14
; Sequence 14, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265, 00220101
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
```

```

; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-14

Query Match      40.7%; Score 33; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 11
DB      2 PPPP 6

RESULT 39
US-10-691-157-14
; Sequence 14, Application US/10691157
; Publication No. US20040266681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUZEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEROF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265, 00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-157-14

Query Match      40.7%; Score 33; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 11
DB      2 PPPP 6

RESULT 40
US-10-691-330-14
; Sequence 14, Application US/10691330
; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy A.
; APPLICANT: HUGHES, Thomas K., Jr.
; APPLICANT: KRUZEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEROF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265, 00390101
```

; CURRENT APPLICATION NUMBER: US/10/691,330
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatencLin version 3.2
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
; US-10-691-330-14

Query Match 40.7%; Score 33; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 PPPPQ 11
|||
Db 2 PPPPQ 6

Search completed: June 7, 2005, 23:31:39
Job time : 68.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:56:36 ; Search time 13.9091 Seconds
(without alignments)
103.763 Million cell updates/sec

Title: US-10-691-157-7
Perfect score: 81
Sequence: 1 VLEMKFPPPPQETVT 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	38.3	17	2	SS7991 hydroxyproline-ric
2	29	35.8	15	2	PT0037 light harvesting c
3	28	34.6	7	2	S71299 IC12 protein - Par
4	28	34.6	10	2	A36454 trypsin-modulating
5	28	34.6	17	2	SS9481 hydroxyproline-ric
6	27	33.3	12	2	B39690 neural cell adhesi
7	27	33.3	13	2	S21152 cryptophyllin-rela
8	27	33.3	16	2	JH0517 inulin-like growt
9	26	32.1	12	2	E45691 probable minor cap
10	26	32.1	13	2	D39690 neural cell adhesi
11	26	32.1	14	2	H64008 hypothetical prote
12	26	32.1	14	2	S12904 protein kinase (RC
13	26	32.1	16	2	ES8503 superoxide dismuta
14	25	30.9	9	2	S26508 collagen alpha 2(V
15	25	30.9	12	2	PN0663 dystrophin-associa
16	24	29.6	11	2	D45900 complement C3b rec
17	24	29.6	11	2	C37196 bradykinin-potent
18	24	29.6	11	2	D37196 bradykinin-potent
19	24	29.6	13	2	A35245 histone H1a - mou
20	24	29.6	13	2	B35245 histone H1c - mou
21	24	29.6	17	2	C33098 223k exoantigen -
22	24	29.6	17	2	A42920 fatty acid ethyl e
23	23	28.4	9	2	S66607 quinolone 2-oxidor
24	23	28.4	10	2	H28027 protein p11 - curl
25	23	28.4	13	2	A05174 cryptophyllin-13 -
26	23	28.4	15	2	F28587 T-cell receptor be
27	23	28.4	15	2	I53284 T-cell receptor be
28	23	28.4	15	2	A28965 ribulose-bisphosph
29	23	28.4	17	2	D53284 T-cell receptor be

30	23	28.4	18	2	A35704 cytochrome P450 o1
31	22.5	27.8	15	2	A54397 ubiquitin-carrier
32	22	27.2	8	2	S16324 hypothetical prote
33	22	27.2	13	2	PN0048 unidentified OM002
34	22	27.2	14	2	PA0104 protein QP20070 -
35	22	27.2	15	2	B39109 hypothetical 1.5K
36	22	27.2	15	2	PA0057 adenylyate isopente
37	21	25.9	10	2	C35389 urase (EC 3.5.1.5
38	21	25.9	11	2	I52980 glucocorticoidase
39	21	25.9	12	2	C39109 hypothetical 1.2K
40	21	25.9	12	2	PH1567 cerebriin 28 - huma
41	21	25.9	13	2	S09716 2S albumin large c
42	21	25.9	13	2	A40207 cell surface glyco
43	21	25.9	14	2	S11129 phosphoprotein, bo
44	21	25.9	15	2	B61457 alpha-glucosidase
45	21	25.9	18	2	PC2280 poly(endorpeptidas
46	21	25.9	18	2	A54195 Na+/K+-exchanging
47	20	24.7	8	2	S21288 lectin - potato (f
48	20	24.7	10	2	B59272 peptide-M4-(N-acet
49	20	24.7	11	1	XASNBA bradykinin-potent
50	20	24.7	11	1	A60654 substance P - quin
51	20	24.7	11	1	SFHO substance P - hors
52	20	24.7	11	1	S23306 substance P - Acta
53	20	24.7	12	2	PE0213 28K protein 4412 -
54	20	24.7	12	2	PA0098 ribosomal protein
55	20	24.7	12	2	S07436 tachykinin - Afri
56	20	24.7	13	2	G37266 Ig heavy chain C r
57	20	24.7	14	2	PH0135 T-cell receptor be
58	20	24.7	14	2	S65392 cytochrome-c oxida
59	20	24.7	14	2	S48685 extension protei
60	20	24.7	17	2	A39111 Ig light chain - P
61	20	24.7	17	2	A49237 45/47K antigen - M
62	20	24.7	17	2	B25348 glycogen(starch) s
63	19	23.5	10	2	C30572 T-cell receptor be
64	19	23.5	10	2	S18396 probable glucose-6
65	19	23.5	11	1	JN0023 bradykinin-potent
66	19	23.5	11	1	XAVIBH substance P - chic
67	19	23.5	11	2	C60409 kaesinin-like pept
68	19	23.5	11	2	B60409 kaesinin-like pept
69	19	23.5	11	2	D60409 kaesinin-like pept
70	19	23.5	14	2	C59137 protein PF3 - gold
71	19	23.5	14	2	A42473 ermk leader peptid
72	19	23.5	15	2	PA0002 photoystem II oxy
73	19	23.5	15	2	PA0014 seed storage prote
74	19	23.5	15	2	PN0173 seed storage prote
75	19	23.5	15	2	A41436 alpha-macroglobuli
76	19	23.5	15	2	PK0031 mixed lymphocyte r
77	19	23.5	15	2	B59137 protein pfl - gold
78	19	23.5	16	2	PH1302 Ig heavy chain DJ
79	19	23.5	16	2	PH0759 T-cell receptor be
80	19	23.5	16	2	PH0759 T-cell receptor be
81	19	23.5	16	2	A45454 ankyrin-binding gl
82	19	23.5	17	2	JT0609 leukocyte chemoat
83	19	23.5	17	2	PT0235 Ig heavy chain CRD
84	19	23.5	18	2	A42576 steroid receptor c
85	19	23.5	18	2	A61049 halo-toxin - Pseud
86	18	22.2	6	2	A19780 transferrin - bovi
87	18	22.2	8	2	S10783 enamein f - bovin
88	18	22.2	8	2	A05169 neuropeptide M-I -
89	18	22.2	9	2	B30572 T-cell receptor be
90	18	22.2	10	1	XASNPC angiotensin-conver
91	18	22.2	12	2	S11286 exo-alpha-sialidas
92	18	22.2	12	2	S67528 napin - rape (frag
93	18	22.2	12	2	JU0356 cycloleucorin -
94	18	22.2	13	2	A60856 inhibin alpha chai
95	18	22.2	13	2	S36668 hypothetical prote
96	18	22.2	13	2	S33800 chaperone, TCPI-re
97	18	22.2	14	2	A60737 pollen allergen lo
98	18	22.2	14	2	S00150 onostatin - duck (
99	18	22.2	14	2	B61280 probable proteolys
100	18	22.2	15	2	S29207 avenin gamma-4 - o

ALIGNMENTS

RESULT 1

S57991

hydroxyproline-rich protein - Seebania rostrata (fragment)

C:Species: Seebania rostrata

C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C:Accession: S57991

R:Gormachy, S.; Valerio-Lepinec, M.; Szczyglowski, K.; van Montagu, M.; Holsters, M.

submitted to the EMBL Data Library, March 1995

A:Description: Use of differential display to identify novel Seebania rostrata genes ent

A:Reference number: S57991

A:Accession: S57991

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-17 <GOO>

A:Cross-references: UNIPROT:Q41400; EMBL:Z48673; NID:G899484; PID:G899485

C:Superfamily: hydroxyproline-rich glycoprotein

Query Match

Best Local Similarity	38.3%;	Score 31;	DB 2;	Length 17;
Matches	5;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;

QY 5 KRPPP 10

DB 8 KSPPP 13

RESULT 2

PT0037

light harvesting complex chain III/D, photosystem I - rice (fragment)

C:Species: Oryza sativa (rice)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: PT0037; PS0205

R:Uchiyama, Y.; Teugite, A.

submitted to JIPID, June 1991

A:Reference number: PS0189

A:Accession: PT0037

A:Molecule type: protein

A:Residues: 1-15 <UCH>

A:Cross-references: UNIPROT:Q7M1V1

Query Match

Best Local Similarity	35.8%;	Score 29;	DB 2;	Length 15;
Matches	5;	Conservative	0;	Mismatches 3;
			Indels	0;
			Gaps	0;

QY 3 EMKFRPPP 10

DB 4 EAAAPPP 11

RESULT 3

S71299

ICL2 protein - Paramecium tetraurelia (fragment)

C:Species: Paramecium tetraurelia

C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999

C:Accession: S71299

R:Madaddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.

Eur. J. Biochem. 238, 121-128, 1996

A:Title: Characterization of centrin genes in Paramecium.

A:Reference number: S71299; MUID:96248429; PMID:8665928

A:Accession: S71299

A:Molecule type: protein

A:Residues: 1-7 <MAD>

A:Experimental source: strain d4-2

C:Genetics:

A:Genetic code: SGCS

Query Match

Best Local Similarity	34.6%;	Score 28;	DB 2;	Length 7;
Matches	4;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY 8 PPPQ 12

DB 3 PPPQ 7

RESULT 4

A6454

trypsin-modulating oostatic factor - yellow fever mosquito

C:Species: Aedes aegypti (yellow fever mosquito)

C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004

C:Accession: A6454; A6130

R:Bobrovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

FASEB J. 4, 3015-3020, 1990

A:Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi.

A:Reference number: A6454; MUID:90367888; PMID:2394318

A:Accession: A6454

A:Molecule type: protein

A:Residues: 1-10 <BOR>

A:Cross-references: UNIPROT:P19425

R:Bobrovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

Insect Biochem. Mol. Biol. 23, 703-712, 1993

A:Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost

A:Reference number: A61630; MUID:93357794; PMID:8353526

A:Accession: A61630

A:Molecule type: protein

A:Residues: 1-10 <BO2>

A:Note: none of the amino acids is modified

C:Function:

A:Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ep

C:Keywords: hormone

Query Match

Best Local Similarity	34.6%;	Score 28;	DB 2;	Length 10;
Matches	4;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY 7 PPP 10

DB 5 PPP 8

RESULT 5

S59481

hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)

C:Species: Phaseolus vulgaris (kidney bean)

C:Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

C:Accession: S59481

R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A:Title: Specificity in the immobilisation of cell wall proteins in response to differen

A:Reference number: S59481; MUID:96011753; PMID:7548825

A:Accession: S59481

A:Molecule type: protein

A:Residues: 1-17 <WOJ>

A:Cross-references: UNIPROT:Q7M1I3

C:Keywords: glycoprotein; hydroxyproline

F:6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match

Best Local Similarity	34.6%;	Score 28;	DB 2;	Length 17;
Matches	4;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY 7 PPP 10

DB 8 PPP 11

RESULT 6

B39690

neural cell adhesion molecule, cardiac splice form +, -, - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999

C:Accession: B39690

R:Reyes, A.A.; Small, S.J.; Akesson, R.

Mol. Cell. Biol. 11, 1654-1661, 1991
 A>Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
 A:Reference number: A39690; MUID:91141516; PMID:1996115
 A:Accession: B39690
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-12 <REV>
 A:Cross-references: GB:M63970
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 33.3%; Score 27; DB 2; Length 12;
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPPPE 12
 |||:
 DB 6 PPPPE 10

RESULT 7

S21152
 tryptophyllin-related peptide - two-colored leaf frog
 C:Species: Phyllomedusa bicolor (two-colored leaf frog)
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
 C:Accession: S21152
 R:Minogima, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erpamer, G.; Kreil, G.
 FEBS Lett. 302, 151-154, 1992
 A>Title: Identification and characterization of two dermorphins from skin extracts of th
 A:Reference number: S21152; MUID:92339502; PMID:1633846
 A:Accession: S21152
 A:Molecule type: protein
 A:Residues: 1-13 <WIG>
 A:Cross-references: UNIPROT:Q7LZ51
 A:Experimental source: skin

Query Match 33.3%; Score 27; DB 2; Length 13;
 Best Local Similarity 62.5%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKPPPP 10
 |||:
 DB 2 EKPFYPP 9

RESULT 8

JH0517
 insulin-like growth factor-binding protein 4 - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C:Accession: JH0517
 R:Coleman, M.E.; Pan, Y.C.E.; Eberton, T.D.
 Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991
 A>Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth
 A:Reference number: JH0515; MUID:92109718; PMID:1722398
 A:Accession: JH0517
 A:Molecule type: protein
 A:Residues: 1-16 <COL>
 A:Cross-references: UNIPROT:P24854
 A:Experimental source: serum
 C:Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat h

Query Match 33.3%; Score 27; DB 2; Length 16;
 Best Local Similarity 66.7%; Pred. No. 3.5e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 PPPPE 12
 |||:
 DB 7 PPPPE 12

RESULT 9
 B55691
 probable minor capsid protein R117a [similarity] - Lactobacillus delbrueckii subsp. lact

C:Species: Lactobacillus delbrueckii subsp. Lactis phage Lh-H
 C>Date: 24-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C:Accession: B55691
 R:Vaasala, A.; Dupont, L.; Baumann, M.; Ritzenhaller, P.; Alatosava, T.
 J. Virol. 67, 3061-3068, 1993
 A>Title: Molecular comparison of the structural proteins encoding gene clusters of two r

A:Reference number: A45691; MUID:93267750; PMID:8497043
 A:Accession: B45691
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-12 <VAS>
 A:Cross-references: UNIPROT:004769
 A:Note: sequence extracted from NCBI Backbone (NCBIN:132363, NCBIPI:132373)

Query Match 32.1%; Score 26; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 3.6e+02;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 MKPPPPQETVT 15
 |||:
 DB 1 MKLPPIPYQWVS 12

RESULT 10

D39690
 neural cell adhesion molecule, cardiac splice form +,-,-,+ - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
 C:Accession: D39690
 R:Reyes, A.A.; Small, S.J.; Akesson, R.
 Mol. Cell. Biol. 11, 1654-1661, 1991
 A>Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mR
 A:Reference number: A39690; MUID:91141516; PMID:1996115
 A:Accession: D39690
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-13 <REV>
 A:Cross-references: GB:M63970
 C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 32.1%; Score 26; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPPQ 11
 |||:
 DB 6 PPPQ 9

RESULT 11

H64008
 hypothetical protein HI0492 - Haemophilus influenzae (strain Rd KW20)
 C:Species: Haemophilus influenzae
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998
 C:Accession: H64008
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
 ; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
 ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
 A>Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: H64000; MUID:95350630; PMID:7542800
 A:Accession: H64008
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-14 <TIGR>
 A:Cross-references: GB:U52731; GB:I42023; NID:g1573465; PID:g1573478; TIGR:HI0492

Query Match 32.1%; Score 26; DB 2; Length 14;
 Best Local Similarity 57.1%; Pred. No. 4.2e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFPFPPQ 11
| | | | |
Db 7 KMPFPRK 13

RESULT 12

S12904
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)
C1Species: Pisaster ochraceus
C1Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C1Accession: S12904
R1Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.
FBS Lett. 273, 223-226, 1990
A1Title: Identification of the sites in myelin basic protein that are phosphorylated by
A1Reference number: S12904; MUID:91032186; PMID:1699809
A1Accession: S12904
A1Status: preliminary
A1Molecule type: protein
A1Residues: 1-14 <SAN>
A1Cross-references: UNIPROT:Q7M3M4
C1Keywords: phosphotransferase

Query Match 32.1%; Score 26; DB 2; Length 14;
Best Local Similarity 36.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VLEMKFPPPPQ 11
: | | | | |
Db 2 IVTPRTPPPSQ 12

RESULT 13

E58503
superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)
N1Alternate names: 21.3X bladder and kidney stone protein
C1Species: unidentified bacterium
C1Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C1Accession: E58503
R1Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A1Description: The proteins of kidney and gallbladder stones.
A1Reference number: A58501
A1Accession: E58503
A1Status: preliminary
A1Molecule type: protein
A1Residues: 1-16 <BIN>
A1Cross-references: UNIPROT:Q7M137
A1Experimental source: human bladder and kidney stones
C1Function:
A1Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C1Keywords: metalloprotein; oxidoreductase

Query Match 32.1%; Score 26; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 LEMKFPFPPQ 12
: | | | | |
Db 1 MEHTLPPLPYE 11

RESULT 14

S26508
collagen alpha 2(VI) chain - bovine (fragment)
C1Species: Bos primigenius taurus (cattle)
C1Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C1Accession: S26508
R1Jander, R.; Rautenberg, J.; Glanville, R.W.
Eur. J. Biochem. 133, 39-46, 1983
A1Title: Further characterization of the three polypeptide chains of bovine and human sh
A1Reference number: S26506; MUID:83209648; PMID:685203
A1Accession: S26508
A1Status: preliminary

A1Molecule type: protein
A1Residues: 1-9 <JAN>
A1Cross-references: UNIPROT:Q7M2M9
C1Keywords: hydroxyproline
F17/Modified site: hydroxyproline (Pro) #status experimental

Query Match 30.9%; Score 25; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.8e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKFPFPP 10
| | | | |
Db 1 LEIKFPFPP 9

RESULT 15

PN0663
dytrophin-associated glycoprotein A3a-II - rabbit (fragment)
C1Species: Oryctolagus cuniculus (domestic rabbit)
C1Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C1Accession: PN0663
R1Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993

A1Title: A dytrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
A1Reference number: PN0662; MUID:94156881; PMID:8113213
A1Accession: PN0663
A1Molecule type: protein
A1Residues: 1-12 <YOS>
C1Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C1Keywords: glycoprotein; skeletal muscle

Query Match 30.9%; Score 25; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 KFPFPPPP 12
| | | | |
Db 1 KAPLPFPP 8

RESULT 16

D45900
complement C3b receptor type 2 - mouse (clone 12) (fragment)
C1Species: Mus musculus (house mouse)
C1Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C1Accession: D45900
R1Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.
J. Immunol. 144, 3581-3591, 1990
A1Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2 gen
A1Reference number: A45900; MUID:90229754; PMID:2139460
A1Accession: D45900
A1Status: preliminary
A1Molecule type: mRNA
A1Residues: 1-11 <KUR>

Query Match 29.6%; Score 24; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKFPFPP 10
| | | | |
Db 4 BISCDFPP 11

RESULT 17

C37196
bradykinin-potentiating peptide 3 - island jararaca
C1Species: Bothrops jararaca (island jararaca)
C1Date: 14-Feb-1993 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C1Accession: C37196
R1Cintrà, A.C.O.; Vieira, C.A.; Giglio, J.R.
U. Protein Chem. 9, 221-227, 1990
A1Title: Primary structure and biological activity of bradykinin potentiating peptides f

A:Reference number: A37196; MUID:90351557; PMID:2386615

A:Accession: C37196

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <CIN>

A:Cross-references: UNIPROT:P30423

C:Keywords: pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 11;

Best Local Similarity 80.0%; Pred. No. 6.5e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPQ 11

Db 4 PPRPQ 8

RESULT 18

D37196

bradykinin-potentiating peptide 4 - island jararaca

C:Species: Bothrops insularis (island jararaca)

C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004

C:Accession: D37196

R:Ajiro, K.; Shibata, K.; Nishikawa, Y.

J. Biol. Chem. 265, 6494-6500, 1990

A:Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differ

A:Reference number: A37196; MUID:90351557; PMID:2386615

A:Accession: D37196

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <CIN>

A:Cross-references: UNIPROT:P30424

C:Keywords: pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 11;

Best Local Similarity 80.0%; Pred. No. 6.5e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPQ 11

Db 4 PPRPQ 8

RESULT 19

A35245

histone H1a - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 31-Oct-1997

C:Accession: A35245

R:Ajiro, K.; Shibata, K.; Nishikawa, Y.

J. Biol. Chem. 265, 6494-6500, 1990

A:Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differ

A:Reference number: A35245; MUID:90202935; PMID:1690730

A:Accession: A35245

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <Aji>

C:Superfamily: histone H1

C:Keywords: chromosomal protein; nucleosome

Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 13;

Best Local Similarity 50.0%; Pred. No. 7.8e+02;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 PPOPTVT 15

Db 5 PPVSELTIT 12

RESULT 20

B35245

histone H1.c - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 31-Oct-1997

C:Accession: B35245

R:Ajiro, K.; Shibata, K.; Nishikawa, Y.

J. Biol. Chem. 265, 6494-6500, 1990

A:Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differ

A:Reference number: A35245; MUID:90202935; PMID:1690730

A:Accession: B35245

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <Aji>

C:Superfamily: histone H1

C:Keywords: chromosomal protein; nucleosome

Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 13;

Best Local Similarity 50.0%; Pred. No. 7.8e+02;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 PPOPTVT 15

Db 5 PPVSELTIT 12

RESULT 21

C33098

233K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum

C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

C:Accession: C33098

R:Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A:Reference number: A33098

A:Accession: C33098

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <NIC>

Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PPOE 12

Db 3 PPOE 6

RESULT 22

A42920

fatty acid ethyl ester synthase-II - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A42920

R:Bora, P.S.; Wu, X.; Spillburg, C.A.; Lange, L.G.

J. Biol. Chem. 267, 13217-13221, 1992

A:Title: Purification and characterization of fatty acid ethyl ester synthase-II from hu

A:Reference number: A42920; MUID:92317032; PMID:1618826

A:Accession: A42920

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-17 <BOR>

A:Cross-references: UNIPROT:Q9UND6

A:Experimental source: myocardium

A>Note: sequence extracted from NCBI backbone (NCBI:P107742)

Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 17;

Best Local Similarity 57.1%; Pred. No. 1e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PPOPT 13

Db 3 PPDPDTT 9

RESULT 23

S66607
 quinoline 2-oxidoreductase beta chain - Comamonas testosteroni (fragment)
 C/Species: Comamonas testosteroni
 C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C/Accession: S66607
 R/Schach, S.; Tehlanaka, B.; Fecner, S.; Lingens, F.
 Eur. J. Biochem. 232, 536-544, 1995
 A/Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from
 A/Reference number: S66606; PMID:96035889; PMID:7556204
 A/Accession: S66607
 A/Molecule type: protein
 A/Residues: 1-9 <SCH>
 A/Experimental source: strain 63

Query Match 28.4%; Score 23; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKFP 7
 ||||
 Db 1 MKFP 4

RESULT 24

H28027
 protein P11 - curled-leaved tobacco (fragment)
 C/Species: Nicotiana glauca (curled-leaved tobacco)
 C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993
 C/Accession: H28027
 R/Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
 A/Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-
 A/Reference number: A94167
 A/Accession: H28027
 A/Molecule type: protein
 A/Residues: 1-10 <BAU>
 A/Note: 4-Val was also found

Query Match 28.4%; Score 23; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 8.2e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MKFP 10
 :|||
 Db 2 TKFGPP 8

RESULT 25

A05174
 tryptophyl11n-13 - Rohde's leaf frog
 C/Species: Phyllomedusa rohdei (Rohde's leaf frog)
 C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
 C/Accession: A05174
 R/Montecucchi, P.C.; Gozzini, L.; Ersamer, V.
 Int. J. Pept. Protein Res. 27, 175-182, 1986
 A/Reference number: A05174
 A/Accession: A05174
 A/Molecule type: protein
 A/Residues: 1-13 <MON>
 A/Cross-references: UNIPROT:P04096
 C/Superfamily: unassigned animal peptides
 C/Keywords: pyroglutamic acid, skin
 F11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.4%; Score 23; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKFP 10
 :|||
 Db 2 EKPYWPP 9

RESULT 26

F28587
 T-cell receptor beta-2 chain J-B2.7 segment - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
 C/Accession: F28587
 R/Tovomaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
 A/Title: Organization and sequences of the diversity, joining, and constant region genes
 A/Reference number: A94081; PMID:86094276; PMID:3866244
 A/Accession: F28587
 A/Molecule type: DNA
 A/Residues: 1-15 <TOY>
 A/Cross-references: GB:M4159; NID:G33852; PID:AAA0681.1; PID:G553692
 C/Keywords: T-cell receptor

Query Match 28.4%; Score 23; DB 2; Length 15;
 Best Local Similarity 46.2%; Pred. No. 1.3e+03;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 EMKFP 15
 :|||
 Db 3 EYFGPGTKLTVT 15

RESULT 27

I53284
 T-cell receptor beta 2 chain J region, Jbeta2.7 - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C/Accession: I53284
 R/Harindranath, N.; Alexander, C.B.; Mage, R.G.
 Mol. Immunol. 28, 881-888, 1991
 A/Title: Evolutionarily conserved organization and sequences of germ-line diversity and J
 A/Reference number: A53284; PMID:91342695; PMID:1678859
 A/Accession: I53284
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-15 <HAR>
 A/Cross-references: GB:S60737; NID:G233916; PID:AA19525.1; PID:G233925
 A/Note: sequence extracted from NCBI Backbone (NCBI:60737, NCBI:P:60747)
 C/Keywords: T-cell receptor

Query Match 28.4%; Score 23; DB 2; Length 15;
 Best Local Similarity 46.2%; Pred. No. 1.3e+03;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 EMKFP 15
 :|||
 Db 3 EYFGPGTKLTVT 15

RESULT 28

A28965
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - spinach (fragments)
 C/Species: Spinacia oleracea (spinach)
 C/Date: 22-Dec-1988 #sequence_revision 22-Dec-1988 #text_change 09-Jul-2004
 C/Accession: A28965
 R/Mulligan, R.M.; Houtz, R.L.; Tolbert, N.E.
 Proc. Natl. Acad. Sci. U.S.A. 85, 1513-1517, 1988
 A/Title: Reaction-intermediate analogue binding by ribulose bisphosphate carboxylase/oxy
 cetylated proline.
 A/Reference number: A28965; PMID:8814446; PMID:3422748
 A/Accession: A28965
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-15 <MUL>
 A/Cross-references: UNIPROT:P00875

Query Match 28.4%; Score 23; DB 2; Length 15;
 Best Local Similarity 46.2%; Pred. No. 1.3e+03;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 5 KRPPEQETV 14
| | | | |
| | | | |

DB 6 KRPPEQETV 15
| | | | |
| | | | |

RESULT 29

D53284

T-cell receptor beta 2 chain J region, Jbeta2.1 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C:Accession: D53284

R:Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 29, 881-888, 1991

A:Title: Evolutionarily conserved organization and sequences of germline diversity and J

A:Reference number: A53284; MUID:91342695; PMID:1678859

A:Accession: D53284

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-17 <HAR>

A:Cross-references: GB:S60737; NID:G233916; PIDN:AB19520.1; PID:G233920

A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:P.60742)

C:Keywords: T-cell receptor

Query Match 28.4%; Score 23; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 3 EMKPPPEQETV 14
| | | | |
| | | | |

DB 5 EMKPPPEQETV 16
| | | | |
| | | | |

RESULT 30

A35704

cytochrome P450 olf2 - bovine (fragment)

M:Contains: oxidoreductase (EC 1.-.-.-)

C:Species: Bos primigenius taurus (cattle)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C:Accession: A35704

R:Laizard, D.; Tal, N.; Rubinstein, M.; Khen, M.; Lancet, D.; Zupko, K.

Biochemistry 29, 7433-7440, 1990

A:Title: Identification and biochemical analysis of novel olfactory-specific cytochrome

A:Reference number: A35704; MUID:91027757; PMID:2121272

A:Accession: A35704

A:Molecule type: protein

A:Residues: 1-18 <LAZ>

A:Cross-references: UNIPROT:P22779

C:Genetics:

A:Gene: CYP2A

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C:Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane protei

Query Match 28.4%; Score 23; DB 2; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 MKPPPEQETV 12
| | | | |
| | | | |

DB 1 MKPPPEQETV 9
| | | | |
| | | | |

RESULT 31

A54397

ubiquitin-carrier protein E2-F1 - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A54397

R:Blumenfeld, N.; Gonen, H.; Mayer, A.; Smith, C.E.; Siegel, N.R.; Schwartz, A.L.; Ciech

J. Biol. Chem. 269, 9574-9581, 1994

A:Title: Purification and characterization of a novel species of ubiquitin-carrier prote

A:Reference number: A54397; MUID:94193635; PMID:8144544

A:Accession: A54397

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <BLU>

A:Cross-references: UNIPROT:Q9T584

A:Experimental source: reticulocyte

A>Note: sequence extracted from NCBI backbone (NCBI:P.146038)

C:Superfamily: human ubiquitin-protein ligase E2

Query Match 27.8%; Score 22.5; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

OY 2 LMKPPPEQETV 11
| | | | |
| | | | |

DB 1 LMKPPPEQETV 15
| | | | |
| | | | |

RESULT 32

S16324

hypothetical protein 2 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000

C:Accession: S16324

R:Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.

EMBO J. 10, 1787-1791, 1991

A:Title: A novel class of plant proteins containing a homeodomain with a closely linked

A:Reference number: S16323; MUID:91265907; PMID:1675603

A:Accession: S16324

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <RUB>

A:Cross-references: EMBL:X58821; NID:916327; PIDN:CAA41624.1; PID:G579259

Query Match 27.2%; Score 22; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 LMKPPPP 9
| | | | |
| | | | |

DB 1 MEYKLLPP 8
| | | | |
| | | | |

RESULT 33

PN0048

unidentified QM0023 protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998

C:Accession: PN0048

R:Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neur

A:Reference number: PN0041

A:Accession: PN0048

A:Molecule type: protein

A:Residues: 1-13 <KAT>

A:Experimental source: neuroblastoma cell

C:Comment: The molecular mass is 30,500 and the pI is 6.19.

C:Keywords: brain

Query Match 27.2%; Score 22; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 10 POETVT 15
| | | | |
| | | | |

DB 8 PNDTIV 13
| | | | |
| | | | |

RESULT 34

PA0104

protein QP200070 - fungus (Fusarium sporotrichioides) (fragment)

C:Species: *Fusarium sporotrichioides*
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0104
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JRPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichi*
A:Reference number: PA0051
A:Accession: PA0104
A:Molecule type: protein
A:Residues: 1-14 <CHO>

Query Match 27.2%; Score 22; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 EMKPPPPQ 11
DB 3 EMKPPPPQ 11

RESULT 35
B39109
hypothetical 1.5K protein - hepatitis C virus
N:Alternate names: hypothetical protein 2
C:Species: hepatitis C virus
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C:Accession: B39109; J01585
R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A:Reference number: A39109; MUID:91156678; PMID:1705704
A:Accession: B39109
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-15 <HAN>
A:Cross-references: GB:M58406
R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992
A:Title: Cloning and sequencing of the structural region and expression of putative core
A:Reference number: J01584; MUID:92300349; PMID:1318944
A:Accession: J01585
A:Molecule type: genomic RNA
A:Residues: 1-15 <KUM>
A:Experimental source: strain U.K.

Query Match 27.2%; Score 22; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 1.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VLEMKPPPOE 12
DB 3 VVQPPGPPLRGE 14

RESULT 36
PA0057
adenylate isopentenyltransferase (EC 2.5.1.27) - fungus (*Fusarium sporotrichioides*) (Fru
C:Species: *Fusarium sporotrichioides*
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0057
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JRPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichi*
A:Reference number: PA0051
A:Accession: PA0057
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: transferase

Query Match 27.2%; Score 22; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 PQETV 14
DB 4 PQORT 8

RESULT 37
C35389
urease (EC 3.5.1.5) 6K chain - *Morganella morganii* (fragment)
C:Species: *Morganella morganii*
C:Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004
C:Accession: C35389
R:Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A:Title: *Morganella morganii* urease: purification, characterization, and isolation of ge
A:Reference number: A35389; MUID:90264298; PMID:2345135
A:Accession: C35389
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <HUA>
A:Cross-references: UNIPROT:P17339
C:Keywords: hydrolase

Query Match 25.9%; Score 21; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 MKPPPPQE 12
DB 1 MOUTPPEVE 9

RESULT 38
I52980
glucocerebrosidase - human (fragment)
C:Species: *Homo sapiens* (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I52980; I65971
R:Reiner, O.; Magerason, M.; Horowitz, M.
DNA 7, 107-116, 1988
A:Title: Structural analysis of the human glucocerebrosidase genes.
A:Reference number: I52980; MUID:88195776; PMID:3355914
A:Accession: I52980
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: GB:M18916; NID:G183023; PIDN:AAA35878.1; PID:G183024
A:Accession: I65971
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-11 <RE2>
A:Cross-references: GB:M18917; NID:G183025; PIDN:AAA35879.1; PID:G183026

Query Match 25.9%; Score 21; DB 2; Length 11;
Best Local Similarity 44.4%; Pred. No. 1.8e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 MKPPPPQE 12
DB 1 MEFSPPVE 9

RESULT 39
C39109
hypothetical 1.2K protein - hepatitis C virus
N:Alternate names: hypothetical protein 3
C:Species: hepatitis C virus
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C:Accession: C39109; J01586
R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A:Reference number: A39109; MUID:91156678; PMID:1705704
A:Accession: C39109

A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-12 <HAN>
 A:Cross-references: GB:MS8406
 R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
 J. Gen. Virol. 73, 1521-1525, 1992
 A:Title: Cloning and sequencing of the structural region and expression of putative core
 A:Reference number: JQ1584; MUID:92300349; PMID:1318944
 A:Accession: JQ1586
 A:Molecule type: genomic RNA
 A:Residues: 1-12 <RUM>
 A:Experimental source: strain U.K.

Query Match 25.9%; Score 21; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred.No. 2e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPOE 12
 |||:
 Db 8 PPOD 11

RESULT 40

PH1567
 cerebrin 28 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
 C:Accession: PH1567
 R:Leone, M.G.; Saao, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.
 J. Neurochem. 61, 533-540, 1993
 A:Title: Micropurification of two human cerebrospinal fluid proteins by high performance
 A:Reference number: PH1566; MUID:93329419; PMID:8336140
 A:Accession: PH1567
 A:Molecule type: Protein
 A:Residues: 1-12 <LEO>
 A:Cross-references: UNIPROT:P41222

Query Match 25.9%; Score 21; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred.No. 2e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 PPOETV 14
 |||:
 Db 2 PPOQVS 8

Search completed: June 7, 2005, 23:20:42
 Job time : 14.9091 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 66 Seconds
(without alignments)
116.382 Million cell updates/sec

Title: US-10-691-157-7

Perfect score: 81

Sequence: 1 VLEKKPPPPQETVT 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0
Maximum DB seq length: 18Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	40.7	15	1 PRP MYCBO	P80149 mycobacteri
2	32	39.5	15	2 O9TR14	O9TR14 bos taurus
3	31	38.3	15	2 O6LBP7	O6LBP7 glycine max
4	31	38.3	17	2 O49225	O49225 glycine max
5	31	38.3	17	2 O41400	O41400 seebania ro
6	30	37.0	15	2 P82439	P82439 nicotiana t
7	29	35.8	15	2 O7M1V1	O7M1V1 oryza sativ
8	28	34.6	10	1 TMOR AEDAF	P19425 aedes aegypt
9	28	34.6	17	2 O9TR22	O9TR22 bos taurus
10	28	34.6	17	2 O7M1I3	O7M1I3 phaseolus v
11	27	33.3	9	2 O6SP94	O6SP94 chlamydomon
12	27	33.3	13	2 O7LZ51	O7LZ51 phyllomedon
13	27	33.3	16	1 IBP4 PIG	P24854 sus scrofa
14	26	32.1	12	2 O9BZ49	O9BZ49 homo sapien
15	26	32.1	14	2 O7M3M4	O7M3M4 plaaster oc
16	26	32.1	16	2 O7M137	O7M137 unidentified
17	26	32.1	18	2 O9UC19	O9UC19 homo sapien
18	25	30.9	9	2 O7M2M9	O7M2M9 bos taurus
19	25	30.9	17	2 O9PRU7	O9PRU7 gallus galli
20	25	30.9	18	2 O6A417	O6A417 archangiopt
21	24	29.6	10	2 O8TV66	O8TV66 polymomaviru
22	24	29.6	10	2 O8TV68	O8TV68 polymomaviru
23	24	29.6	10	2 O8TV70	O8TV70 polymomaviru
24	24	29.6	10	2 O8TV72	O8TV72 polymomaviru
25	24	29.6	10	2 O8TV74	O8TV74 polymomaviru
26	24	29.6	10	2 O8TV76	O8TV76 polymomaviru
27	24	29.6	10	2 O8TV80	O8TV80 polymomaviru
28	24	29.6	10	2 O8TV82	O8TV82 polymomaviru
29	24	29.6	10	2 O9Q0V7	O9Q0V7 polymomaviru
30	24	29.6	10	2 O9Q0V9	O9Q0V9 polymomaviru
31	24	29.6	10	2 O9Q0W1	O9Q0W1 polymomaviru

32	24	29.6	10	2 O9Q0W3	O9Q0W3 polymomaviru
33	24	29.6	10	2 O9Q0W5	O9Q0W5 polymomaviru
34	24	29.6	10	2 O9Q0W7	O9Q0W7 polymomaviru
35	24	29.6	10	2 O9Q0W9	O9Q0W9 polymomaviru
36	24	29.6	10	2 O9Q0X1	O9Q0X1 polymomaviru
37	24	29.6	10	2 O9Q0X3	O9Q0X3 polymomaviru
38	24	29.6	10	2 O9Q0X5	O9Q0X5 polymomaviru
39	24	29.6	10	2 O9Q0X9	O9Q0X9 polymomaviru
40	24	29.6	11	1 BPP3 BORTN	P30423 boehrops in
41	24	29.6	11	1 BPP4 BORTN	P30424 boehrops in
42	24	29.6	13	2 O9UDC6	O9UDC6 homo sapien
43	24	29.6	14	1 TY13 BOWVA	P84215 bombina var
44	24	29.6	15	2 O9BXK4	O9BXK4 homo sapien
45	24	29.6	15	2 O6LCH6	O6LCH6 mus musculu
46	24	29.6	17	2 O9UDD6	O9UDD6 homo sapien
47	24	29.6	17	2 O6PUY4	O6PUY4 hepatitis c
48	24	29.6	17	2 O6PUY5	O6PUY5 hepatitis c
49	24	29.6	17	2 O6PUY8	O6PUY8 hepatitis c
50	24	29.6	17	2 O6PUZ0	O6PUZ0 hepatitis c
51	24	29.6	17	2 O6PUZ1	O6PUZ1 hepatitis c
52	23	28.4	9	2 O99193	O99193 pseudomonas
53	23	28.4	10	1 Q2OB COMTE	P80465 comamonas t
54	23	28.4	13	1 TY13 PHYRO	P04096 phyllomedus
55	23	28.4	17	1 RAYE RAMES	P83663 rana esculie
56	23	28.4	17	2 O9R4T1	O9R4T1 rhodobacter
57	23	28.4	17	2 O6PUY7	O6PUY7 hepatitis c
58	23	28.4	18	1 CPAX BOVIN	P23779 bos taurus
59	23	28.4	18	2 O8NFB4	O8NFB4 homo sapien
60	23	28.4	18	2 O9H1I3	O9H1I3 homo sapien
61	22	27.2	12	1 PIFI SARBUR	P83349 sarcophaga
62	22	27.2	12	1 HS9A RAT	P82995 rattus norv
63	22	27.2	13	2 O81761	O81761 hepatitis c
64	22	27.2	15	2 O9TRA6	O9TRA6 bos taurus
65	22	27.2	15	2 O9S8N8	O9S8N8 hordaeum vul
66	22	27.2	15	2 O9S929	O9S929 glycine max
67	22	27.2	16	1 IEC DELRE	P83511 delonix reg
68	22	27.2	16	2 O6ZZ04	O6ZZ04 lychnis cha
69	22	27.2	16	2 O6ZZ06	O6ZZ06 atocion arm
70	22	27.2	16	2 O6ZZ07	O6ZZ07 agrostemma
71	22	27.2	16	2 O6ZZ08	O6ZZ08 silene ajan
72	22	27.2	16	2 O6ZZ10	O6ZZ10 lychnis aby
73	22	27.2	16	2 O6ZZ11	O6ZZ11 silene frut
74	22	27.2	16	2 O6ZZ13	O6ZZ13 silene berg
75	22	27.2	16	2 O6ZZ15	O6ZZ15 silene scha
76	22	27.2	16	2 O6ZZ17	O6ZZ17 silene bac
77	22	27.2	16	2 O6ZZ19	O6ZZ19 silene acan
78	22	27.2	16	2 O6ZZ20	O6ZZ20 silene coel
79	22	27.2	16	2 O6ZZ22	O6ZZ22 lychnis flo
80	22	27.2	16	2 O9PRU6	O9PRU6 gallus galli
81	22	27.2	17	1 APID BOWPA	P81464 bombus pasc
82	22	27.2	17	2 O6ZZ24	O6ZZ24 silene bac
83	22	27.2	17	2 O9ULAV	O9ULAV mus musculu
84	22	27.2	18	2 O9UR42	O9UR42 homo sapien
85	22	27.2	18	2 O9UIR9	O9UIR9 mus musculu
86	22	27.2	18	2 O84129	O84129 influenza a
87	22	27.2	18	2 O6WTX0	O6WTX0 eleutheroda
88	22	27.2	18	2 O6WTZ8	O6WTZ8 eleutheroda
89	22	27.2	18	2 O6WU54	O6WU54 eleutheroda
90	22	27.2	18	2 O6WU67	O6WU67 eleutheroda
91	21	25.9	10	1 URE3 MORWO	P17339 morganella
92	21	25.9	11	2 O6PKO1	O6PKO1 homo sapien
93	21	25.9	11	2 O9C057	O9C057 homo sapien
94	21	25.9	11	2 P82436	P82436 nicotiana t
95	21	25.9	12	1 ODO2 COMAC	P82436 c dihydroli
96	21	25.9	13	2 O7M3T0	O7M3T0 zea mays (m
97	21	25.9	13	2 O7M3T0	O7M3T0 dictyosteli
98	21	25.9	15	1 SODM STRGR	P80733 streptomyce
99	21	25.9	15	2 O9TR45	O9TR45 bos taurus
100	21	25.9	15	2 O6WFA4	O6WFA4 sturnus vul

ALIGNMENTS

RESULT 1
 PRP MYCBO STANDARD; PRT; 15 AA.
 AC P80149;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT- 01-JUL-1993 (Rel. 26, Last sequence update)
 DT- 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Proline-rich protein (Fragment).
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 NCBI_TaxID=1765;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=BCG / Paris 1173 P2;
 RA MEDLINE=93281750; PubMed=8506381;
 RA Roman F., Augier J., Pescher P., Marchal G.A.;
 RT "Isolation of a proline-rich mycobacterial protein eliciting delayed-
 RT type hypersensitivity reactions only in guinea pigs immunized with
 RT living mycobacteria."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5322-5326(1993).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: Immunodominant for delayed-type hypersensitivity
 CC reactions in guinea pigs.
 KW Direct protein sequencing.
 FT NON TER
 SQ SEQUENCE 15 AA; 1612 MW; 22659F848B922773 CRC64;

Query Match 40.7%; Score 33; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
 |||||
 Db 7 PPPPQ 11

RESULT 2
 Q9TR14 PRELIMINARY; PRT; 15 AA.
 AC Q9TR14;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Tropomyosin-T homolog/proteolysis CONDITIONING INDICATOR peptide
 DE (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96187584; PubMed=8611748;
 RA Nakai Y., Nishimura T., Shinizu M., Arai S.;
 RT "Effects of freezing on the proteolysis of beef during storage at 4
 RT degrees C."
 RL BioSci Biotechnol. Biochem. 59:2255-2258(1995).
 SQ SEQUENCE 15 AA; 1597 MW; C98A5B44A79E4777 CRC64;

Query Match 39.5%; Score 32; DB 2; Length 15;
 Best Local Similarity 83.3%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PPPPQ 12
 |||||
 Db 2 PPPPQ 7

RESULT 3
 Q6LBP7 PRELIMINARY; PRT; 15 AA.

AC Q6LBP7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Glycine B(1b) subunit (15 AA) (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90332420; PubMed=2377465;
 RA Kitamura Y., Arahira M., Itoh Y., Fukazawa C.;
 RT "The complete nucleotide sequence of soybean glycinin A2b1a gene
 RT spanning to another glycinin gene AlaB1d."
 RL Nucleic Acids Res. 18:4245-4245(1990).
 DR EMBL; X53404; CAA37479.1; -.
 FT NON TER
 SQ SEQUENCE 15 AA; 1698 MW; 68D29896D30C431C CRC64;

Query Match 38.3%; Score 31; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 6.2e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFPFPQET 13
 |||||
 Db 1 KFLVPPQES 9

RESULT 4
 O49225 PRELIMINARY; PRT; 17 AA.
 ID O49225
 AC O49225;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hydroxyproline-rich glycoprotein (Fragment).
 GN Name=hrgp;
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Roots;
 RX MEDLINE=94211912; PubMed=8159793; DOI=10.1104/pp.104.2.793;
 RA Hong J.C., Cheong Y.H., Nagao R.T., Bahk J.D., Cho M.J., Key J.L.;
 RT "Isolation and characterization of three soybean extensin cDNAs."
 RL Plant Physiol. 104:793-796(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Roots;
 RA Mahalingam R., Knapp H.T.;
 RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF047052; AAC03558.1; -.
 FT NON TER
 SQ SEQUENCE 17 AA; 2149 MW; 285E5874515A2222 CRC64;

Query Match 38.3%; Score 31; DB 2; Length 17;
 Best Local Similarity 83.3%; Pred. No. 7.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KFPFPQ 10
 |||||
 Db 9 KSPPPP 14

RESULT 5
 Q41400 PRELIMINARY; PRT; 17 AA.
 ID Q41400
 AC Q41400;

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DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, last annotation update)
DE Hydroxyproline-rich protein (Fragment).
OS Sesbania rostrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.
OX NCBI_TaxId=3895;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bacterial infected stem located root primordia;
RX MEDLINE=9612737; PubMed=8664492;
RA Goormachtig S., Valerio-Leprincet M., Szczylowski K., Van Montagu M.,
RA Holsters M., De Brulin F.;
RT "Use of differential display to identify novel Sesbania rostrata genes
RT enhanced by Azorhizobium caulinodans infection.";
RL Mol. Plant Microbe Interact. 8:816-824(1995).
DR EMBL, 248673; CAA8592.1; -.
DR PIR, S57991; S57991.
FT NON TER
SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;

Query Match
Best Local Similarity 38.3%; Score 31; DB 2; Length 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KPPPP 10
DB 8 KPPPP 13

RESULT 6
P82439 PRELIMINARY; PRT; 15 AA.
ID P82439;
AC P82439;
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, last sequence update)
DR 01-JUN-2003 (TREMBLrel. 24, last annotation update)
DE 200 kDa cell wall protein (fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxId=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
DR GO: GO:0005618; C:cell wall; IEA.
KM Cell wall; Hydroxylation.
FT MOD RES
FT NON TER
SQ SEQUENCE 15 AA; 1870 MW; 3E1E05A20A3C5681 CRC64;

Query Match
Best Local Similarity 37.0%; Score 30; DB 2; Length 15;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPP 12
DB 7 PPPPP 12

RESULT 7
Q7M1V1 PRELIMINARY; PRT; 15 AA.
ID Q7M1V1

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AC Q7M1V1;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
DE Light harvesting complex chain III/b, photosystem I (fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP SEQUENCE.
RA Uchiyama Y., Tsugita A.;
RL Submitted (JUN-1991) to the PIR data bank.
DR PIR, P70037; P70037.
DR Gramene; Q7M1V1; -.
FT NON TER
FT NON TER
SQ SEQUENCE 15 AA; 1441 MW; 3D92222733333672 CRC64;

Query Match
Best Local Similarity 35.8%; Score 29; DB 2; Length 15;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKPPPP 10
DB 4 EMKPPPP 11

RESULT 8
TMOF_AEDAE STANDARD; PRT; 10 AA.
ID TMOF_AEDAE
AC P19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, last sequence update)
DT 25-OCT-2004 (Rel. 45, last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
OX NCBI_TaxId=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like
RT enzyme biosynthesis in the midgut.";
RL PASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=8353526; DOI=10.1016/0965-1748(93)90044-S;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
RT modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -1- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
CC in the midgut which indirectly reduces the vitellogenin
CC concentration in the hemolymph resulting in inhibition of oocyte
CC development.
CC -1- DEVELOPMENTAL STAGE: Synthesized and released from follicular
CC epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs
CC and drops at 56 hrs.
DR PIR, A36454; A36454.
KM Direct protein sequencing; Hormone.
FT VARIANT
FT VARIAT YD -> DY (in TMOF(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A77777776DC7 CRC64;

Query Match
Best Local Similarity 34.6%; Score 28; DB 1; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 7 PPPP 10
 ||||
 Db 5 PPPP 8

RESULT 9

Q9TR22 PRELIMINARY; PRT; 17 AA.
 AC Q9TR22;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE NONAMELOGENIN glycoprotein (Fragment).
 OS Bos taurus (Bovine).
 CC Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP MEDLINE=96126798; PubMed=8564801;
 RA Punzi J.S., DenBesten P.K.;
 RT "Purification of nonameloogenin proteins from bovine secretory enamel.";
 RL Calif. Tissue Int. 57:379-384(1995).
 SQ SEQUENCE 17 AA; 2032 MW; 9D811C8228B615D CRC64;

Query Match 34.6%; Score 28; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
 ||||
 Db 8 PPPP 11

RESULT 10
 Q7ML13 PRELIMINARY; PRT; 17 AA.
 AC Q7ML13;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hydroxyproline-rich cell wall glycoprotein, 230K (Fragment).
 OS Phaseolus vulgaris (Kidney bean) (French bean).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
 OC NCBI_TaxID=3885;
 RN [1]
 RP MEDLINE=96011753; PubMed=7548825;
 RA Wojtaszek P., Trethowan J., Botwell G.P.;
 RT "Specificity in the immobilisation of cell wall proteins in response to different elicitor molecules in suspension-cultured cells of French bean (Phaseolus vulgaris L.)."
 RL Plant Mol. Biol. 28:1075-1087(1995).
 DR PIR: S59481; S59481.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 1929 MW; 7C0525B0179CE555 CRC64;

Query Match 34.6%; Score 28; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
 ||||
 Db 8 PPPP 11

RESULT 11

Q6SP94 PRELIMINARY; PRT; 9 AA.
 AC Q6SP94;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE PF26 (Fragment).
 OS Chlamydomonas reinhardtii.
 CC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
 OC NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CC-2290;
 RX MEDLINE=22570934; PubMed=12684385; DOI=10.1128/EC.2.2.362-379.2003;
 RA Kahler P., Laviole M., Brazelton W.J., Haas N.A., Lefebvre P.A., Silflow C.D.;
 RT "Molecular map of the Chlamydomonas reinhardtii nuclear genome.";
 RL Eukaryotic Cell 2:362-379(2003).
 DR EMBL: AY454155; AAR20844.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1012 MW; DB0AAB1B1B07776D CRC64;

Query Match 33.3%; Score 27; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 PPPP 12
 . ||||
 Db 1 PAPPE 6

RESULT 12
 Q7LZ51 PRELIMINARY; PRT; 13 AA.
 AC Q7LZ51;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Trypophyllin-related peptide.
 OS Phyllomedusa bicolor (Two-colored leaf frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Phyllomedusinae; Phyllomedusa.
 OC NCBI_TaxID=8393;
 RN [1]
 RP MEDLINE=92339502; PubMed=1633846; DOI=10.1016/0014-5793(92)80427-I;
 RA Mignogna G., Severini C., Simmaco M., Negri L., Falconieri Espamer G., Kreil G., Barra D.;
 RT "Identification and characterization of two dermorphins from skin extracts of the Amazonian frog Phyllomedusa bicolor.";
 RL FEBS Lett. 302:151-154(1992).
 DR PIR: S21152; S21152.
 SQ SEQUENCE 13 AA; 1575 MW; 094C3A21BC5777B CRC64;

Query Match 33.3%; Score 27; DB 2; Length 13;
 Best Local Similarity 62.5%; Pred. No. 2e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKEPPPP 10
 ||||
 Db 2 EKPFYPP 9

RESULT 13
 IBP4_PIG STANDARD; PRT; 16 AA.
 AC P24854;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4) (IGF-

DE binding protein 4) (Fragment).
 GN Name:IGFBP4;
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sue.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92109718; PubMed=1722398;
 RA Coleman M.E., Pan Y.-C.E., Ehterton T.D.;
 RT "Identification and NH₂-terminal amino acid sequence of three insulin-like growth factor-binding proteins in porcine serum."
 RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
 CC -1- FUNCTION: IGF-binding proteins prolong the half-life of the IGFs and have been shown to either inhibit or stimulate the growth promoting effects of the IGFs on cell culture. They alter the interaction of IGFs with their cell surface receptors.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 IGFBP domain.
 DR PIR: JH0517; JH0517.
 DR InterPro: IPR000867; Insl_gro_fac_pr.
 DR InterPro: IPR000716; Thyroglobulin_1.
 DR PROSITE: PS00222; IGF_BINDING; PARTIAL.
 DR PROSITE: PS00484; THYROGLOBULIN_1; PARTIAL.
 KM Direct protein sequencing; Growth factor binding.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1799 MW; 409888400965582 CRC64;

Query Match 33.1%; Score 27; DB 1; Length 16;
 Best Local Similarity 66.7%; Pred. No. 2.5e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 7 PPPPQ 12
 Db 7 PPPSE 12

RESULT 14
 O9B249 PRELIMINARY; PRT; 12 AA.
 AC O9B249;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Glycophorin C (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Patel S.S., Mehlotra R.K., Kastens W., Ngone C.S., Kazura J.W., Zimmerman P.A.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF342984; AAK01459.1; -.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;
 Query Match 32.1%; Score 26; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 PPPQ 11
 Db 9 PPPQ 12

RESULT 15
 O7M3M4 PRELIMINARY; PRT; 14 AA.
 AC O7M3M4;
 DT 07M3M4;

DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Protein kinase (EC 2.7.1.37).
 OS Pisaster ochraceus (Sea star).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
 OC Asteroidea; Forcipulatacea; Forcipulataida; Asteriidae; Pisaster.
 OX NCBI_TaxID=7612;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91032186; PubMed=1699809; DOI=10.1016/0014-5793(90)81090-B;
 RA Sanghera J.S., Abercrombie R., Morrison H.D., Bures E.J., Pelech S.L.;
 RT "Identification of the sites in myelin basic protein that are phosphorylated by meiosis-activated protein kinase p44 (mpk)."
 RL FEBS Lett. 273:223-226(1990).
 DR PIR: S12904; S12904.
 DR GO: GO:004672; F:protein kinase activity; IEA.
 SQ SEQUENCE 14 AA; 1492 MW; 90E7368373068171 CRC64;

Query Match 32.1%; Score 26; DB 2; Length 14;
 Best Local Similarity 36.4%; Pred. No. 3e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 VLEMKPPPPQ 11
 Db 2 IVTPRTPPPSQ 12

RESULT 16
 O7M137 PRELIMINARY; PRT; 16 AA.
 AC O7M137;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Superoxide dismutase (EC 1.15.1.1) (Fragment).
 OS unidentified bacterium.
 OC Bacteria; environmental samples.
 OX NCBI_TaxID=2338;
 RN [1]
 RP SEQUENCE.
 RA Binette J.P., Binette M.B.;
 RL Submitted (OCT-1996) to the PIR data bank.
 CC -1- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase family.
 DR PIR: E58503; E58503.
 DR GO: GO:0046872; F:metal ion binding; IEA.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 DR GO: GO:0004784; F:superoxide dismutase activity; IEA.
 DR GO: GO:0006801; F:superoxide metabolism; IEA.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; Sod_Fe_N; 1.
 KM Oxidoreductase.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 16 AA; 1828 MW; 12DE78949AC43609 CRC64;
 Query Match 32.1%; Score 26; DB 2; Length 16;
 Best Local Similarity 45.5%; Pred. No. 3.4e+03;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 2 LEMKPPPPQ 12
 Db 1 MEHTLPPLPYE 11

RESULT 17
 O9UCT9 PRELIMINARY; PRT; 18 AA.
 AC O9UCT9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE PRG-PROLINE-rich glycoprotein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91373355; PubMed=1894623;
 RA Gillette-Castro B.L., Prakobphol A., Burlingame A.L., Leflier H.,
 RA Fisher S.U.;
 RT "Structure and bacterial receptor activity of a human salivary
 RT proline-rich glycoprotein."
 RL J. Biol. Chem. 266:17358-17368(1991).
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0008368; F:Gram-negative bacterial binding; NAS.
 DR GO; GO:0009618; P:response to pathogenic bacteria; NAS.
 FT NON_TER 1 1
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1780 MW; 961F6P8A83D2E40 CRC64;

Query Match 32.1%; Score 26; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PPOQ 11
 ||||
 Db 14 PPOQ 17

RESULT 18
 O7M2M9 PRELIMINARY; PRT; 9 AA.
 AC O7M2M9;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
 DE Collagen alpha 2(VI) chain (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83209648; PubMed=6852033;
 RA Jander R., Rautenberg J., Gianvillie R.W.;
 RT "Further characterization of the three polypeptide chains of bovine
 RT and human short-chain collagen (intima collagen).";
 RL Eur. J. Biochem. 133:39-46(1983).
 DR PIR: S26508; S26508.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 876 MW; 681467776867605B CRC64;

Query Match 30.9%; Score 25; DB 2; Length 9;
 Best Local Similarity 55.6%; Pred. No. 1.6e+06;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 LEMKEPPPP 10
 ||||
 Db 1 LEMKEPPPP 9

RESULT 19
 O9PRU7 PRELIMINARY; PRT; 17 AA.
 AC O9PRU7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-CRK in VIVO

DE (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95105151; PubMed=7806494;
 RA Sakai R., Iwamoto A., Hirano N., Ogawa S., Tanaka T., Nishida J.,
 RA Yazaki Y., Hirai H.;
 RT "Characterization, partial purification, and peptide sequencing of
 RT p130, the main phosphoprotein associated with v-Crk oncoprotein."
 RL J. Biol. Chem. 269:32740-32746(1994).
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1608 MW; 52EAB880A931F887 CRC64;

Query Match 30.9%; Score 25; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 5.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 PPOQ 11
 ||||
 Db 13 PPOQ 17

RESULT 20
 O6A417 PRELIMINARY; PRT; 18 AA.
 AC O6A417;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, last annotation update)
 DE Ribulose biphosphate carboxylase large subunit (EC 4.1.1.39)
 DE (Fragment).
 GN Name=rdcl;
 OS Archangiopteris somai.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Monilliformes; Filicophyta; Marattiopsida; Marattiales;
 OC Marattiaceae; Archangiopteris.
 OX NCBI_TaxID=203826;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chiang T., Chiang Y., Chou C., Cheng Y., Chiou W.;
 RT "Phylogeography and conservation of Archangiopteris somai and A. itoi
 RT (Marattiaceae, Pteridophyta) based on nucleotide variation of cpDNA
 RT atp-rbcL intergenic spacer."
 RL Submitted (Aug-2004) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chiang Y.C.;
 RL Submitted (Aug-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ505216; CAD43797.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0016984; F:ribulose-biphosphate carboxylase activity; IEA.
 KW Chloroplast; lyase.
 FT NON_TER 18 18
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1924 MW; AAEC25AA8268869 CRC64;

Query Match 30.9%; Score 25; DB 2; Length 18;
 Best Local Similarity 62.5%; Pred. No. 5.4e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 8 PPOETVT 15
 ||||
 Db 2 PPOETVT 9

RESULT 21
 O8JVV66

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ID Q8JV66 PRELIMINARY; PRT; 10 AA.
AC Q8JV66;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxId=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Boffill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to vitrons or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304389; AAM97808.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KPPP 9
DB 5 KTRPP 9

RESULT 22
Q8JV68 PRELIMINARY; PRT; 10 AA.
ID Q8JV68;
AC Q8JV68;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxId=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Boffill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to vitrons or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304388; AAM97806.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KPPP 9
DB 5 KTRPP 9

RESULT 23
Q8JV70 PRELIMINARY; PRT; 10 AA.
ID Q8JV70;
AC Q8JV70;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.

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OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxId=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Boffill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to vitrons or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304387; AAM97804.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KPPP 9
DB 5 KTRPP 9

RESULT 24
Q8JV72 PRELIMINARY; PRT; 10 AA.
ID Q8JV72;
AC Q8JV72;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxId=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Boffill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to vitrons or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304386; AAM97802.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KPPP 9
DB 5 KTRPP 9

RESULT 25
Q8JV74 PRELIMINARY; PRT; 10 AA.
ID Q8JV74;
AC Q8JV74;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxId=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Boffill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,

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RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA."
RL J. Virol. 75:10290-10299(2001).
DR EMBL, AF303948; AAM97800.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KEPPP 9
|
|
|
|
DB 5 KTRPP 9

RESULT 26

ID Q8JV76 PRELIMINARY; PRT; 10 AA.
AC Q8JV76;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
RX DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA."
RL J. Virol. 75:10290-10299(2001).
DR EMBL, AF303947; AAM97798.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KEPPP 9
|
|
|
|
DB 5 KTRPP 9

RESULT 27

ID Q8JV80 PRELIMINARY; PRT; 10 AA.
AC Q8JV80;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
RX DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA."
RL J. Virol. 75:10290-10299(2001).
DR EMBL, AF303945; AAM97794.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KEPPP 9
|
|
|
|
DB 5 KTRPP 9

RESULT 28

ID Q8JV82 PRELIMINARY; PRT; 10 AA.
AC Q8JV82;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
RX DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA."
RL J. Virol. 75:10290-10299(2001).
DR EMBL, AF303944; AAM97792.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KEPPP 9
|
|
|
|
DB 5 KTRPP 9

RESULT 29

ID Q9Q0V7 PRELIMINARY; PRT; 10 AA.
AC Q9Q0V7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087544; PubMed=10618230;
RX Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage."
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL, AF119356; AAF24118.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KEPPP 9
|
|
|
|
DB 5 KTRPP 9

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RESULT 30
O9Q0V9 PRELIMINARY; PRT; 10 AA.
ID O9Q0V9
AC O9Q0V9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
RT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
OS Polyomavirus JC.
OC Viruses; dcdna viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119355; AAF24116.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 KPPP 9
Db 5 KPPP 9

RESULT 31
O9Q0W1 PRELIMINARY; PRT; 10 AA.
ID O9Q0W1
AC O9Q0W1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
RT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
OS Polyomavirus JC.
OC Viruses; dcdna viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119354; AAF24114.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 KPPP 9
Db 5 KPPP 9

RESULT 32
O9Q0W3 PRELIMINARY; PRT; 10 AA.
ID O9Q0W3
AC O9Q0W3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
RT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
OS Polyomavirus JC.
OC Viruses; dcdna viruses, no RNA stage; Polyomaviridae; Polyomavirus.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;
```

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OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119353; AAF24112.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 KPPP 9
Db 5 KPPP 9

RESULT 33
O9Q0W5 PRELIMINARY; PRT; 10 AA.
ID O9Q0W5
AC O9Q0W5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
RT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
OS Polyomavirus JC.
OC Viruses; dcdna viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119352; AAF24110.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 KPPP 9
Db 5 KPPP 9

RESULT 34
O9Q0W7 PRELIMINARY; PRT; 10 AA.
ID O9Q0W7
AC O9Q0W7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
RT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
OS Polyomavirus JC.
OC Viruses; dcdna viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119351; AAF24108.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;
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Query Match 29.6%; Score 24; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KRPPP 9
 |
 |
 |
 |
 DB 5 KRPPP 9

RESULT 35
 Q9Q0W9 PRELIMINARY; PRT; 10 AA.
 AC Q9Q0W9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20087544; PubMed=10618230;
 RA BoFilli-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119350; AAF24106.1; --
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A9771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KRPPP 9
 |
 |
 |
 |
 DB 5 KRPPP 9

RESULT 36
 Q9Q0X1 PRELIMINARY; PRT; 10 AA.
 AC Q9Q0X1;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20087544; PubMed=10618230;
 RA BoFilli-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119349; AAF24104.1; --
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A9771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KRPPP 9
 |
 |
 |
 |
 DB 5 KRPPP 9

RESULT 37

Q9Q0X3 PRELIMINARY; PRT; 10 AA.
 AC Q9Q0X3;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20087544; PubMed=10618230;
 RA BoFilli-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119348; AAF24102.1; --
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A9771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KRPPP 9
 |
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 |
 |
 DB 5 KRPPP 9

RESULT 38
 Q9Q0X5 PRELIMINARY; PRT; 10 AA.
 AC Q9Q0X5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20087544; PubMed=10618230;
 RA BoFilli-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119347; AAF24100.1; --
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A9771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KRPPP 9
 |
 |
 |
 |
 DB 5 KRPPP 9

RESULT 39
 Q9Q0X9 PRELIMINARY; PRT; 10 AA.
 AC Q9Q0X9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=20087544; PubMed=10618230;
 RA Boffill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RL populations by studying their presence in urban sewage."; Appl. Environ. Microbiol. 66:238-245(2000).
 [2]
 RN SEQUENCE FROM N.A.
 RA Boffill-Mas S., Pina S., Girones R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF119345; AAF24096.1; -.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KPPPP 9
 | | | | |
 Db 5 KTRPP 9

RESULT 40
 BPP3_BOTIN
 ID BPP3_BOTIN STANDARD; PRT; 11 AA.
 AC P30423;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OC NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintrá A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom."; J. Protein Chem. 9:221-227(1990).
 RL J. FUNCTION: This peptide both inhibits the activity of the
 CC -I- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it. It acts
 CC as an indirect hypotensive agent.
 DR PIR: C37196; C37196.
 KM Direct protein sequencing; Hypotensive agent;
 KM Pyroglutamate carboxylic acid.
 KW MOD_RES 1
 FT MOD_RES 1
 SQ SEQUENCE 11 AA; 1199 MW; 20B25813C741777 CRC64;

Query Match 29.6%; Score 24; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 4.5e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 PPPPQ 11
 | | | | |
 Db 4 PPRPQ 8

Search completed: June 7, 2005, 23:19:03
 Job time : 67 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 80.7273 Seconds
(without alignments)
71.864 Million cell updates/sec

Title: US-10-691-157-8
Perfect score: 82
Sequence: 1 LKPFKLVKVEFPFP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 366760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A: Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	15	4	AA072507 Colostrin
2	82	100.0	15	4	AA059313 Ewe colos
3	82	100.0	15	4	AA072253 Colostrin
4	82	100.0	15	4	AA072539 Colostrin
5	82	100.0	15	5	AA014584 Neural ce
6	82	100.0	15	5	AA051043 Colostrin
7	82	100.0	15	5	AA020235 Colostrin
8	82	100.0	15	8	AA060302 Constitue
9	82	100.0	15	8	AA074389 Ewe col
10	82	100.0	16	4	AA059344 Ewe colos
11	82	100.0	14	7	AA014848 T cell st
12	82	100.0	14	7	AA014527 Eptlope o
13	82	100.0	14	7	AA014511 Gluteu-de
14	82	100.0	14	7	AA014519 Eptlope o
15	82	100.0	14	7	AA014535 Eptlope o
16	82	100.0	14	7	AA014824 Glutidin r
17	82	100.0	14	8	AA048879 Cyclic pe
18	82	100.0	14	2	AA048904 Cyclic pe
19	82	100.0	18	4	AA041738 Peptide #
20	82	100.0	18	4	AA055535 Peptide #
21	82	100.0	18	4	AA025488 Protein #
22	82	100.0	18	4	AA075423 Human Don
23	82	100.0	18	4	AA062611 Human bra
24	82	100.0	18	4	AA057176 Human liv
25	82	100.0	18	5	AA045003 Human pep

26	36	43.9	18	4	AA072520 Colostrin
27	36	43.9	18	4	AA059330 Ewe colos
28	36	43.9	18	4	AA072267 Colostrin
29	36	43.9	18	4	AA072552 Colostrin
30	36	43.9	18	5	AA014598 Neural ce
31	36	43.9	18	5	AA051056 Colostrin
32	36	43.9	18	5	AA020249 Colostrin
33	36	43.9	18	8	AA060316 Constitue
34	36	43.9	18	8	AA074406 Ewe col
35	35	42.7	16	8	AA014831 Glutidin r
36	35	42.7	18	8	AA014841 Glutidin r
37	34.5	42.1	11	4	AA070188 Colostrin
38	34.5	42.1	11	4	AA070198 Colostrin
39	34.5	42.1	14	2	AA048877 Cyclic pe
40	34.5	42.1	14	2	AA048878 Cyclic pe
41	34	41.5	10	4	AA070187 Colostrin
42	34	41.5	15	4	AA072504 Colostrin
43	34	41.5	15	4	AA059322 Ewe colos
44	34	41.5	15	4	AA072250 Colostrin
45	34	41.5	15	4	AA072536 Colostrin
46	34	41.5	15	5	AA014581 Neural ce
47	34	41.5	15	5	AA051040 Colostrin
48	34	41.5	15	5	AA020232 Colostrin
49	34	41.5	15	8	AA060299 Constitue
50	34	41.5	15	8	AA074398 Ewe col
51	34	41.5	16	4	AA059352 Ewe colos
52	34	41.5	17	8	AA014827 Glutidin r
53	34	41.5	18	8	AA014832 Glutidin r
54	33.5	40.9	14	2	AA048905 Cyclic pe
55	33	40.2	14	2	AA058339 Hypotenai
56	33	40.2	14	7	AA014518 Eptlope o
57	33	40.2	14	7	AA014510 Gluteu-de
58	33	40.2	14	7	AA014534 Eptlope o
59	33	40.2	14	7	AA014847 T cell st
60	33	40.2	14	7	AA014526 Eptlope o
61	33	40.2	14	8	AA037024 Bovine ca
62	33	40.2	17	8	AA014823 Glutidin r
63	33	40.2	18	2	AA014821 Glutidin r
64	32.5	39.6	14	8	AA048906 Cyclic pe
65	32	39.0	9	5	AA001855 158P1D7 r
66	32	39.0	9	5	AA001751 158P1D7 r
67	32	39.0	9	5	AA001966 158P1D7 r
68	32	39.0	10	5	AA001907 158P1D7 r
69	32	39.0	10	5	AA001366 158P1D7 r
70	32	39.0	13	7	AA075628 Potential
71	32	39.0	14	7	AA014852 T cell st
72	32	39.0	14	7	AA014531 Eptlope o
73	32	39.0	14	7	AA014523 Eptlope o
74	32	39.0	14	7	AA014539 Eptlope o
75	32	39.0	14	7	AA014515 Gluteu-de
76	32	39.0	16	2	AA038528 S. pneumo
77	32	39.0	16	5	AA077148 Cibaical
78	32	39.0	16	6	AA082437 G protein
79	32	39.0	17	6	AA034141 T-cell st
80	31.5	38.4	12	2	AA093361 LYN prote
81	31.5	38.4	14	2	AA048876 Cyclic pe
82	31.5	38.4	14	5	AA081248 GS14K4 an
83	31.5	38.4	17	4	AA001835 Wheat Gli
84	31.5	38.4	17	8	AA014595 Glutidin r
85	31.5	38.4	17	8	AA016198 Glutidin r
86	31.5	38.4	17	8	AA014663 Glutidin r
87	31	37.8	13	4	AA074265 Exemplyar
88	31	37.8	13	4	AA080871 Angiostatic
89	31	37.8	13	5	AA097548 Antiangio
90	31	37.8	14	7	AA014522 Eptlope o
91	31	37.8	14	7	AA014851 T cell st
92	31	37.8	14	7	AA014538 Eptlope o
93	31	37.8	14	7	AA014514 Gluteu-de
94	31	37.8	14	7	AA014530 Eptlope o
95	30.5	37.2	15	8	AA091447 Immunogen
96	30.5	37.2	15	8	AA093461 GST-P13K
97	30.5	37.2	17	4	AA001804 Wheat A-g
98	30.5	37.2	17	4	AA001816 Wheat Gli

99 30.5 37.2 17 4 AAU01798
100 30.5 37.2 17 4 AAU01803

AAU01798 Wheat A-g
AAU01803 Wheat A-g

ALIGNMENTS

RESULT 1

AA072507
ID AAB72507 strand; peptide; 15 AA.

AC AAB72507;

DT 09-MAY-2001 (first entry)

DE Colostriin peptide #8.

KW Dermatological; oxidative stress regulator; colostriin.

OS Unidentified.

PN WO200112650-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022665.

PR 17-AUG-1999; 99US-0149310P.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Stanton GJ, Hughes TK, Boldogh I;

DR MPI; 2001-218342/22.

PT Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostriin, its constituent peptide, analog or their combinations.

PS Claim 6; Page 25; 48pp; English.

CC The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostriin, or its constituent peptide (e.g. the present peptide), CC to change the level of an oxidizing species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient

SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 6.2e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKFPFKLKVFPFP 15
1 LKFPFKLKVFPFP 15

Db 1 LKFPFKLKVFPFP 15

RESULT 2

AA059313
ID AAB59313 strand; peptide; 15 AA.

AC AAB59313;

DT 21-MAR-2001 (first entry)

DE Ewe colostriin peptide fragment A-4.

KW Sheep; colostriin; proline rich polypeptide; colostrum; immune disorder;

KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

OS Ovis sp.

PN WO200075173-A2.

PD 14-DEC-2000.

PF 02-JUN-2000; 2000WO-GB002128.

PR 02-JUN-1999; 99GB-00012852.

PA (REGG-) REGEN THERAPEUTICS PLC.

PI Georgiades JA;

DR MPI; 2001-071058/08.

PT Peptides having an N-terminal amino acid sequence isolated from colostriin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques.

PS Claim 7; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides found in ewe's colostriin. Colostriin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques

SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 6.2e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKFPFKLKVFPFP 15
1 LKFPFKLKVFPFP 15

Db 1 LKFPFKLKVFPFP 15

RESULT 3

AA072253
ID AAB72253 strand; peptide; 15 AA.

AC AAB72253;

DT 14-MAY-2001 (first entry)

DE Colostriin derived cytokine inducing peptide SEQ ID 8.

KW Colostriin; immune response; cytokine; blood cell proliferation;

KW central nervous system disorder; neurological disorder; mental disorder;

KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;

KW neurosis; infection.

OS Synthetic.

PN WO200111937-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022818.

PR 17-AUG-1999; 99US-0149311P.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2001-202804/20.
XX Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial, and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator.
XX
XX
PS Claim 1; Page 34; 50pp; English.
XX
CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The peptides
CC have immune response modulatory activity, and are capable of inducing
CC cytokines. Colostrinin and its derived peptides are useful for inducing
CC cytokine production, for modulating an immunological response and for
CC inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 82; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKPPKLVKVEVPPF 15
DB 1 LKPPKLVKVEVPPF 15
RESULT 4
AAB72539
ID AAB72539 standard; peptide; 15 AA.
XX
AC AAB72539;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #8.
XX
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
OS Unidentified.
XX
PN WO200112651-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US022774.
XX
PR 17-AUG-1999; 99US-0149633P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Boldogh I;
XX
XX WPI; 2001-226545/23.
DR
XX
PT Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating damaged
PT neural cells in a patient.
XX
PS Claim 6; Page 21; 35pp; English.
XX
CC The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKPPKLVKVEVPPF 15
DB 1 LKPPKLVKVEVPPF 15
RESULT 5
AA014584
ID AA014584 standard; peptide; 15 AA.
XX
AC AA014584;
XX
DT 27-MAY-2002 (first entry)
XX
DE Neural cell regulatory colostrinin peptide 8.
XX
KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
KW neural cell treatment.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 15 /note="Optional C-terminal amide"
XX
PN WO200213851-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022777.
XX
PR 17-AUG-2000; 2000WO-US022777.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Boldogh I, Stanton JG, Hughes TK;
XX
DR WPI; 2002-269152/31.
XX
PT Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX
PS Claim 7; Page 21; 37pp; English.
XX
CC The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 82; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKPPKLVKVEVPPF 15
DB 1 LKPPKLVKVEVPPF 15
RESULT 6
AAM51043

ID AAM51043 standard; peptide, 15 AA.
XX AAM51043;
AC
XX
XX 30-MAY-2002 (first entry)
DT
XX Colostrinin constituent peptide.
DB,
XX Colostrinin constituent peptide.
XX Colostrinin; colostrum; immunomodulator; cardiovascular;
KM blood cell regulator; cytokine inducer; human.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 15
FT /note= "optional C-terminal amidation"
FT
XX
XX WO200213849-A1.
PN
XX
XX 21-FEB-2002.
PD
XX
XX 17-AUG-2000; 2000WO-US022775.
PF
XX
XX 17-AUG-2000; 2000WO-US022775.
PR
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
XX
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
PI
XX WPI, 2002-269150/31.
DR
XX
XX Modulation of blood cell proliferation in a patient involves use of blood
PT cell regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX
XX Claim 1; Page 34; 54pp; English.
PS
XX
XX The present sequence is that of a colostrinin constituent peptide that is
CC preferred for use as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. Methods are claimed for:
CC inducing a cytokine in a cell by contact with an immunological regulator,
CC where the cell is present in a cell culture, a tissue, an organ or an
CC organism, and the cell is mammalian, including human; modulating an
CC immune response in a cell by contact with the immunological regulator
CC under conditions effective to induce a cytokine; modulating an immune
CC response in a patient by administering an immunological regulator under
CC conditions effective to induce a cytokine, where the immunological
CC regulator is administered topically or as part of a dietary supplement,
CC and where the immune response is specific or non specific, an interferon
CC response or an antibody response; modulating blood cell proliferation by
CC contacting blood cells with a blood cell regulator, where the blood cells
CC are present in a cell culture or an organism, are mammalian or human, and
CC where the blood cells are increased in number or differentiated; and a
CC method for modulating blood cell proliferation in a patient. A claimed
CC cytokine-inducing composition comprises a pharmaceutical carrier and an
CC active agent such as the present peptide. Cytokines induced by this
CC peptide in human leucocyte cultures include interferon-gamma, tumour
CC necrosis factor-alpha, interleukin-6 and interleukin-10
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 82; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFPFKLKVVPFP 15
| | | | | | | | | | | | | | |
Db 1 LKFPFKLKVVPFP 15

RESULT 7
AAE20235

ID AAE20235 standard; peptide, 15 AA.
XX AAE20235;
AC
XX
XX 18-JUN-2002 (first entry)
DT
XX Colostrinin constituent peptide #8.
DE
XX Colostrinin; colostrum; immunomodulator; cardiovascular;
KM blood cell regulator; cytokine inducer; human.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 15
FT /note= "Optionally C-terminal amide"
FT
XX
XX WO200213850-A1.
PN
XX
XX 21-FEB-2002.
PD
XX
XX 17-AUG-2000; 2000WO-US022776.
PF
XX
XX 17-AUG-2000; 2000WO-US022776.
PR
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
XX
XX Stanton GJ, Hughes TK, Boldogh I;
PI
XX WPI, 2002-269151/31.
DR
XX
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog.
XX
XX Claim 6; Page 25; 51pp; English.
PS
XX
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress level
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
CC organ, or organism; or for treating oxidative damage to the skin of a
CC patient e.g. animal or human; to modulate oxidative stress during/ after
CC a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 82; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFPFKLKVVPFP 15
| | | | | | | | | | | | | | |
Db 1 LKFPFKLKVVPFP 15

RESULT 8
ADN60302
ID ADN60302 standard; peptide, 15 AA.
XX

AC ADN60302;
XX
XX 29-JUL-2004 (first entry)
DE Constituent peptide of colostrinin SEQ ID NO:8.
XX
XX
KW modulator; colostrinin; intracellular signaling molecule modulator;
KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;
KW DNA damage; beta-amyloid; retinoic acid; cyclostatic; 4HNE inhibitor;
KW 4HNE-protein adduct formation reduction;
KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;
KW c-Jun NH2-terminal kinase inhibition.
XX
OS Synthetic.
XX
XX WO2004037851-A2.
XX
XX 06-MAY-2004.
XX
XX 22-OCT-2003; 2003WO-US033423.
XX
XX 22-OCT-2002; 2002US-0420369P.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX PA (BOLD/) BOLDG I.
XX PA (STAN/) STANTON J G.
XX PA (GEOR/) GEORGIADIS J A.
XX PA (HUGH/) HUGHES T K.
XX PA (KRUZ/) KRUZEL M.
XX
XX Boldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;
XX WPI; 2004-365494/34.
XX
XX Use of colostrinin for e.g. modulating an intracellular signaling
XX molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a
XX cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
XX a cell.
XX
XX Claim 6; SEQ ID NO 8; 46pp; English.
XX
XX The present invention describes the use of a modulator selected from
XX colostrinin, its constituent peptide, its active analogue, and a
XX combination of these, for modulating an intracellular signaling molecule
XX in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,
XX inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
XX and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
XX The modulator has cyostatic activity, and can be used as a 4HNE
XX inhibitor. The modulator is useful in the manufacture of a medicament for
XX reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated
XX glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,
XX and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.
XX Colostrinin, or its constituent peptide or active analogue is useful for
XX inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
XX or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
XX The present sequence represents a synthetic constituent peptide of
XX colostrinin, which can be used as a modulator in the present invention.
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 82; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. NO. 6.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKPPFKLKVVEVPPF 15
DB 1 LKPPFKLKVVEVPPF 15
RESULT 9
ADS74389
ID ADS74389 standard; peptide; 15 AA.
XX

AC ADS74389;
XX
XX 16-DEC-2004 (first entry)
XX
XX Ovine colostrinin peptide.
DE
XX
XX Colostrinum; colostrinin; sheep; peptide purification.
KW
XX
OS Ovis aries.
XX
XX WO2004081038-A1.
XX
XX 23-SEP-2004.
XX
XX 10-MAR-2004; 2004WO-GB001014.
XX
XX 11-MAR-2003; 2003GB-00005552.
XX
XX 08-MAR-2004; 2004GB-00005190.
XX
XX (REGG-) REGEN THERAPEUTICS PLC.
XX
XX Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;
XX WPI; 2004-677519/66.
XX
XX Recovering peptides such as colostrinin from mammalian colostrum, by
XX mixing colostrum with alcohol to form alcohol phase containing peptides
XX and precipitate, separating alcohol phase from precipitate, and
XX recovering alcohol phase.
XX
XX Disclosure; SEQ ID NO 4; 41pp; English.
XX
XX The present sequence is that of a peptide that can be recovered from
XX ovine colostrinum using the method of the invention. The invention
XX provides a method for the recovery of peptides (especially colostrinin)
XX from colostrum in substantially pure, biologically active form and in
XX high yield. The method involves mixing the colostrum with an alcohol to
XX form an alcohol phase containing the colostrinin and a precipitate
XX containing higher molecular weight caseins and other proteins. Best
XX results are obtained using methanol or ethanol of at least 80%, and
XX preferably up to 100%, purity. The alcohol phase is then separated from
XX the precipitate, and the colostrinin is separated from the alcohol,
XX preferably by evaporation, to form a colostrinin-rich phase, which is
XX recovered. A precipitation agent, such as ammonium sulfate, may be added
XX either to the alcohol phase or, preferably, to the colostrinin-rich phase
XX to induce precipitation of the colostrinin peptides. The method is
XX generally applicable to the separation of peptides from fluids containing
XX higher molecular weight proteins, lipids, carbohydrates and/or nucleic
XX acids.
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 82; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. NO. 6.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKPPFKLKVVEVPPF 15
DB 1 LKPPFKLKVVEVPPF 15
RESULT 10
AAB59344
ID AAB59344 standard; peptide; 16 AA.
XX
XX AAB59344;
XX
XX 21-MAR-2001 (first entry)
XX
XX Ewe colostrinin peptide fragment derived sequence #4.
DE
XX
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX

XX OS Ovis sp.
 XX PN WO20075173-A2.
 XX PD 14-DEC-2000.
 XX PF 02-JUN-2000; 2000WO-GB002128.
 XX PR 02-JUN-1999; 99GB-00012852.
 XX PA (REG-) REGEN THERAPEUTICS PLC.
 XX PI Georgiades JA;
 XX DR WPI; 2001-071058/08.
 XX PT Peptides having an N-terminal amino acid sequence isolated from
 PT colostrin for treating e.g. disorders of the central nervous system and
 PT immune system, viral and bacterial infections, and diseases characterized
 PT by amyloid plaques.
 XX PS Claim 8; Page 27; 63pp; English.
 XX CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques
 XX SQ Sequence 16 AA;
 XX Query Match 100.0%; Score 82; DB 4; Length 16;
 XX Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LKFPKLVKVEPPFP 15
 DB 2 LKFPKLVKVEPPFP 16
 XX RESULT 11
 XX ADF14848
 XX ID ADF14848 standard; peptide; 14 AA.
 XX AC ADF14848;
 XX DT 12-FEB-2004 (first entry)
 XX DE T cell stimulatory pool-derived peptide 4.
 XX KW plant; deamidation; tissue transglutaminase; celiac disease; CD;
 KW gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; sjogren syndrome; diabetes;
 KW immunosuppressive; antirheumatic; antiarthritic; antidiabetic;
 KW dermatological; antiinflammatory; T cell stimulatory pool.
 XX OS Unidentified.
 XX PN EPI332760-A1.
 XX PD 06-AUG-2003.
 XX PF 04-FEB-2002; 2002EP-00075456.
 XX PR 04-FEB-2002; 2002EP-00075456.
 XX PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
 XX DR WPI; 2003-647889/62.

XX PT New gluten peptides or epitopes prone to deamidation by tissue
 PT transglutaminase, useful for treating celiac disease or an autoimmune
 PT disease, rheumatoid arthritis, multiple sclerosis, systemic lupus
 PT erythematosus, or diabetes.
 XX PS Disclosure; Fig 2B; 143pp; English.
 XX CC The invention relates to a novel peptide or epitope which is prone to
 CC deamidation by tissue transglutaminase (tTG) and is a causative factor of
 CC celiac disease (CD, gluten intolerance) or an autoimmune disease such as
 CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
 CC sjogren syndrome or diabetes. The peptide of the invention demonstrates
 CC immunosuppressive, antirheumatic, antiarthritic, antidiabetic,
 CC dermatological and antiinflammatory activities whilst pharmaceutical
 CC compositions comprising the peptides or epitopes may be useful for the
 CC treatment of a celiac disease or an autoimmune disease such as rheumatoid
 CC arthritis, multiple sclerosis, systemic lupus erythematosus, sjogren
 CC syndrome or diabetes. Gluten-derived peptides may be useful in the
 CC preparation of therapeutic agents capable of eliminating a subset of
 CC cells, particularly gluten-sensitive or auto-antigen sensitive T cells.
 CC The current sequence is that of the T cell stimulatory pool-derived
 CC peptide of the invention.
 XX SQ Sequence 14 AA;
 XX Query Match 46.3%; Score 38; DB 7; Length 14;
 XX Best Local Similarity 53.8%; Pred. No. 16;
 XX Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 OY 3 PPKLVKLVKVEPPFP 15
 DB 1 PPKLVKLVKVEPPFP 13
 XX RESULT 12
 XX ADF14527
 XX ID ADF14527 standard; peptide; 14 AA.
 XX AC ADF14527;
 XX DT 12-FEB-2004 (first entry)
 XX DE Epitope of gluten-derived tTG substrate peptide - SEQ ID 20.
 XX KW plant; deamidation; tissue transglutaminase; celiac disease; CD;
 KW gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; sjogren syndrome; diabetes;
 KW immunosuppressive; antirheumatic; antiarthritic; antidiabetic;
 KW dermatological; antiinflammatory; substrate epitope.
 XX OS Unidentified.
 XX PN EPI332760-A1.
 XX PD 06-AUG-2003.
 XX PF 04-FEB-2002; 2002EP-00075456.
 XX PR 04-FEB-2002; 2002EP-00075456.
 XX PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
 XX DR WPI; 2003-647889/62.
 XX PT New gluten peptides or epitopes prone to deamidation by tissue
 PT transglutaminase, useful for treating celiac disease or an autoimmune
 PT disease, rheumatoid arthritis, multiple sclerosis, systemic lupus
 PT erythematosus, or diabetes.
 XX PS Claim 2; SEQ ID NO 20; 143pp; English.
 XX CC The invention relates to a novel peptide or epitope which is prone to

CC deamidation by tissue transglutaminase (tTG) and is a causative factor of
 CC celiac disease (CD, gluten intolerance) or an autoimmune disease such as
 CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
 CC Sjogren syndrome or diabetes. The peptide of the invention demonstrates
 CC immunosuppressive, antirheumatic, antidiabetic, antidiabetic,
 CC dermatological and antiinflammatory activities whilst pharmaceutical
 CC compositions comprising the peptides or epitopes may be useful for the
 CC treatment of a celiac disease or an autoimmune disease such as rheumatoid
 CC arthritis, multiple sclerosis, systemic lupus erythematosus, Sjogren
 CC syndrome or diabetes. Gluten-derived peptides may be useful in the
 CC preparation of therapeutic agents capable of eliminating a subset of
 CC cells, particularly gluten-sensitive or auto-antigen sensitive T cells.
 CC The current sequence is that of the epitope of the gluten-derived tTG
 CC substrate peptide of the invention.

CC Sequence 14 AA;

Query Match 46.3%; Score 38; DB 7; Length 14;
 Best Local Similarity 53.8%; Pred. No. 16;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPKLKVVFPP 15
 |||:|:|
 Db 1 PPKLKVVFPP 13

RESULT 13

ADP14511
 ID ADP14511 standard; peptide; 14 AA.

AC ADP14511;

DT 12-FEB-2004 (first entry)

DE Gluten-derived tissue transglutaminase substrate peptide - SEQ ID 4.

XX plant; deamidation; tissue transglutaminase; tTG; celiac disease; CD;

XX gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;

XX systemic lupus erythematosus; Sjogren syndrome; diabetes;

XX immunosuppressive; antirheumatic; antidiabetic; antidiabetic;

XX dermatological; antiinflammatory; substrate.

OS Unidentified.

XX EP1332760-A1.

PD 06-AUG-2003.

PF 04-FEB-2002; 2002EP-00075456.

PR 04-FEB-2002; 2002EP-00075456.

PS (ZIER-) ACAD ZIEKENHUIS LEIDEN.

XX WPI; 2003-647889/62.

DR New gluten peptides or epitopes prone to deamidation by tissue

XX transglutaminase, useful for treating celiac disease or an autoimmune

PT disease, rheumatoid arthritis, multiple sclerosis, systemic lupus

XX erythematosus, or diabetes.

PS Claim 1; SEQ ID NO 4; 143pp; English.

XX The invention relates to a novel peptide or epitope which is prone to

CC deamidation by tissue transglutaminase (tTG) and is a causative factor of

CC celiac disease (CD, gluten intolerance) or an autoimmune disease such as

CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,

CC Sjogren syndrome or diabetes. The peptide of the invention demonstrates

CC immunosuppressive, antirheumatic, antidiabetic, antidiabetic,

CC dermatological and antiinflammatory activities whilst pharmaceutical

CC compositions comprising the peptides or epitopes may be useful for the

CC treatment of a celiac disease or an autoimmune disease such as rheumatoid

CC arthritis, multiple sclerosis, systemic lupus erythematosus, Sjogren

CC syndrome or diabetes. Gluten-derived peptides may be useful in the
 CC preparation of therapeutic agents capable of eliminating a subset of
 CC cells, particularly gluten-sensitive or auto-antigen sensitive T cells.
 CC The current sequence is that of the gluten-derived tissue
 CC transglutaminase substrate peptide of the invention.

CC Sequence 14 AA;

Query Match 46.3%; Score 38; DB 7; Length 14;
 Best Local Similarity 53.8%; Pred. No. 16;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPKLKVVFPP 15
 |||:|:|
 Db 1 PPKLKVVFPP 13

RESULT 14

ADP14519
 ID ADP14519 standard; peptide; 14 AA.

AC ADP14519;

DT 12-FEB-2004 (first entry)

DE Epitope of gluten-derived tTG substrate peptide - SEQ ID 12.

XX plant; deamidation; tissue transglutaminase; tTG; celiac disease; CD;

XX gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;

XX systemic lupus erythematosus; Sjogren syndrome; diabetes;

XX immunosuppressive; antirheumatic; antidiabetic; antidiabetic;

XX dermatological; antiinflammatory; substrate epitope.

OS Unidentified.

XX EP1332760-A1.

PD 06-AUG-2003.

PF 04-FEB-2002; 2002EP-00075456.

PR 04-FEB-2002; 2002EP-00075456.

PS (ZIER-) ACAD ZIEKENHUIS LEIDEN.

XX WPI; 2003-647889/62.

DR New gluten peptides or epitopes prone to deamidation by tissue

XX transglutaminase, useful for treating celiac disease or an autoimmune

PT disease, rheumatoid arthritis, multiple sclerosis, systemic lupus

XX erythematosus, or diabetes.

PS Claim 2; SEQ ID NO 12; 143pp; English.

XX The invention relates to a novel peptide or epitope which is prone to

CC deamidation by tissue transglutaminase (tTG) and is a causative factor of

CC celiac disease (CD, gluten intolerance) or an autoimmune disease such as

CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,

CC Sjogren syndrome or diabetes. The peptide of the invention demonstrates

CC immunosuppressive, antirheumatic, antidiabetic, antidiabetic,

CC dermatological and antiinflammatory activities whilst pharmaceutical

CC compositions comprising the peptides or epitopes may be useful for the

CC treatment of a celiac disease or an autoimmune disease such as rheumatoid

CC arthritis, multiple sclerosis, systemic lupus erythematosus, Sjogren

Query Match 46.3%; Score 38; DB 7; Length 14;

Best Local Similarity 53.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 3 PPKLKVEVFP 15
|||:|:|
Db 1 PFPQLQPPQPP 13

RESULT 15

ADP14535
ID ADP14535 standard; peptide; 14 AA.

AC ADP14535;

DT 12-FEB-2004 (first entry)

DE Epitope of gluten-derived cTG substrate peptide - SEQ ID 28.

XX plant; deamidation; tissue transglutaminase; cTG; celiac disease; CD;
XX gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;
XX celiac disease; autoimmune; Sjogren syndrome; diabetes;
XX immunosuppressive; antirheumatic; antidiabetic;
XX dermatological; antiinflammatory; substrate epitope.

OS Unidentified.

PN EP132760-A1.

PD 06-AUG-2003.

PF 04-FEB-2002; 2002EP-00075456.

PR 04-FEB-2002; 2002EP-00075456.

PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.

DR WPI; 2003-647889/62.

XX New gluten peptides or epitopes prone to deamidation by tissue
XX transglutaminase, useful for treating celiac disease or an autoimmune
XX disease, rheumatoid arthritis, multiple sclerosis, systemic lupus
XX erythematosus, or diabetes.

PS Claim 2; SEQ ID NO 28; 143pp; English.

XX The invention relates to a novel peptide or epitope which is prone to
XX deamidation by tissue transglutaminase (TG) and is a causative factor of
XX celiac disease (CD, gluten intolerance) or an autoimmune disease such as
XX rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
XX Sjogren syndrome or diabetes. The peptide of the invention demonstrates
XX immunosuppressive, antirheumatic, antidiabetic, antidiabetic,
XX dermatological and antiinflammatory activities whilst pharmaceutical
XX compositions comprising the peptide or epitopes may be useful for the
XX treatment of a celiac disease or an autoimmune disease such as rheumatoid
XX arthritis, multiple sclerosis, systemic lupus erythematosus, Sjogren
XX syndrome or diabetes. Gluten-derived peptides may be useful in the
XX preparation of therapeutic agents capable of eliminating a subset of
XX cells, particularly gluten-sensitive or auto-antigen sensitive T cells.
XX The current sequence is that of the epitope of the gluten-derived cTG
XX substrate peptide of the invention.

SQ Sequence 14 AA;

Query Match 46.3%; Score 38; DB 7; Length 14;

Best Local Similarity 53.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 3 PPKLKVEVFP 15
|||:|:|
Db 1 PFPQLQPPQPP 13

RESULT 16

ADH14824
ID ADH14824 standard; peptide; 17 AA.

AC ADH14824;

DT 11-MAR-2004 (first entry)

DE Gliadin related epitope peptide.

XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
XX vaccine.

OS Synthetic.

PN WO2003104273-A2.

PD 18-DEC-2003.

PF 05-JUN-2003; 2003WO-GB002450.

PR 05-JUN-2002; 2002GB-00012885.

PA (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2004-043640/04.

XX Preventing or treating coeliac disease comprises administering agent
XX which are wheat gliadin T cell epitope capable of being recognized by T
XX cell receptor.

PS Example 13; Page 95; 177pp; English.

XX The present invention describes a method (M1) for preventing or treating
XX coeliac disease. M1 comprises administering an agent (A) comprising a
XX gliadin T cell epitope, which is capable of being recognised by a T cell
XX receptor, to an individual. Gliadin is a component of gluten. (A) has
XX gastrointestinal activity, and can be used in vaccines. The agent (A) can
XX be used in the preparation of a medicament for treating or preventing
XX coeliac disease. (A) can also be used in the preparation of a diagnostic
XX means for use in diagnosing coeliac disease, or susceptibility to coeliac
XX disease, in an individual, which involves determining whether T cells of
XX the individual recognise the agent, recognition by the T cells indicating
XX that the individual has, or is susceptible to, coeliac disease. The
XX present sequence represents a peptide which is used in the
XX exemplification of the present invention.

SQ Sequence 17 AA;

Query Match 46.3%; Score 38; DB 8; Length 17;

Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 LKPPKLVFP 15
|||:|:|
Db 2 LQFPQPPQPP 16

RESULT 17

AAW48879
ID AAW48879 standard; peptide; 14 AA.

AC AAW48879;

DT 23-SEP-1998 (first entry)

DE Cyclic peptide gramicidin S14 (GS14) analogue 3.

XX Cyclic: gramicidin S14; GS; beta-pleated structure; therapeutic index;
XX hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;
XX mycoplasma; food additive; antimicrobial activity; GS14.

OS Synthetic.
 XX WO9816549-A1.
 XX 23-APR-1998.
 PD
 XX 10-OCT-1997; 97WO-US018693.
 XX PF
 XX 11-OCT-1996; 96US-0028315P.
 XX PR
 XX (PENCE-) PENCE INC.
 XX PA (DEHL/) DEHLINGER P J.
 XX PI Kondejewski LH, Hodges RS, Wishart DS, Hancock RM, McElhaney R;
 XX PI Premier EJ, Lewis RNAH;
 XX DR WPI; 1998-251231/22.
 XX
 PT Cyclic peptide analogues of gramicidin S with broad spectrum
 PT antimicrobial activity - and reduced haemolytic activity, have beta-
 PT pleated sheet structure disrupted or eliminated by amino acid
 PT substitutions.
 XX
 XX PS Claim 39; Page 65; 88pp; English.
 XX
 CC The invention provides for cyclic peptide analogues of gramicidin S14
 CC (GS14; AAM48876) such as the present one. These cyclic peptide GS14
 CC analogues do not have the beta-pleated structure present in GS as, for
 CC e.g., residues 2, 4, 5 and 8-11 of the present cyclic peptide would be
 CC substituted with the respective D-form residue. These analogues are
 CC claimed to have an advantage over GS as they have broad spectrum
 CC antimicrobial activity and an increased therapeutic index because they
 CC lack the hemolytic effect of GS. The cyclic peptide GS14 analogues are
 CC also claimed to be useful therapeutically in human or veterinary medicine
 CC to kill or inhibit Gram-positive and Gram-negative bacteria, fungi and
 CC mycoplasma. They may also be used to control mycoplasma contamination of
 CC cultured cells and as food additives
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 45.7%; Score 37.5; DB 2; Length 14;
 Best Local Similarity 69.2%; Pred. No. 19;
 Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 QY 1 LKPPKLVKVEVP 13
 ||| ||| ||| |||
 Db 3 LKVFP-LKVQLFP 14
 XX
 RESULT 18
 AAM48904
 ID AAM48904 standard; peptide; 14 AA.
 XX
 AC AAM48904;
 XX
 DT 23-SEP-1998 (first entry)
 XX
 DE Cyclic peptide gramicidin S14 analogue Y2/F2.
 XX
 KW Cyclic; gramicidin S; GS; beta-pleated structure; therapeutic index;
 KW hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;
 KW mycoplasma; food additive; antimicrobial activity.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1..14
 FT /note= "Residue 1 is in a peptide linkage with residue
 FT 14"
 FT Misc-difference 4
 FT /note= "D-form residue"
 FT 6
 FT Misc-difference
 FT /note= "D-form residue"

FT Misc-difference 13
 FT /note= "D-form residue"
 FT
 XX WO9816549-A1.
 XX 23-APR-1998.
 PD
 XX 10-OCT-1997; 97WO-US018693.
 XX PF
 XX 11-OCT-1996; 96US-0028315P.
 XX PR
 XX (PENCE-) PENCE INC.
 XX PA (DEHL/) DEHLINGER P J.
 XX PI Kondejewski LH, Hodges RS, Wishart DS, Hancock RM, McElhaney R;
 XX PI Premier EJ, Lewis RNAH;
 XX DR WPI; 1998-251231/22.
 XX
 PT Cyclic peptide analogues of gramicidin S with broad spectrum
 PT antimicrobial activity - and reduced haemolytic activity, have beta-
 PT pleated sheet structure disrupted or eliminated by amino acid
 PT substitutions.
 XX
 XX PS Disclosure; Page 45; 88pp; English.
 XX
 CC The invention provides for cyclic peptide analogues of gramicidin S14
 CC (GS14; AAM48876), such as the present one. These cyclic peptide GS14
 CC analogues do not have the beta-pleated structure present in gramicidin S
 CC (GS). These analogues are claimed to have an advantage over GS as they
 CC have broad spectrum antimicrobial activity and an increased therapeutic
 CC index because they lack the hemolytic effect of GS. The cyclic peptide
 CC GS14 analogues are also claimed to be useful therapeutically in human or
 CC veterinary medicine to kill or inhibit Gram-positive and -negative
 CC bacteria, fungi and mycoplasma. They may also be used to control
 CC mycoplasma contamination of cultured cells and as food additives
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 45.7%; Score 37.5; DB 2; Length 14;
 Best Local Similarity 69.2%; Pred. No. 19;
 Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 QY 1 LKPPKLVKVEVP 13
 ||| ||| ||| |||
 Db 3 LKVFP-LKVQLFP 14
 XX
 RESULT 19
 ABB41738
 ID ABB41738 standard; peptide; 18 AA.
 XX
 AC ABB41738;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Peptide #9244 encoded by human foetal liver single exon probe.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.
 KW
 OS Homo sapiens.
 OS
 XX WO200157277-A2.
 XX
 XX 09-AUG-2001.
 XX
 PD 30-JAN-2001; 2001WO-US000669.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.

```
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 34373; 639bp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 18 AA;

Query Match          45.1%; Score 37; DB 4; Length 18;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      8 KVEVFPFP 15
       :||| |||
       3 RVEAFPPF 10
DB
XX
RESULT 20
ID AAM35535 standard; protein; 18 AA.
XX
AC AAM35535;
XX
XX 17-OCT-2001 (first entry)
DT
XX Peptide #9572 encoded by probe for measuring placental gene expression.
DE
XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 35804; 654bp; English.
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XX
XX The present invention relates to single exon nucleic acid probes (SENPs;
CC see A431315-A4157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
XX Sequence 18 AA;

Query Match          45.1%; Score 37; DB 4; Length 18;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      8 KVEVFPFP 15
       :||| |||
       3 RVEAFPPF 10
DB
XX
RESULT 21
ID ABB25488 standard; protein; 18 AA.
XX
AC ABB25488;
XX
XX 23-JAN-2002 (first entry)
DT
XX Protein #7487 encoded by probe for measuring heart cell gene expression.
DE
XX Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
XX Claim 15; SEQ ID NO 27258; 530bp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
```

SQ Sequence 18 AA;

Query Match 45.1%; Score 37; DB 4; Length 18;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 KVEVFPFP 15
 :|||
 Db 3 RVEAFPPF 10

RESULT 22

AAM75423
 ID AAM75423 standard; protein; 18 AA.

AC AAM75423;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 35729.

KW Human; bone marrow expressed exon; gene expression analysis; probe;
 microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human bone marrow.

XX Example 4; SEQ ID NO 35729; 658bp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention

Query Match 45.1%; Score 37; DB 4; Length 18;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 KVEVFPFP 15
 :|||
 Db 3 RVEAFPPF 10

RESULT 23

AAM62611
 ID AAM62611 standard; protein; 18 AA.

AC AAM62611;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 34716.

KW Human; brain expressed exon; gene expression analysis; probe; microarray;
 Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

OS Homo sapiens.

PN WO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000667.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human

XX brains.

CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention

XX Sequence 18 AA;

Query Match 45.1%; Score 37; DB 4; Length 18;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 KVEVFPFP 15
 :|||
 Db 3 RVEAFPPF 10

RESULT 24

ABG57176
 ID ABG57176 standard; peptide; 18 AA.

AC ABG57176;

DT 25-FEB-2003 (first entry)

DE Human liver peptide, SEQ ID NO 35824.

KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 hypercholesterolaemia; coronary heart disease.

OS Homo sapiens.

PN WO200157273-A2.

PD 09-AUG-2001.

```

XX PF 30-JAN-2001; 2001WO-US000664.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PT Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488898/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human adult liver.
XX PS Claim 27; SEQ ID NO 35824; 658bp; English.
XX CC The invention relates to a single exon nucleic acid probe (SENP) (1) for
XX CC measuring human gene expression in a sample derived from human adult
XX CC liver, comprising one of 13109 defined nucleotide sequences given in the
XX CC specification (or complements/ fragments). The probe hybridizes at high
XX CC stringency to a nucleic acid molecule expressed in the human adult liver.
XX CC (1) may be used for predicting, measuring and displaying gene expression
XX CC in samples derived from human adult liver. The genes identified may be
XX CC involved in genetic liver diseases such as cirrhosis,
XX CC hyperlipoproteinemia, hyperlipidaemia and hypercholesterolaemia which is
XX CC associated with coronary heart disease. ABG47348-ABG59930 represent human
XX CC liver single exon encoded peptides of the invention. Note: The sequence
XX CC information for this patent does not appear in the printed specification
XX CC but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 18 AA;
XX
XX Query Match 45.1%; Score 37; DB 4; Length 18;
XX Best Local Similarity 75.0%; Pred. No. 31;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 8 KVEVPPFP 15
XX :|||
XX Db 3 RVEAPFP 10
XX
XX RESULT 25
XX ID ABG45003
XX ID ABG45003 standard; peptide; 18 AA.
XX AC ABG45003;
XX DT 19-AUG-2002 (first entry)
XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 34668.
XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX KW chronic obstructive pulmonary disease; interstitial lung disease;
XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
XX KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX KW primary ciliary dyskinesia; pulmonary hypertension;
XX KW hyaline membrane disease.
XX XX Homo sapiens.
XX OS
XX XX MO200186003-A2.
XX PN
XX XX 15-NOV-2001.
XX PD

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XX PF 30-JAN-2001; 2001WO-US000665.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PT Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2002-114183/15.
XX PT Spatially-addressable set of single exon nucleic acid probes, used to
XX PT measure gene expression in human lung samples.
XX PS Claim 27; SEQ ID NO 34668; 634p; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human lung comprising single exon nucleic acid probes having one of
XX CC 12614 nucleic acid sequences mentioned in the specification, or their
XX CC complements or the 12387 open reading frames derived from the 12614
XX CC probes. Also included are a microarray comprising the novel set of probes
XX CC ; the novel set of probes which hybridize at high stringency to a nucleic
XX CC acid expressed in the human lung; measuring gene expression in a sample
XX CC collected from human lung; contacting the array with a
XX CC collection of detectably labeled nucleic acids derived from human lung
XX CC mRNA, and (b) measuring the label detectably bound to each probe of the
XX CC array; identifying exons in a eukaryotic genome, comprising (a)
XX CC algorithmically predicting at least one exon from genomic sequences of
XX CC the eukaryote; and (b) detecting specific hybridization of detectably
XX CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX CC having a fragment identical to the predicted exon, the probe is included
XX CC in the above mentioned microarray; assigning exons to a single gene,
XX CC comprising (a) identifying exons from genomic sequence by the method
XX CC 'above and (b) measuring the expression of each of the exons in several
XX CC tissues and/or cell types using hybridization to a single exon
XX CC microarrays having a probe with the exon, where a common pattern of
XX CC expression of the exons in the tissues and/or cell types indicates that
XX CC the exons should be assigned to a single gene; a peptide comprising one
XX CC of 12011 sequences, mentioned in the specification, or encoded by the
XX CC probes/open reading frames (ORF). The probes are used for gene expression
XX CC analysis, and for identifying exons in a gene, particularly using human
XX CC lung derived mRNA and for the study of lung diseases such as asthma, lung
XX CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
XX CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
XX CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
XX CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
XX CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
XX CC Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary
XX CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
XX CC present sequence is a peptide/protein encoded by a single exon probe of
XX CC the invention. Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 18 AA;
XX
XX Query Match 45.1%; Score 37; DB 5; Length 18;
XX Best Local Similarity 75.0%; Pred. No. 31;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 8 KVEVPPFP 15
XX :|||
XX Db 3 RVEAPFP 10
XX
XX RESULT 26

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AAB72520
 ID AAB72520 standard; peptide; 18 AA.
 XX
 AC AAB72520;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostretin peptide #21.
 XX
 KW Dermatological; oxidative stress regulator; colostretin.
 OS
 XX Unidentified.
 PN WO200112650-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US022665.
 XX
 PR 17-AUG-1999; 99US-0149310P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2001-218342/22.
 XX
 PT Modulating oxidative stress level in a cell, involves contacting the cell
 PT with an oxidative stress regulator selected from colostretin, its
 PT constituent peptide, analog or their combinations.
 PS
 XX Claim 6; Page 26; 48pp; English.
 CC
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostretin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient
 XX
 SQ Sequence 18 AA;

 QY Query Match 43.9%; Score 36; DB 4; Length 18;
 Best Local Similarity 70.0%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0
 DB 3 PPKKAKVEVP 12
 5 PPKKYPVEVP 14

 RESULT 27
 AAB59330
 ID AAB59330 standard; peptide; 18 AA.
 XX
 AC AAB59330;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Ewe colostretin peptide fragment C-5.
 XX
 KW Sheep; colostretin; proline rich polypeptide; colostrum; immune disorder;
 KM central nervous system disorder; dietary supplement; beta-amyloid plaque.
 OS
 XX Ovis sp.
 PN WO200075173-A2.
 XX
 PD 14-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-GB002128.
 XX

XX	DR	02-JUN-1999;	99GB-00012852.
XX	PA	(REGG-) REGEN THERAPEUTICS PLC.	
XX	P1	Georgiades JA;	
XX	DR	WPI; 2001-071056/08.	
XX	PT	Peptides having an N-terminal amino acid sequence isolated from	
XX	PT	colostriatin for treating e.g. disorders of the central nervous system and	
XX	PT	immune system, viral and bacterial infections, and diseases characterized	
XX	PT	by amyloid plaques.	
XX	PS	Claim 7; Page 27; 63pp; English.	
XX	CC	The present invention provides the sequences of a number of peptides	
XX	CC	found in ewe's colostrum. Colostrin is the proline-rich polypeptide	
XX	CC	fragment of colostrum. These peptides can be used in the treatment of	
XX	CC	central nervous system disorders such as senile dementia, Parkinson's	
XX	CC	disease, Alzheimer's disease, psychosis and neurosis, immune system	
XX	CC	disorders such as bacterial and viral infections, to improve the	
XX	CC	development of a child's immune system, as a dietary supplement, and to	
XX	CC	promote the dissolution of beta-amyloid plaques	
SQ		Sequence 18 AA;	
OY		Query Match 43.9%; Score 36; DB 4; Length 18;	
Dd		Best Local Similarity 70.0%; Pred. No. 46;	
		Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
		3 PEPKATVEVF 12	
		5 PPKCYVPEPF 14	
RESULT 28			
AAB72267	ID	AAB72267 standard; peptide; 18 AA.	
AAB72267;	AC		
.14-MAY-2001	DT	(first entry)	
Colostrin derived cytokine inducing peptide SEQ ID 22.	DE		
Colostrin; immune response; cytokine; blood cell proliferation;	DS		
central nervous system disorder; neurological disorder; mental disorder;	KM		
dementia; neurodegenerative disease; Alzheimer's disease; psychosis;	KW		
neurosis; infection.	KX		
Synthetic.	OS		
WO200111937-A2.	PN		
22-FEB-2001.	PD		
17-AUG-2000; 2000MO-US022818.	PF		
17-AUG-1999; 99US-0149311P.	PR		
(TEKA) UNIV TEXAS SYSTEM.	XA		
(REGG-) REGEN THERAPEUTICS PLC.	PA		
Stanton GJ, Hughes TK, Boldogh I, Georgiades J;	PI		
WPI; 2001-202804/20.	WP		
Inducing a cytokine and modulating an immune response, useful for	PT		
treating central nervous system diseases and bacterial and viral	PT		
infections, comprises administering colostrin as an immunological	PT		
regulator.	PT		
Claim 1; Page 34; 50pp; English.	XS		

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XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The peptides
CC have immune response modulatory activity, and are capable of inducing
CC cytokine production, for modulating an immunological response and for
CC inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies
XX
SQ Sequence 18 AA;

Query Match      43.9%; Score 36; DB 4; Length 18;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPKLKVEVF 12
   |||||
DB 5 PPKKYPVEPF 14

RESULT 29
AAB72552
ID AAB72552 standard; peptide; 18 AA.
XX
AC AAB72552;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #21.
XX
KW Neuropeptide; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
OS Unidentified.
XX
PN WO200112651-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US022774.
XX
PR 17-AUG-1999; 99US-0149633P.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Boldogh I;
XX
PI WPI; 2001-226545/23.
XX
DR
XX
PT Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating damaged
PT neural cells in a patient.
XX
PS Claim 6; Page 21; 35pp; English.
XX
CC The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
XX
SQ Sequence 18 AA;

Query Match      43.9%; Score 36; DB 4; Length 18;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPKLKVEVF 12
   |||||
DB 5 PPKKYPVEPF 14

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RESULT 30
AA014598
ID AA014598 standard; peptide; 18 AA.
XX
AC AA014598;
XX
DT 27-MAY-2002 (first entry)
XX
DE Neural cell regulatory colostrinin peptide 21.
XX
KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
KW neural cell treatment.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FH Modified-site 18 /note="Optional C-terminal amide"
FT
FT
XX
PN WO200213851-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022777.
XX
PR 17-AUG-2000; 2000WO-US022777.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Boldogh I, Stanton JG, Hughes TK;
XX
PI WPI; 2002-269152/31.
XX
DR
XX
PT Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX
PS Claim 7; Page 21; 37pp; English.
XX
CC The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention
XX
SQ Sequence 18 AA;

Query Match      43.9%; Score 36; DB 5; Length 18;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPKLKVEVF 12
   |||||
DB 5 PPKKYPVEPF 14

RESULT 31
AAM51056
ID AAM51056 standard; peptide; 18 AA.
XX
AC AAM51056;
XX
DT 30-MAY-2002 (first entry)
XX
DE Colostrinin constituent peptide (casein amino acids 121-138).
XX

```

KW Colostrotin; colostrotin; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; beta-casein; human.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT Modified-site 18
FT /note="optional C-terminal amidation"
XX
XX WO200213849-A1.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US022775.
XX
XX 17-AUG-2000; 2000WO-US022775.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX (REGS-) REGEN THERAPEUTICS PLC.
XX
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX WPI; 2002-269150/31.
XX
XX Modulation of blood cell proliferation in a patient involves use of blood
PT cell regulator selected from colostrotin, its constituent peptide and/or
PT analog.
XX
XX Claim 1; Page 34; 54pp; English.
XX
XX The present sequence is that of a colostrotin constituent peptide that is
CC preferred for use as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. It is classified as having
CC a beta-casein homologue precursor, and corresponds to casein amino acids
CC 121-138. Methods are claimed for: inducing a cytokine in a cell by
CC contact with an immunological regulator, where the cell is present in a
CC cell culture, a tissue, an organ or an organism, and the cell is
CC mammalian, including human; modulating an immune response in a cell by
CC contract with the immunological regulator under conditions effective to
CC induce a cytokine; modulating an immune response in a patient by
CC administering an immunological regulator under conditions effective to
CC induce a cytokine, where the immunological regulator is administered
CC topically or as part of a dietary supplement, and where the immune
CC response is specific or non specific, an interferon response or an
CC antibody response; modulating blood cell proliferation by contacting
CC blood cells with a blood cell regulator, where the blood cells are
CC present in a cell culture or an organism, are mammalian or human, and
CC where the blood cells are increased in number or differentiated; and a
CC method for modulating blood cell proliferation in a patient. A claimed
CC cytokine-inducing composition comprises a pharmaceutical carrier and an
CC active agent such as the present peptide. Cytokines induced by this
CC peptide in human leucocyte cultures include interferon-gamma, tumour
CC necrosis factor-alpha and interleukin-10
XX
XX SQ Sequence 18 AA;
XX
XX Query Match 43.9%; Score 36; DB 5; Length 18;
XX Best Local Similarity 70.0%; Pred. No. 46;
XX Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 3 PPKPKVEVF 12
XX |||||
XX 5 PPKKYPVEPF 14
XX
XX Db
XX
XX RESULT 32
XX AAE20249
XX ID AAE20249 standard; peptide; 18 AA.
XX
XX AC AAE20249;
XX
XX 18-JUN-2002 (first entry)
XX

DE Colostrotin constituent peptide #21.
XX
XX Blood cell regulator; colostrotin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnery.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FT Modified-site 18
FT /note="Optionally C-terminal amide"
XX
XX WO200213850-A1.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US022776.
XX
XX 17-AUG-2000; 2000WO-US022776.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
XX WPI; 2002-269151/31.
XX
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrotin, its
PT constituent peptide and/or analog.
XX
XX Claim 6; Page 26; 51pp; English.
XX
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrotin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress level
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
CC organ, or organism; or for treating oxidative damage to the skin of a
CC patient e.g. animal or human; to modulate oxidative stress during/ after
CC a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrotin constituent peptide
XX
XX SQ Sequence 18 AA;
XX
XX Query Match 43.9%; Score 36; DB 5; Length 18;
XX Best Local Similarity 70.0%; Pred. No. 46;
XX Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 3 PPKPKVEVF 12
XX |||||
XX 5 PPKKYPVEPF 14
XX
XX Db
XX
XX RESULT 33
XX ADN60316
XX ID ADN60316 standard; peptide; 18 AA.
XX
XX AC ADN60316;
XX
XX 29-JUL-2004 (first entry)
XX
XX Constituent peptide of colostrotin SEQ ID NO:22.
XX

KM modulator; colostretin; intracellular signaling molecule modulator;
 KM 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibitor;
 KM DNA damage; beta-amyloid; retinoic acid; cytosolic; 4HNE inhibitor;
 KM 4HNE-protein adduct formation reduction;
 KM 4HNE-mediated glutathione depletion inhibition; p53 inhibition;
 KM c-Jun NH2-terminal Kinase inhibition.
 XX Synthetic.
 XX WO2004037851-A2.
 XX PD 06-MAY-2004.
 XX PF 22-OCT-2003; 2003WO-US033423.
 XX PR 22-OCT-2002; 2002US-0420369P.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PA (BOLD) BOLDG I.
 XX PA (STAN) STANTON J G.
 XX PA (GEOR) GEORGIADIS J A.
 XX PA (HUGH) HUGHES T K.
 XX PA (KRUI) KRUIZEL M.
 XX PT Boldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;
 XX WPI; 2004-365494/34.
 XX DR Use of colostretin for e.g. modulating an intracellular signaling
 PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a
 PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
 PT a cell.
 XX PS Claim 6; SEQ ID NO 22; 46pp; English.
 XX CC The present invention describes the use of a modulator selected from
 CC colostretin, its constituent peptide, its active analogue, and a
 CC combination of these, for modulating an intracellular signaling molecule
 CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
 CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
 CC The modulator has cytostatic activity, and can be used as a 4HNE
 CC inhibitor. The modulator is useful in the manufacture of a medicament for
 CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated
 CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,
 CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.
 CC Colostretin, or its constituent peptide or active analogue is useful for
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
 CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
 CC The present sequence represents a synthetic constituent peptide of
 CC colostretin, which can be used as a modulator in the present invention.
 XX CC
 XX SQ Sequence 18 AA;
 SQ
 Query Match 43.9%; Score 36; DB 8; Length 18;
 Best Local Similarity 70.0%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 PPKKLVVEVF 12
 DB 5 PPKKLVVEVF 14
 RESULT 34
 ADS74406
 ID ADS74406 standard; peptide; 18 AA.
 AC ADS74406;
 XX
 XX DT 16-DEC-2004 (first entry)
 XX DE Ovine colostretin peptide.
 XX

KM Colostretum; colostretin; sheep; peptide purification.
 XX Ovis aries.
 XX OS
 XX WO2004081038-A1.
 XX PN
 XX PD 23-SEP-2004.
 XX PF 10-MAR-2004; 2004WO-GB001014.
 XX PR 11-MAR-2003; 2003GB-00005552.
 XX PR 08-MAR-2004; 2004GB-00005190.
 XX PA (REGG) REGEN THERAPEUTICS PLC.
 XX PI Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;
 XX WPI; 2004-677519/66.
 XX DR Recovering peptides such as colostretin from mammalian colostretum, by
 PT mixing colostretum with alcohol to form alcohol phase containing peptides
 PT and precipitate, separating alcohol phase from precipitate, and
 PT recovering alcohol phase.
 XX PS Disclosure; SEQ ID NO 23; 41pp; English.
 XX CC The present sequence is that of a peptide that can be recovered from
 CC ovine colostretin using the method of the invention. The invention
 CC provides a method for the recovery of peptides (especially colostretin)
 CC from colostretum in substantially pure, biologically active form and in
 CC high yield. The method involves mixing the colostretum with an alcohol to
 CC form an alcohol phase containing the colostretin and a precipitate
 CC containing higher molecular weight caseins and other proteins. Best
 CC results are obtained using methanol or ethanol of at least 80%, and
 CC preferably up to 100%, purity. The alcohol phase is then separated from
 CC the precipitate, and the colostretin is separated from the alcohol,
 CC preferably by evaporation, to form a colostretin-rich phase, which is
 CC recovered. A precipitation agent, such as ammonium sulfate, may be added
 CC either to the alcohol phase or, preferably, to the colostretin-rich phase
 CC to induce precipitation of the colostretin peptides. The method is
 CC generally applicable to the separation of peptides from fluids containing
 CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic
 CC acids.
 XX CC
 XX SQ Sequence 18 AA;
 SQ
 Query Match 43.9%; Score 36; DB 8; Length 18;
 Best Local Similarity 70.0%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 PPKKLVVEVF 12
 DB 5 PPKKLVVEVF 14
 RESULT 35
 ADH14831
 ID ADH14831 standard; peptide; 16 AA.
 AC ADH14831;
 XX
 XX DT 11-MAR-2004 (first entry)
 XX DE Gliadin related epitope peptide.
 XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 XX vaccine.
 XX OS Synthetic.
 XX PN WO2003104273-A2.
 XX PD 18-DEC-2003.
 XX

CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostriin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostriin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostriin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child. The
 CC present sequence is colostriin peptide 4 related to the invention

CC Sequence 10 AA;

Query Match 42.1%; Score 34.5; DB 4; Length 10;
 Best Local Similarity 81.8%; Pred. No. 43;
 Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 5 PRLKXVEVPFP 15
 |||||
 Db 1 PRLKXVEV-PEP 10

RESULT 38

AAE07198 standard; peptide; 11 AA.

AAE07198;
 06-NOV-2001 (first entry)

Modified colostriin cyclic peptide #4.

Colostriin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 central nervous system disorder; neurodegenerative disorder; weight loss;
 beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 acquired immunological deficiency; neurological disorder; dementia;
 antiviral; cyclic.

Synthetic.

Key Location/Qualifiers
 Modified-site 1 /note="N-terminal acetyl; this residue forms a cyclic
 linkage with Pro found at the C-terminal end"

WO20015199-A1.

02-AUG-2001.

26-JAN-2001; 2001WO-GB000329.

26-JAN-2000; 2000GB-00001825.

(REGG-) REGEN THERAPEUTICS PLC.

Georgiades JA;

WPI; 2001-488775/53.

Peptide useful as an interalia in the treatment of e.g. disorders of the
 immune system and the central nervous system comprises ten amino-terminal
 amino acid sequence derived from peptides present in colostriin.

Example 2; Page 8; 40pp; English.

The invention relates to colostriin peptide fragments which are useful,
 inter alia, in the treatment of chronic disorders of the immune system
 and the central nervous system. Colostriin peptides are used as a

CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostriin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostriin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostriin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child. The
 CC present sequence is modified colostriin cyclic peptide #4 related to the
 CC invention

CC Sequence 11 AA;

Query Match 42.1%; Score 34.5; DB 4; Length 11;
 Best Local Similarity 81.8%; Pred. No. 48;
 Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 5 PRLKXVEVPFP 15
 |||||
 Db 2 PRLKXVEV-PEP 11

RESULT 39

AAW48877 standard; peptide; 14 AA.

AAW48877;

23-SEP-1998 (first entry)

Cyclic peptide gramicidin S14 (GS14) analogue 1.

Cyclic; gramicidin S14; GS; beta-pleated structure; therapeutic index;
 hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;
 mycoplasma; food additive; antimicrobial activity; GS14.

Synthetic.

Key Location/Qualifiers
 Misc-difference 1..14 /note="Residue 1 is in a peptide linkage with residue
 14"

Misc-difference 2 /note="Optionally D-form residue"

Misc-difference 4 /note="Optionally D-form residue"

Misc-difference 5 /note="Optionally D-form residue"

Misc-difference 6 /note="Optionally D-form residue"

Misc-difference 8 /note="D-form residue"

Misc-difference 9 /note="Optionally D-form residue"

Misc-difference 10 /note="Optionally D-form residue"

Misc-difference 11 /note="Optionally D-form residue"

Misc-difference 13 /note="Optionally D-form residue"

WO9816549-A1.

23-APR-1998.

10-OCT-1997; 97WO-US018693.

```

XX 11-OCT-1996; 96US-0028315P.
PR (PENC-) PENCE INC.
XX (DEHL/) DEHLINGER P J.
PA Kondejowski LH, Hodges RS, Wishart DS, Hancock REM, McElhaney R;
XX Premier EJ, Lewis RNAH;
XX WPI; 1998-251231/22.
DR
XX
XX Cyclic peptide analogues of gramicidin S with broad spectrum
PT antimicrobial activity - and reduced haemolytic activity, have beta-
PT pleated sheet structure disrupted or eliminated by amino acid
PT substitutions.
XX
XX Claim 39; Page 65; 88pp; English.
PS
XX The invention provides for cyclic peptide analogues of gramicidin S14
CC (GS14; AAM48876) such as the present one. These cyclic peptide GS14
CC analogues do not have the beta-pleated structure present in GS as, for
CC e.g. residues 2, 4, 5 and 8-11 of the present cyclic peptide would be
CC substituted with the respective D-form residue. These analogues are
CC claimed to have an advantage over GS as they have broad spectrum
CC antimicrobial activity and an increased therapeutic index because they
CC lack the hemolytic effect of GS. The cyclic peptide GS14 analogues are
CC also claimed to be useful therapeutically in human or veterinary medicine
CC to kill or inhibit Gram-positive and Gram-negative bacteria, fungi and
CC mycoplasma. They may also be used to control mycoplasma contamination of
CC cultured cells and as food additives
XX
XX Sequence 14 AA:
SQ
Query Match 42.1%; Score 34.5; DB 2; Length 14;
Best Local Similarity 61.5%; Pred. No. 62;
Matches 8; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
QY 1 LKPPKLYEVFP 13
Db 3 LKVP-LKVKLP 14
RESULT 40
AAM48878
ID AAM48878 standard; peptide; 14 AA.
XX
XX AAM48878;
AC
XX
XX 23-SEP-1998 (first entry)
DT
XX
XX Cyclic peptide gramicidin S14 (GS14) analogue 2.
DE
XX Cyclic; gramicidin S14; GS; beta-pleated structure; therapeutic index;
KW hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;
XX mycoplasma; food additive; antimicrobial activity; GS14.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 1.14
FT /note= "Residue 1 is in a peptide linkage with residue
FT 14"
FT Misc-difference 2
FT /note= "Optionally D-form residue"
FT Misc-difference 4
FT /note= "Optionally D-form residue"
FT Misc-difference 5
FT /note= "Optionally D-form residue"
FT Misc-difference 6
FT /note= "D-form residue"
FT Misc-difference 8
FT /note= "Optionally D-form residue"
FT Misc-difference 9

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FT /note= "Optionally D-form residue"
FT Misc-difference 10
FT /note= "Optionally D-form residue"
FT Misc-difference 11
FT /note= "Optionally D-form residue"
FT Misc-difference 13
FT /note= "D-form residue"
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XX WO9816549-A1.
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XX 23-APR-1998.
XX
XX 10-OCT-1997; 97WO-US018693.
XX
XX 11-OCT-1996; 96US-0028315P.
XX
XX (PENC-) PENCE INC.
PA (DEHL/) DEHLINGER P J.
XX
XX Kondejowski LH, Hodges RS, Wishart DS, Hancock REM, McElhaney R;
PI Premier EJ, Lewis RNAH;
XX WPI; 1998-251231/22.
DR
XX
XX Cyclic peptide analogues of gramicidin S with broad spectrum
PT antimicrobial activity - and reduced haemolytic activity, have beta-
PT pleated sheet structure disrupted or eliminated by amino acid
PT substitutions.
XX
XX Claim 39; Page 65; 88pp; English.
PS
XX
XX The invention provides for cyclic peptide analogues of gramicidin S14
CC (GS14; AAM48876) such as the present one. These cyclic peptide GS14
CC analogues do not have the beta-pleated structure present in GS as, for
CC e.g. residues 2, 4, 5 and 8-11 of the present cyclic peptide would be
CC substituted with the respective D-form residue. These analogues are
CC claimed to have an advantage over GS as they have broad spectrum
CC antimicrobial activity and an increased therapeutic index because they
CC lack the hemolytic effect of GS. The cyclic peptide GS14 analogues are
CC also claimed to be useful therapeutically in human or veterinary medicine
CC to kill or inhibit Gram-positive and Gram-negative bacteria, fungi and
CC mycoplasma. They may also be used to control mycoplasma contamination of
CC cultured cells and as food additives
XX
XX Sequence 14 AA:
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Query Match 42.1%; Score 34.5; DB 2; Length 14;
Best Local Similarity 61.5%; Pred. No. 62;
Matches 8; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
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Db 3 LKVP-LKVKLP 14
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OM protein - protein search, using sw model

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Minimum DB seq length: 0
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	31	37.8	16	1	US-07-906-871-3
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7	28	34.1	14	3	US-09-369-364A-29
8	27.5	33.5	14	3	US-08-949-059A-7
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12	27	32.9	11	4	US-09-129-366-25
13	27	32.9	12	4	US-09-095-639A-3
14	27	32.9	12	4	US-09-095-639A-4
15	27	32.9	14	3	US-09-092-000-1
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18	27	32.9	15	4	US-09-774-633-257
19	27	32.9	16	1	US-08-335-844A-16
20	27	32.9	16	3	US-08-335-844A-10
21	27	32.9	16	4	US-09-129-366-40
22	26.5	32.3	13	3	US-08-915-314-22
23	26.5	32.3	13	3	US-08-702-054B-28
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26	26.5	32.3	13	4	US-09-030-619-100
27	26.5	32.3	13	4	US-09-667-486-22

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37	26	31.7	17	4	US-09-552-802B-40	Sequence 40, Appl
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57	25	30.5	16	4	US-09-489-887-252	Sequence 252, App
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94	24	29.3	9	3	US-09-231-797-128	Sequence 128, App
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96	24	29.3	9	3	US-08-933-843-128	Sequence 128, App
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100	24	29.3	9	3	US-09-413-492-128	Sequence 128, App

ALIGNMENTS

RESULT 1
US-09-641-803-8
; Sequence 8, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-8

Query Match 100.0%; Score 82; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPPKLVKVEVFPF 15
| | | | | | | | | | | | | | |
DB 1 LKPPKLVKVEVFPF 15

RESULT 2
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; Sequence 22, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-22

Query Match 43.9%; Score 36; DB 4; Length 18;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPKKLVKVEVFP 12
| | | | | | | | | | | | | | |
DB 5 PPKKLVKVEVFP 14

RESULT 3
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; Sequence 5, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-5

Query Match 41.5%; Score 34; DB 4; Length 15;
Best Local Similarity 70.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLKLVKVEVFPF 14
| | | | | | | | | | | | | | |
DB 5 PVLKLVKVEVFPF 14

RESULT 4
US-09-385-442-39
; Sequence 39, Application US/09385442
; Patent No. 6200954
; GENERAL INFORMATION:
; APPLICANT: Ge, Ruowen
; APPLICANT: KIM, R. Manjunatha
; TITLE OF INVENTION: Small Peptides Having Potent Anti-Angiogenic Activity
; FILE REFERENCE: 1781-170P
; CURRENT APPLICATION NUMBER: US/09/385,442
; PRIOR FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 60/099,313
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 13
; TYPE: PRT
; ORGANISM: mammalian
; FEATURE:
; OTHER INFORMATION: SHPLT2
US-09-385-442-39

Query Match 37.8%; Score 31; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKPPKLVKVEVFP 12
| | | | | | | | | | | | | | |
DB 1 LVPLPKKINSTR 12

RESULT 5
US-07-906-871-3
; Sequence 3, Application US/07906871
; Patent No. 5340739

GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: HEMATOPOIETIC CELL SPECIFIC
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY ELEMENTS OF SERGLYCIN AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,871
FILING DATE: 19920103
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/07/816,289
FILING DATE: 03 JAN 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/635,544
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03051
FILING DATE: 13-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/224,035
FILING DATE: 13-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.2830004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)833-8716
FAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: AMINO ACID
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-906-871-3

Query Match 37.8%; Score 31; DB 1; Length 16;
Best Local Similarity 44.4%; Pred. No. 1e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 PKLXKVEVP 13
|:|:|:|:|:
Db 5 PRLRTDLP 13

RESULT 6
US-08-477-928A-26
Sequence 26, Application US/08477928A
Patent No. 6207389
GENERAL INFORMATION:
APPLICANT: Dosch, Hans M.
TITLE OF INVENTION: METHODS FOR CONTROLLING T
TITLE OF INVENTION: LYMPHOCYTE MEDIATED IMMUNE RESPONSES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS
STREET: 1299 Pennsylvania Avenue
CITY: Washington D.C.

STATE: California
COUNTRY: U.S.A.
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,928A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36902
REFERENCE/DOCKET NUMBER: 19060-0105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 639 7700
FAX: (202) 639 7890
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-928A-26

Query Match 35.4%; Score 29; DB 3; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KPPLKXVEY 11
|:|:|:|:|:
Db 4 KNFDLKNVD 13

RESULT 7
US-09-369-364A-29
Sequence 29, Application US/09369364A
Patent No. 6391610
GENERAL INFORMATION:
APPLICANT: Apte, Suneel
APPLICANT: Hurekainen, Tina L.
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 14
TYPE: PRT
ORGANISM: synthetic construct
US-09-369-364A-29

Query Match 34.1%; Score 28; DB 3; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKPPKXK 8
|:|:|:|:|:
Db 6 LKPPKXK 13

RESULT 8
US-08-949-059A-7
Sequence 7, Application US/08949059A
Patent No. 6358921
GENERAL INFORMATION:
APPLICANT: Kondejewski, Leslie H.
APPLICANT: Hodges, Robert S.

```
/ APPLICANT: Wishart, David S.
/ APPLICANT: Hancock, Robert E.W.
/ APPLICANT: McElhane, Ronald N.
/ APPLICANT: Premier, Elmer J.
/ APPLICANT: Lewis, Ruthven N.A.H
/ TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
/ TITLE OF INVENTION: METHOD
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: SEED AND BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/949,059A
/ FILING DATE: 10-OCT-1997
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mcmasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 660081.412
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: cyclic
/ MOLECULE TYPE: Peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 13
/ OTHER INFORMATION: /note="Residue is a D-Tyrosine"
/
US-08-949-059A-7

Query Match 33.5%; Score 27.5; DB 3; Length 14;
Best Local Similarity 53.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

OY 1 LKPPKLVKVEVP 13
||| ||||:|
DB 3 LKVP-LKVKLP 14

RESULT 9
US-08-949-059A-14
/ Sequence 14, Application US/08949059A
/ Patent No. 6358921
/ GENERAL INFORMATION:
/ APPLICANT: Kondejewski, Leslie H.
/ APPLICANT: Hodges, Robert S.
/ APPLICANT: Wishart, David S.
/ APPLICANT: Hancock, Robert E.W.
/ APPLICANT: McElhane, Ronald N.
/ APPLICANT: Premier, Elmer J.
/ APPLICANT: Lewis, Ruthven N.A.H
/ TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
/ TITLE OF INVENTION: METHOD
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: SEED AND BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
```

```
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/949,059A
/ FILING DATE: 10-OCT-1997
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mcmasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 660081.412
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: cyclic
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 6
/ OTHER INFORMATION: /note="Residue is a D-Tyrosine"
/
US-08-949-059A-14

Query Match 33.5%; Score 27.5; DB 3; Length 14;
Best Local Similarity 53.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

OY 1 LKPPKLVKVEVP 13
||| ||||:|
DB 3 LKVP-LKVKLP 14

RESULT 10
US-08-347-198A-1
/ Sequence 1, Application US/08347198A
/ Patent No. 5747046
/ GENERAL INFORMATION:
/ APPLICANT: MUNN, Edward A.
/ APPLICANT: SMITH, Trevor S.
/ TITLE OF INVENTION: PRODUCTION AND USE OF ANTHELMINTIC
/ TITLE OF INVENTION: AGENTS AND PROTECTIVE IMMUNOGENS
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: NIKAI DO, MARWELSTEIN, MURRAY & ORAM LLP
/ STREET: 655 Fifteenth Street, N. W., Suite 330 - G
/ CITY: Street Lobby
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 20005-5701
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/347,198A
/ FILING DATE: 21-NOV-1994
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/020,526
```


FILING DATE: 22-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/761,749
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00416
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 89906156.8
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: KITTIS, Monica C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P443-1289
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-347-198A-1

Query Match 32.9%; Score 27; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPKLKVVEF 12
: : : : :
Db 3 YPVVKEEF 11

RESULT 11
US-08-335-844A-25
Sequence 25, Application US/08335844A
Patent No. 6065503
GENERAL INFORMATION:
APPLICANT: GRAHAM, MARGARET
APPLICANT: SMITH, TREVOR STANLEY
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: KNOX, DAVID PATRICK
APPLICANT: OLIVER, JOANNA JANE
APPLICANT: NEWTON, SUSAN ELIZABETH
TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, F199, Ernst & Kurtz
STREET: Suite 701-E, 555 Thirteenth St., N.W
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,844A
FILING DATE: 09-JAN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9209936
FILING DATE: 08-MAY-1992
ATTORNEY/AGENT INFORMATION:

NAME: WALKER, Barbara W.
REGISTRATION NUMBER: 35,400
REFERENCE/DOCKET NUMBER: 1181-223A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-335-844A-25

Query Match 32.9%; Score 27; DB 3; Length 11;
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPKLKVVEF 12
: : : : :
Db 3 YPVVKEEF 11

RESULT 12
US-09-129-366-25
Sequence 25, Application US/09129366
Patent No. 6534638
GENERAL INFORMATION:
APPLICANT: GRAHAM, MARGARET
APPLICANT: SMITH, TREVOR STANLEY
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: KNOX, DAVID PATRICK
APPLICANT: OLIVER, JOANNA JANE
APPLICANT: NEWTON, SUSAN ELIZABETH
TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, F199, Ernst & Kurtz
STREET: Suite 701-E, 555 Thirteenth St., N.W
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/129,366
FILING DATE: 05-AUG-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/335,844
FILING DATE: 09-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9209936
FILING DATE: 08-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1181-241A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-129-366-25

Query Match 32.9%; Score 27; DB 4; Length 11;
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPKLVEVF 12
|:|:|:|:
DB 3 YPVVKEEF 11

RESULT 13
US-09-095-639A-3
; Sequence 3, Application US/09095639A
; Patent No. 6750203

GENERAL INFORMATION:
APPLICANT: POZZILI Paolo
TITLE OF INVENTION: Product derived from milk
TITLE OF INVENTION: substantially free of beta casein from non-human
TITLE OF INVENTION: mammals and relative use.

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESSEE: HEDMAN, GIBSON & COSTIGAN

STREET: 1185 Avenue of the Americas

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

COMPUTER: IBM PC/2

OPERATING SYSTEM: DOS

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,639A

FILING DATE: JUNE 6, 1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM 95 A 000850

FILING DATE: 27-DEC-1995

ATTORNEY/AGENT INFORMATION:
NAME: Costigan, James V.

REGISTRATION NUMBER: 25,669

REFERENCE/DOCKET NUMBER: 515-4111

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 302-8989

TELEFAX: (212) 302-8998

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-095-639A-3

Query Match 32.9%; Score 27; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 VPPFP 15
|:|:|:|:
DB 3 YVPFP 7

RESULT 14
US-09-095-639A-4
; Sequence 4, Application US/09095639A

Patent No. 6750203
GENERAL INFORMATION:
APPLICANT: POZZILI Paolo
TITLE OF INVENTION: Product derived from milk
TITLE OF INVENTION: substantially free of beta casein from non-human
TITLE OF INVENTION: mammals and relative use.

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESSEE: HEDMAN, GIBSON & COSTIGAN

STREET: 1185 Avenue of the Americas

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

COMPUTER: IBM PC/2

OPERATING SYSTEM: DOS

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,639A

FILING DATE: JUNE 6, 1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM 95 A 000850

FILING DATE: 27-DEC-1995

ATTORNEY/AGENT INFORMATION:
NAME: Costigan, James V.

REGISTRATION NUMBER: 25,669

REFERENCE/DOCKET NUMBER: 515-4111

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 302-8989

TELEFAX: (212) 302-8998

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-095-639A-4

Query Match 32.9%; Score 27; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 VPPFP 15
|:|:|:|:
DB 3 YVPFP 7

RESULT 15
US-09-092-000-1
; Sequence 1, Application US/09092000
; Patent No. 6339139
GENERAL INFORMATION:
APPLICANT: Gu, Jian-ren
APPLICANT: Tian, Peikun
TITLE OF INVENTION: Receptor-Mediated Gene Transfer System for Targeting
TITLE OF INVENTION: Tumor Gene Therapy
FILE REFERENCE: Gu
CURRENT APPLICATION NUMBER: US/09/092,000
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 96 116557.X
EARLIER FILING DATE: 1996-10-31
EARLIER APPLICATION NUMBER: PCT/CN97/00106
EARLIER FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Ligand
OTHER INFORMATION: oligopeptide for the receptor region of IGF I and
OTHER INFORMATION: IGF II
US-09-092-000-1

Query Match 32.9%; Score 27; DB 3; Length 14;
Best Local Similarity 46.2%; Pred. No. 3.9e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 2 KPF--PKKVEVP 12
DB 1 EPPRSPKLALEY 13

RESULT 16
US-09-514-245-80

Sequence 80, Application US/09514245
Patent No. 6703023

GENERAL INFORMATION:

APPLICANT: JESTIN, Andre

APPLICANT: ALBINA, Emanuel

APPLICANT: Le CANN, Pierre

APPLICANT: BLANCHARD, Philippe

APPLICANT: HUTET, Evelyne

APPLICANT: ARNAULD, Claire

APPLICANT: MAHE, Catherine

APPLICANT: CARIOLET, Roland

APPLICANT: MADRC, Francois

TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE

FILE REFERENCE: 065691/0176

CURRENT APPLICATION NUMBER: US/09/514,245

CURRENT FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: FR 97/15396

PRIOR FILING DATE: 1997-12-05

NUMBER OF SEQ ID NOS: 170

SOFTWARE: Patentin version 3.0

SEQ ID NO 80

LENGTH: 15

TYPE: PRT

ORGANISM: Type B FMD circovirus

US-09-514-245-80

Query Match 32.9%; Score 27; DB 4; Length 15;
Best Local Similarity 62.5%; Pred. No. 4.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 KKKVEVP 13
DB 8 KKKVEFP 15

RESULT 17
US-09-514-245-81

Sequence 81, Application US/09514245
Patent No. 6703023

GENERAL INFORMATION:

APPLICANT: JESTIN, Andre

APPLICANT: ALBINA, Emanuel

APPLICANT: Le CANN, Pierre

APPLICANT: BLANCHARD, Philippe

APPLICANT: HUTET, Evelyne

APPLICANT: ARNAULD, Claire

APPLICANT: MAHE, Catherine

APPLICANT: CARIOLET, Roland

APPLICANT: MADRC, Francois

TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE

FILE REFERENCE: 065691/0176

CURRENT APPLICATION NUMBER: US/09/514,245

CURRENT FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: FR 97/15396

PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
SEQ ID NO 81
LENGTH: 15
TYPE: PRT

ORGANISM: Type B FMD circovirus
US-09-514-245-81

Query Match 32.9%; Score 27; DB 4; Length 15;
Best Local Similarity 62.5%; Pred. No. 4.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 KKKVEVP 13
DB 4 KKKVEFP 11

RESULT 18
US-09-774-639-257

Sequence 257, Application US/09774639
Patent No. 6806351

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 90 Human Secreted Proteins

FILE REFERENCE: P2013P1

CURRENT APPLICATION NUMBER: US/09/774,639

CURRENT FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04

NUMBER OF SEQ ID NOS: 371

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 257

LENGTH: 15

TYPE: PRT

ORGANISM: Homo sapiens

US-09-774-639-257

Query Match 32.9%; Score 27; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 KKKVEFP 15
DB 2 KKKVEFP 9

RESULT 19
US-08-347-198A-16

Sequence 16, Application US/08347198A
Patent No. 5747046

GENERAL INFORMATION:

APPLICANT: MUNN, Edward A.

APPLICANT: SMITH, Trevor S.

TITLE OF INVENTION: PRODUCTION AND USE OF ANTHELMINTIC

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESS: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP

STREET: 655 Fifteenth Street, N. W., Suite 330 - G

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,198A

FILING DATE: 21-NOV-1994

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/020,526
FILING DATE: 22-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/761,749
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00416
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 89906156.8
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: KITS, Monica C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P443-1289
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-347-198A-16

Query Match 32.9%; Score 27; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPKLKVVF 12
:|:|||||
Db 3 YPVVKVEEF 11

RESULT 20
US-08-335-844A-40
Sequence 40, Application US/08335844A
Patent No. 6066503
GENERAL INFORMATION:
APPLICANT: GRAHAM, MARGARET
APPLICANT: SMITH, TREVOR STANLEY
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: KNOX, DAVID PATRICK
APPLICANT: OLIVER, JOANNA JANE
APPLICANT: NEWTON, SUSAN ELIZABETH
TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figs, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,844A
FILING DATE: 09-JAN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9209936
FILING DATE: 08-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: WALKER, Barbara W.
REGISTRATION NUMBER: 35,400
REFERENCE/DOCKET NUMBER: 1181-223A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-335-844A-40

Query Match 32.9%; Score 27; DB 3; Length 16;
Best Local Similarity 55.6%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPKLKVVF 12
:|:|||||
Db 3 YPVVKVEEF 11

RESULT 21
US-09-129-366-40
Sequence 40, Application US/09129366
Patent No. 6534658
GENERAL INFORMATION:
APPLICANT: GRAHAM, MARGARET
APPLICANT: SMITH, TREVOR STANLEY
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: KNOX, DAVID PATRICK
APPLICANT: OLIVER, JOANNA JANE
APPLICANT: NEWTON, SUSAN ELIZABETH
TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figs, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/129,366
FILING DATE: 05-AUG-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/335,844
FILING DATE: 09-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9209936
FILING DATE: 08-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1181-241A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040

TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-129-366-40

Query Match 32.9%; Score 27; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LKPKLVEVP 12
DB 3 YPVVKEEP 11

RESULT 22

US-08-915-314-22
; Sequence 22, Application US/08915314
; Patent No. 6180604
; GENERAL INFORMATION:
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Ertle, Douglas
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,314
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6180604tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 660081.405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-915-314-22

Query Match 32.3%; Score 26.5; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

QY 1 LKPKLVEVP 14
DB 2 LKKEP-----FPF 10

RESULT 23

US-08-702-054B-28
; Sequence 28, Application US/08702054B
; Patent No. 6191254
; GENERAL INFORMATION:
; APPLICANT: Falls, Timothy J.
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; TITLE OF INVENTION: AND METHODS OF SCREENING FOR THE SAME
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,054B
; FILING DATE: 23-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,687
; FILING DATE: 23-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/013001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-702-054B-28

Query Match 32.3%; Score 26.5; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

QY 1 LKPKLVEVP 14
DB 2 LKKEP-----FPF 10

RESULT 24

US-08-702-054B-29
; Sequence 29, Application US/08702054B
; Patent No. 6191254
; GENERAL INFORMATION:
; APPLICANT: Falls, Timothy J.
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; TITLE OF INVENTION: AND METHODS OF SCREENING FOR THE SAME
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,054B
FILING DATE: 23-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,687
FILING DATE: 23-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07420/013001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-702-054B-29

Query Match 32.3%; Score 26.5; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 LKPPKLVKVEVPPF 14
|||
Db 2 LKKFP-----FFPF 10

RESULT 25
US-09-030-619-93
Sequence 93, Application US/09030619B
PATENT NO. 6503881
GENERAL INFORMATION:
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfile, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 93
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-93

Query Match 32.3%; Score 26.5; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 LKPPKLVKVEVPPF 14
|||
Db 2 LKKFP-----FFPF 10

RESULT 26
US-09-030-619-100
Sequence 100, Application US/09030619B
PATENT NO. 6503881
GENERAL INFORMATION:

APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfile, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 100
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-100

Query Match 32.3%; Score 26.5; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 LKPPKLVKVEVPPF 14
|||
Db 2 LKKFP-----FFPF 10

RESULT 27
US-09-667-486-22
Sequence 22, Application US/09667486
PATENT NO. 6538106
GENERAL INFORMATION:
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfile, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/667,486
FILING DATE: 22-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/915,214
FILING DATE: 20-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: No. 6538106tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids

TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-667-486-22

Query Match 32.3%; Score 26.5; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

QY 1 LKPPKLVKVEVPF 14
|||
Db 2 LKKFP-----FPFP 10

RESULT 28
US-10-225-087-8
Sequence 8, Application US/10225087
Patent No. 6835536
GENERAL INFORMATION:
APPLICANT: Krieger, Timothy J.
APPLICANT: McInicol, Patricia J.
APPLICANT: Frazer, Janet R.
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES AND
TITLE OF INVENTION: FORMULATIONS THEREOF
FILE REFERENCE: 660081.417
CURRENT APPLICATION NUMBER: US/10/225,087
CURRENT FILING DATE: 2003-01-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Indolizidin analog
US-10-225-087-8

Query Match 32.3%; Score 26.5; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

QY 1 LKPPKLVKVEVPF 14
|||
Db 2 LKKFP-----FPFP 10

RESULT 29
US-08-477-928A-46
Sequence 46, Application US/08477928A
Patent No. 6207389
GENERAL INFORMATION:
APPLICANT: Dosch, Hans M.
TITLE OF INVENTION: METHODS FOR CONTROLLING T
TITLE OF INVENTION: LYMPHOCYTE MEDIATED IMMUNE RESPONSES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS
STREET: 1299 Pennsylvania Avenue
CITY: Washington D.C.
STATE: California
COUNTRY: U.S.A.
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,928A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James
REGISTRATION NUMBER: 36902
REFERENCE/DOCKET NUMBER: 19060-0105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 639-7700
TELEFAX: (202) 639-7890
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-928A-46

Query Match 31.7%; Score 26; DB 3; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.1e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PPKLKVEV 11
|||:
Db 1 FDKLMKV 8

RESULT 30
5459077-5
Patent No. 5459077
APPLICANT: MOORE, GRAHAM J.; MATSOUKAS, JOHN M.
TITLE OF INVENTION: METHODS FOR MODELLING TERTIARY STRUCTURES
OF BIOLOGICALLY ACTIVE LIGANDS AND FOR MODELLING AGONISTS AND
ANTAGONISTS THERETO
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/27,561
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 458,926
FILING DATE: 29-DEC-1989
SEQ ID NO: 5;
LENGTH: 8
5459077-5

Query Match 31.7%; Score 26; DB 6; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 KYEVPF 14
:
Db 2 RYIYRPF 8

RESULT 31
5459077-5
Patent No. 5459077
APPLICANT: MOORE, GRAHAM J.; MATSOUKAS, JOHN M.
TITLE OF INVENTION: METHODS FOR MODELLING TERTIARY STRUCTURES
OF BIOLOGICALLY ACTIVE LIGANDS AND FOR MODELLING AGONISTS AND
ANTAGONISTS THERETO
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/27,561
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 458,926
FILING DATE: 29-DEC-1989
SEQ ID NO: 5;
LENGTH: 8
5459077-5

Query Match 31.7%; Score 26; DB 6; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 KVEVEFP 14
: |||
Db 2 RVIYEPF 8

RESULT 32

US-08-347-198A-7
; Sequence 7, Application US/08347198A
; Patent No. 5747046
; GENERAL INFORMATION:
; APPLICANT: MUNN, Edward A.
; TITLE OF INVENTION: PRODUCTION AND USE OF ANTHELMINTIC
; TITLE OF INVENTION: AGENTS AND PROTECTIVE IMMUNOGENS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIKO, MARWELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; STREET: Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,198A
; FILING DATE: 21-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/020,526
; FILING DATE: 22-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/761,749
; FILING DATE: 17-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB90/00416
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 89906156.8
; FILING DATE: 17-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTs, Monica C.
; REGISTRATION NUMBER: 36,105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-347-198A-7

Query Match 31.7%; Score 26; DB 1; Length 12;
Best Local Similarity 55.6%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 PPKKVEVP 12
: |||
Db 3 PPLVTVEAF 11

RESULT 33
US-08-335-844A-31
; Sequence 31, Application US/08335844A
; Patent No. 6066503

; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figs, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,844A
; FILING DATE: 09-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-335-844A-31

Query Match 31.7%; Score 26; DB 3; Length 12;
Best Local Similarity 55.6%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 PPKKVEVP 12
: |||
Db 3 PPLVTVEAF 11

RESULT 34
US-09-129-366-31
; Sequence 31, Application US/09129366
; Patent No. 6534638
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
; NUMBER OF SEQUENCES: 73

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
;; STREET: Suite 701-E, 555 Thirteenth St., N.W
;; CITY: Washington
;; STATE: D. C.
;; COUNTRY: U.S.A.
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/129,366
;; FILING DATE: 05-AUG-1998
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/335,844
;; FILING DATE: 09-JAN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB PCT/GB93/00943
;; FILING DATE: 06-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9209936
;; FILING DATE: 08-MAY-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ERNST, Barbara G.
;; REGISTRATION NUMBER: 30,377
;; REFERENCE/DOCKET NUMBER: 1181-241A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)783-6031
;; TELEFAX: (202)783-6040
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-129-366-31

Query Match 31.7%; Score 26; DB 4; Length 12;
Best Local Similarity 55.6%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 PPKLYEVF 12
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Db 3 PFLVTVFAF 11

RESULT 35
US-08-325-509-34
; Sequence 34, Application US/08325509
; Patent No. 5543308
; GENERAL INFORMATION:
; APPLICANT: MORGAN, RICHARD D.
; TITLE OF INVENTION: ISOLATED DNA ENCODING THE Fcε2
; TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND RELATED METHODS FOR
; TITLE OF INVENTION: PRODUCING THE SAME
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREGORY D. WILLIAMS, NEW ENGLAND
; ADDRESS: BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/325,509
;; FILING DATE: 18-OCT-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WILLIAMS, GREGORY D.
;; REGISTRATION NUMBER: 30901
;; REFERENCE/DOCKET NUMBER: NEB-104
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (508) 927-5054
;; TELEFAX: (508) 927-1705
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; US-08-325-509-34

Query Match 31.7%; Score 26; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 EYVPPP 15
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Db 4 ELFPFP 9

RESULT 36
US-08-347-198A-19
; Sequence 19, Application US/08347198A
; Patent No. 5747046
; GENERAL INFORMATION:
; APPLICANT: MGN, Edward A.
; APPLICANT: SMITH, Trevor S.
; TITLE OF INVENTION: PRODUCTION AND USE OF ANTHELMINTIC
; TITLE OF INVENTION: AGENTS AND PROTECTIVE IMMUNOGENS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,198A
; FILING DATE: 21-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/020,526
; FILING DATE: 22-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/761,749
; FILING DATE: 17-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB90/00416
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 89906156.8
; FILING DATE: 17-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTIS, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P443-1289
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-347-198A-19

Query Match 31.7%; Score 26; DB 1; Length 15;
Best Local Similarity 55.6%; Pred. No. 6.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 PPKLVEVP 12
DB 3 PPLVTVEAP 11

RESULT 37
US-09-552-802B-40
; Sequence 40, Application US/09552802B
; Patent No. 6562943
; GENERAL INFORMATION:
; APPLICANT: Peakman, Mark
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: PEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
; FILE REFERENCE: CD4+ T LYMPHOCYTES
; CURRENT APPLICATION NUMBER: US/09/552,802B
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/295,868
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: US 60/130,355
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-552-802B-40

Query Match 31.7%; Score 26; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 KLKVEVP 13
DB 1 KLKVESSP 8

RESULT 38
US-08-396-385-4
; Sequence 4, Application US/08396385
; Patent No. 6001349
; GENERAL INFORMATION:
; APPLICANT: Schlom, Jeffrey
; APPLICANT: Panicali, Dennis
; TITLE OF INVENTION: GENERATION OF HUMAN CYTOTOXIC T-CELLS
; TITLE OF INVENTION: SPECIFIC FOR CARCINOMA SELF-ASSOCIATED ANTIGENS AND USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEWALL P. BRONSTEIN, DIKE, BRONSTEIN, ROBERTS
; ADDRESS: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/396,385
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44933
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STR UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-08-396-385-4

Query Match 30.5%; Score 25; DB 3; Length 11;
Best Local Similarity 55.6%; Pred. No. 6.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 KLKVEVP 14
DB 1 KLKVESSP 9

RESULT 39
US-09-287-221-4
; Sequence 4, Application US/09287221
; Patent No. 6319496
; GENERAL INFORMATION:
; APPLICANT: Schlom, Jeffrey
; APPLICANT: Panicali, Dennis
; TITLE OF INVENTION: GENERATION OF HUMAN CYTOTOXIC T-CELLS
; TITLE OF INVENTION: SPECIFIC FOR CARCINOMA SELF-ASSOCIATED ANTIGENS AND USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEWALL P. BRONSTEIN, DIKE, BRONSTEIN, ROBERTS
; ADDRESS: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/287,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/396,385
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44933
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STR UR
; INFORMATION FOR SEQ ID NO: 4:

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OM protein - protein search, using sw model

Run on: June 7, 2005, 23:00:52 ; Search time 67.5 Seconds
(without alignments)
85.185 Million cell updates/sec

Title: US-10-691-157-8
Perfect score: 82
Sequence: 1 LKPPKXKLVKVFPPF 15

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Gapop 10.0 , Gapext 0.5

Searched: 171039 seqs, 38334425 residues

Total number of hits satisfying chosen parameters: 309695

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	15	US-10-281-652-8	Sequence 8, Appl1
2	82	100.0	15	US-10-691-157-8	Sequence 8, Appl1
3	82	100.0	15	US-10-691-330-8	Sequence 8, Appl1
4	37	45.1	18	US-09-864-761-40786	Sequence 40786, A
5	36	43.9	18	US-10-281-652-22	Sequence 22, Appl1
6	36	43.9	18	US-10-691-157-22	Sequence 22, Appl1
7	36	43.9	18	US-10-691-330-22	Sequence 22, Appl1
8	34.5	42.1	10	US-10-182-110-4	Sequence 4, Appl1
9	34	41.5	10	US-10-182-110-3	Sequence 3, Appl1
10	34	41.5	15	US-10-281-652-5	Sequence 5, Appl1
11	34	41.5	15	US-10-691-157-5	Sequence 5, Appl1

12	41.5	15	US-10-691-330-5	Sequence 5, Appl1
13	39.0	9	US-09-935-430-451	Sequence 451, App
14	39.0	9	US-09-935-430-555	Sequence 555, App
15	39.0	9	US-10-277-292-451	Sequence 451, App
16	39.0	9	US-10-277-292-555	Sequence 555, App
17	39.0	9	US-10-280-340-451	Sequence 451, App
18	39.0	9	US-10-280-340-555	Sequence 555, App
19	39.0	10	US-09-935-430-66	Sequence 66, Appl1
20	39.0	10	US-09-935-430-607	Sequence 607, App
21	39.0	10	US-10-277-292-66	Sequence 66, Appl1
22	39.0	10	US-10-277-292-607	Sequence 607, App
23	39.0	10	US-10-280-340-66	Sequence 66, Appl1
24	39.0	10	US-10-280-340-607	Sequence 607, App
25	39.0	16	US-10-225-667A-1110	Sequence 1110, App
26	39.0	17	US-10-474-955-64	Sequence 64, Appl1
27	37.8	13	US-09-766-412-39	Sequence 39, Appl1
28	37.2	18	US-10-226-007-1525	Sequence 1525, App
29	36.6	17	US-10-302-547-121	Sequence 121, App
30	35.4	9	US-10-884-862-93	Sequence 93, Appl1
31	35.4	12	US-09-281-717-31	Sequence 31, Appl1
32	35.4	12	US-09-281-717-33	Sequence 33, Appl1
33	35.4	12	US-09-281-717-35	Sequence 35, Appl1
34	34.1	8	US-10-333-235A-67	Sequence 67, Appl1
35	34.1	9	US-09-935-430-333	Sequence 333, App
36	34.1	9	US-10-277-292-333	Sequence 333, App
37	34.1	9	US-10-280-340-333	Sequence 333, App
38	34.1	9	US-10-884-862-63	Sequence 63, Appl1
39	34.1	9	US-10-884-862-146	Sequence 146, Appl1
40	34.1	10	US-09-935-430-269	Sequence 269, App
41	34.1	10	US-09-935-430-356	Sequence 356, App
42	34.1	10	US-10-033-662-35	Sequence 35, Appl1
43	34.1	10	US-10-277-292-269	Sequence 269, App
44	34.1	10	US-10-277-292-356	Sequence 356, App
45	34.1	10	US-10-280-340-269	Sequence 269, App
46	34.1	10	US-10-280-340-356	Sequence 356, App
47	34.1	14	US-09-918-171A-29	Sequence 29, Appl1
48	34.1	16	US-09-947-124-5	Sequence 5, Appl1
49	34.1	18	US-10-474-955-67	Sequence 67, Appl1
50	32.9	10	US-09-988-493-133	Sequence 133, App
51	32.9	10	US-10-014-340-127	Sequence 127, App
52	32.9	10	US-10-014-340-428	Sequence 428, App
53	32.9	10	US-10-203-334-2	Sequence 2, Appl1
54	32.9	10	US-10-601-837-131	Sequence 131, App
55	32.9	10	US-10-700-330-140	Sequence 140, App
56	32.9	11	US-10-100-049-25	Sequence 25, Appl1
57	32.9	12	US-10-340-458-24	Sequence 24, Appl1
58	32.9	12	US-10-500-804-2	Sequence 2, Appl1
59	32.9	13	US-10-474-955-110	Sequence 110, App
60	32.9	14	US-10-226-007-1513	Sequence 1513, App
61	32.9	14	US-10-308-128-144	Sequence 144, App
62	32.9	15	US-09-774-639-257	Sequence 257, App
63	32.9	15	US-09-969-730-339	Sequence 339, App
64	32.9	15	US-10-226-007-1514	Sequence 1514, App
65	32.9	15	US-10-226-007-1516	Sequence 1516, App
66	32.9	15	US-10-621-363-339	Sequence 339, App
67	32.9	15	US-10-682-420-80	Sequence 80, Appl1
68	32.9	15	US-10-682-420-81	Sequence 81, Appl1
69	32.9	15	US-10-409-613-80	Sequence 80, Appl1
70	32.9	15	US-10-409-613-81	Sequence 81, Appl1
71	32.9	15	US-10-442-180-80	Sequence 80, Appl1
72	32.9	15	US-10-442-180-81	Sequence 81, Appl1
73	32.9	15	US-10-474-955-109	Sequence 109, App
74	32.9	15	US-10-718-266-80	Sequence 80, Appl1
75	32.9	15	US-10-718-266-81	Sequence 81, Appl1
76	32.9	15	US-10-775-337-80	Sequence 80, Appl1
77	32.9	15	US-10-775-337-81	Sequence 81, Appl1
78	32.9	15	US-10-637-011-81	Sequence 80, Appl1
79	32.9	15	US-10-637-011-80	Sequence 81, Appl1
80	32.9	16	US-10-100-049-40	Sequence 40, Appl1
81	32.9	16	US-10-226-007-1515	Sequence 1515, App
82	32.9	16	US-10-226-007-1517	Sequence 1517, App
83	32.9	16	US-10-226-007-1519	Sequence 1519, App
84	32.9	17	US-09-754-831A-34	Sequence 34, Appl1

85	27	32.9	17	14	US-10-226-007-1518	Sequence 1518, Ap
86	27	32.9	17	14	US-10-226-007-1520	Sequence 1520, Ap
87	27	32.9	17	14	US-10-226-007-1522	Sequence 1522, Ap
88	27	32.9	17	16	US-10-302-547-120	Sequence 120, Appl
89	27	32.9	17	17	US-10-671-317-120	Sequence 34, Appl
90	27	32.9	18	14	US-10-226-007-1521	Sequence 1521, Appl
91	27	32.9	18	14	US-10-226-007-1523	Sequence 1523, Ap
92	26.5	32.3	13	9	US-09-030-619-93	Sequence 93, Appl
93	26.5	32.3	13	9	US-09-030-619-100	Sequence 100, Appl
94	26.5	32.3	13	14	US-10-229-368-8	Sequence 8, Appl
95	26.5	32.3	13	14	US-10-225-087-8	Sequence 8, Appl
96	26.5	32.3	13	15	US-10-277-232-93	Sequence 93, Appl
97	26.5	32.3	13	15	US-10-277-232-100	Sequence 100, Appl
98	26.5	32.3	13	15	US-10-277-233-93	Sequence 93, Appl
99	26.5	32.3	13	15	US-10-277-233-100	Sequence 100, Appl
100	26.5	32.3	13	15	US-10-351-985-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-10-281-652-8
; Sequence 8, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265, 00220101
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/10/281,652
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-8

Query Match 100.0%; Score 82; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPPKLVKVEVPP 15
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DB 1 LKPPKLVKVEVPP 15
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RESULT 2

US-10-691-157-8
; Sequence 8, Application US/10691157
; Publication No. US2004026681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265, 00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-157-8

Query Match 100.0%; Score 82; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPPKLVKVEVPP 15
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DB 1 LKPPKLVKVEVPP 15
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RESULT 3

US-10-691-330-8
; Sequence 8, Application US/10691330
; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: Bolodogh, Istvan
; APPLICANT: Stanton, G. John
; APPLICANT: Hughes, Thomas A.
; APPLICANT: Kruezel, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265,00390101
; CURRENT APPLICATION NUMBER: US/10/691,330
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-330-8

Query Match 100.0%; Score 82; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPPKLVKVEVPP 15
 |||||

DB 1 LKPPKLVKVEVPP 15
 |||||

RESULT 4

US-09-864-761-40786
; Sequence 40786, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

```

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40786
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC023296.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; US-09-864-761-40786

Query Match      45.1%; Score 37; DB 9; Length 18;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 KYEVPFP 15
       :|||
       3 REVAFPFP 10

RESULT 5
US-10-281-652-22
; Sequence 22, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
```

```

; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265,00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-10-281-652-22

Query Match      43.9%; Score 36; DB 14; Length 18;
Best Local Similarity 70.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 PPKIKYVPF 12
       :|||
       5 PPKYVPFP 14

RESULT 6
US-10-691-157-22
; Sequence 22, Application US/10691157
; Publication No. US2004026681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUEZEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; FILE REFERENCE: 265,00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
; US-10-691-157-22

Query Match      43.9%; Score 36; DB 16; Length 18;
Best Local Similarity 70.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 PPKIKYVPF 12
       :|||
       5 PPKYVPFP 14

RESULT 7
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US-10-691-330-22
; Sequence 22, Application US/10691330
; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: Boldogh, Istvan
; APPLICANT: Stanton, G. John
; APPLICANT: Georgiades, Jerzy A.
; APPLICANT: Hughes, Thomas K., Jr.
; APPLICANT: Kruszal, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265,00390101
; CURRENT APPLICATION NUMBER: US/10/691,330
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-330-22

Query Match 43.9%; Score 36; DB 17; Length 18;
Best Local Similarity 70.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPKLKEVEF 12
| | | | |
DB 5 PPKLKEVEF 14
| | | | |
RESULT 8
US-10-182-110-4
; Sequence 4, Application US/10182110
; Publication No. US20040171553A1
; GENERAL INFORMATION:
; APPLICANT: Regen Therapeutics plc
; APPLICANT: Georgiades, Jerzy A.
; TITLE OF INVENTION: Peptide Fragments of Colostrinin And Their Use
; FILE REFERENCE: AAT-14173
; CURRENT APPLICATION NUMBER: US/10/182,110
; PRIOR FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: GB0001825.9
; PRIOR FILING DATE: 2000-01-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Truncated version of a peptide found in colostrinin
US-10-182-110-4

Query Match 42.1%; Score 34.5; DB 16; Length 10;
Best Local Similarity 81.8%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 5 PPKLKEVEF 15
| | | | |
DB 1 PPKLKEVEF 10
| | | | |
RESULT 9
US-10-182-110-3
; Sequence 3, Application US/10182110
; Publication No. US20040171553A1
; GENERAL INFORMATION:
; APPLICANT: Regen Therapeutics plc

; APPLICANT: Georgiades, Jerzy A
; TITLE OF INVENTION: Peptide Fragments of Colostrinin And Their Use
; FILE REFERENCE: AAT-14173
; CURRENT APPLICATION NUMBER: US/10/182,110
; PRIOR FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: GB0001825.9
; PRIOR FILING DATE: 2000-01-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Truncated version of a peptide found in colostrinin
US-10-182-110-3

Query Match 41.5%; Score 34; DB 16; Length 10;
Best Local Similarity 70.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PPKLKEVEF 14
| | | | |
DB 1 PPKLKEVEF 10
| | | | |
RESULT 10
US-10-281-652-5
; Sequence 5, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265,00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-5

Query Match 41.5%; Score 34; DB 14; Length 15;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PPKLKEVEF 14
| | | | |
DB 5 PPKLKEVEF 14
| | | | |
RESULT 11
US-10-691-157-5
; Sequence 5, Application US/10691157
; Publication No. US20040266681A1
; GENERAL INFORMATION:
; APPLICANT: Boldogh, Istvan
; APPLICANT: Stanton, G. John
; APPLICANT: Georgiades, Jerzy
; APPLICANT: Hughes, Thomas
; APPLICANT: Kruszal, Marian


```
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEROOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265.00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-157-5

Query Match          41.5%; Score 34; DB 16; Length 15;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
Qy 5 PVLKVEPPPF 14
Db 5 PVLKVEPPPF 14

RESULT 12
US-10-691-330-5
; Sequence 5, Application US/10691330
; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, G. John
; APPLICANT: Georgiades, Verzy A.
; APPLICANT: Hughes, Thomas K., Jr.
; APPLICANT: Kruzel, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; FILE REFERENCE: 265.00390101
; CURRENT APPLICATION NUMBER: US/10/691,330
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-330-5

Query Match          41.5%; Score 34; DB 17; Length 15;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALIVITA-BID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 451
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-451

Query Match          39.0%; Score 32; DB 10; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 PPKLKLV 9
Db 2 PPKLKLV 8

RESULT 14
US-09-935-430-555
; Sequence 555, Application US/09935430
; Publication No. US200300117466A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALIVITA-BID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 555
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-555

Query Match          39.0%; Score 32; DB 10; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
RESULT 13
US-09-935-430-451
; Sequence 451, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
```

Db 2 PMPKLV 8

RESULT 15

US-10-277-292-451
; Sequence 451, Application US/10277292
; Publication No. US2003019470A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBYTZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 451
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-451

Query Match 39.0%; Score 32; DB 14; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PMPKLV 9
| | | | |
Db 2 PMPKLV 8

RESULT 16

US-10-277-292-555
; Sequence 555, Application US/10277292
; Publication No. US2003019470A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBYTZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 555
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-555

Query Match 39.0%; Score 32; DB 14; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PMPKLV 9
| | | | |
Db 2 PMPKLV 8

RESULT 17

US-10-280-340-451
; Sequence 451, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBYTZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 451
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-451

Query Match 39.0%; Score 32; DB 15; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PMPKLV 9
| | | | |
Db 2 PMPKLV 8

RESULT 18

US-10-280-340-555
; Sequence 555, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBYTZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7

```

; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 555
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-555
```

```

Query Match          39.0%; Score 32; DB 15; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 PPKLKV 9
Db 2 PMPKLKV 8
```

```

RESULT 19
US-09-935-430-66
; Sequence 66, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-ELD, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-66
```

```

Query Match          39.0%; Score 32; DB 10; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 PPKLKV 9
Db 2 PMPKLKV 8
```

```

RESULT 20
US-09-935-430-607
```

```

; Sequence 607, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-ELD, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 607
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-607
```

```

Query Match          39.0%; Score 32; DB 10; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 PPKLKV 9
Db 2 PMPKLKV 8
```

```

RESULT 21
US-10-277-292-66
; Sequence 66, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-ELD, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-66
```

Query Match 39.0%; Score 32; DB 14; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPKLKV 9
| | | | |
DB 2 PMPKLKV 8

RESULT 22

US-10-277-292-607
; Sequence 607, Application US/10277292
; Publication No. US2003019470A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 607
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-607

Query Match 39.0%; Score 32; DB 14; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPKLKV 9
| | | | |
DB 2 PMPKLKV 8

RESULT 23

US-10-280-340-66
; Sequence 66, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098

; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-66

Query Match 39.0%; Score 32; DB 15; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPKLKV 9
| | | | |
DB 2 PMPKLKV 8

RESULT 24

US-10-280-340-607
; Sequence 607, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 607
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-607

Query Match 39.0%; Score 32; DB 15; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPKLKV 9
| | | | |
DB 2 PMPKLKV 8

RESULT 25

US-10-225-567A-1110
; Sequence 110, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.

```
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1110
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1110

Query Match      39.0%; Score 32; DB 14; Length 16;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKPPPK 6
       :|:|:|:|
Db      8 LKPPPK 13

RESULT 26
US-10-474-955-64
; Sequence 64, Application US/10474955
; Publication No. US20040241161A1
; GENERAL INFORMATION:
; APPLICANT: Drifflout, Jan W.
; APPLICANT: Konig, Stephan N.
; APPLICANT: McAdam, Stephen N.
; APPLICANT: Ludwig, Solid Magne
; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
; FILE REFERENCE: 2799/71244-PCT-US
; CURRENT APPLICATION NUMBER: US/10/474,955
; CURRENT FILING DATE: 2003-10-13
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 64
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Peptide sequence in pool 54
; NAME/KEY: MISC FEATURE
; LOCATION: (17)-(18)
; OTHER INFORMATION: "Y" on position 17 is P/S
US-10-474-955-64

Query Match      39.0%; Score 32; DB 16; Length 17;
Best Local Similarity 46.7%; Pred. No. 3e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 4; Gaps 1;

QY      1 LKPPPKLKVVPFP 15
       :|:|:|:|
Db      3 LQPPQPPQ----PFP 13

RESULT 27
US-09-766-412-39
; Sequence 39, Application US/09766412
; Patent No. US20020103129A1
; GENERAL INFORMATION:
; APPLICANT: GE, Rucmen et al.
; TITLE OF INVENTION: SMALL PEPTIDES HAVING ANTI-ANGIOGENIC AND ENDOTHELIAL CELL INHIBI
; FILE REFERENCE: 1781-0215P
; CURRENT APPLICATION NUMBER: US/09/766,412
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 50
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 39
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mammalian
; FEATURES:
; NAME/KEY: misc feature
; OTHER INFORMATION: SHFLT2
US-09-766-412-39

Query Match      37.8%; Score 31; DB 9; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 LKPPPKLKVVPFP 12
       :|:|:|:|
Db      1 LVPPLPKIKNSTP 12

RESULT 28
US-10-226-007-1525
; Sequence 1525, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1525
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Lymphocytic choriomeningitis virus
US-10-226-007-1525

Query Match      37.2%; Score 30.5; DB 14; Length 18;
Best Local Similarity 50.0%; Pred. No. 5.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY      3 PFP-RLKLVVPFP 15
       :|:|:|:|
Db      1 PLPTLTKISTAPSP 14

RESULT 29
US-10-302-547-121
; Sequence 121, Application US/10302547
; Publication No. US20040142448A1
; GENERAL INFORMATION:
; APPLICANT: MORPHY, BRIAN R.
; APPLICANT: COLLINS, PETER L.
; APPLICANT: SKIADOPOULOS, MARIO H.
; APPLICANT: NEWMAN, JASON T.
; TITLE OF INVENTION: RECOVERY OF RECOMBINANT HUMAN PARAINFLUENZA VIRUS TYPE
; TITLE OF INVENTION: 1 (HPIV1) FROM CDNA AND USE OF RECOMBINANT HPIV1 IN
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AND AS VECTORS TO ELICIT
; FILE REFERENCE: 2303-37-3
; CURRENT APPLICATION NUMBER: US/10/302,547
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/331,961
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO: 121
; LENGTH: 17
```

;; TYPE: PRT
;; ORGANISM: Murine parainfluenza virus 1
US-10-302-547-121

Query Match 36.6%; Score 30; DB 16; Length 17;
Best Local Similarity 50.0%; Pred. No. 6.3e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LKPPKLVKVEVPF 14
Db 4 LKDPFKRYEVEHPY 17

RESULT 30
US-10-884-862-93
; Sequence 93, Application US/10884862
; Publication No. US20050048071A1
; GENERAL INFORMATION:
; APPLICANT: BAE, Joo-eun
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES
; FILE REFERENCE: 047940-0239
; CURRENT APPLICATION NUMBER: US/10/884,862
; CURRENT FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: US 60/484689
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-862-93

Query Match 35.4%; Score 29; DB 17; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKPPKLVK 9
Db 1 LKPPKLVK 9

RESULT 31
US-09-281-717-31
; Sequence 31, Application US/09281717
; Patent No. US20020061539A1
; GENERAL INFORMATION:
; APPLICANT: Baxter, John D.
; APPLICANT: Dairmont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletterick, Robert J.
; APPLICANT: Kushner, Peter J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: West, Brian
; APPLICANT: Yamamoto, Keith R.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: UCAL-253/02US
; CURRENT APPLICATION NUMBER: US/09/281,717
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 60/079,956
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (5)
; OTHER INFORMATION: Leu --> Arg (L454R)
; FEATURE:

;; NAME/KEY: MUTAGEN
;; LOCATION: (7)
;; OTHER INFORMATION: Leu --> Arg (L456R)
;; FEATURE:
;; NAME/KEY: MUTAGEN
;; LOCATION: (8)
;; OTHER INFORMATION: Glu --> Lys (E457K)
US-09-281-717-31

Query Match 35.4%; Score 29; DB 9; Length 12;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FPKLVKVEVPF 12
Db 2 FPKLVKVEVPF 10

RESULT 32
US-09-281-717-33
; Sequence 33, Application US/09281717
; Patent No. US20020061539A1
; GENERAL INFORMATION:
; APPLICANT: Baxter, John D.
; APPLICANT: Dairmont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletterick, Robert J.
; APPLICANT: Kushner, Peter J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: West, Brian
; APPLICANT: Yamamoto, Keith R.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: UCAL-253/02US
; CURRENT APPLICATION NUMBER: US/09/281,717
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 60/079,956
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-281-717-33

Query Match 35.4%; Score 29; DB 9; Length 12;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FPKLVKVEVPF 12
Db 2 FPKLVKVEVPF 10

RESULT 33
US-09-281-717-35
; Sequence 35, Application US/09281717
; Patent No. US20020061539A1
; GENERAL INFORMATION:
; APPLICANT: Baxter, John D.
; APPLICANT: Dairmont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletterick, Robert J.
; APPLICANT: Kushner, Peter J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: West, Brian
; APPLICANT: Yamamoto, Keith R.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: UCAL-253/02US
; CURRENT APPLICATION NUMBER: US/09/281,717
; CURRENT FILING DATE: 1999-03-30

EARLIER APPLICATION NUMBER: US 60/079,956
EARLIER FILING DATE: 1998-03-30
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-281-717-35

Query Match 35.4%; Score 29; DB 9; Length 12;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PPKLKVFP 12
Db 2 PPKLKVFP 10

RESULT 34
US-10-333-235A-67
Sequence 67, Application US/10333235A
Publication No. US20040132007A1
GENERAL INFORMATION:
APPLICANT: GOT-A-GENE AB
APPLICANT: Lelf, Lindholm
APPLICANT: Karin, Nord
APPLICANT: Pierre, Boulanger
APPLICANT: Rebecca, Gardner
TITLE OF INVENTION: Modified Virus
FILE REFERENCE: 9.7.72728/001
CURRENT APPLICATION NUMBER: US/10/333,235A
CURRENT FILING DATE: 2003-12-04
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
SEQ ID NO 67
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Linker peptide
US-10-333-235A-67

Query Match 34.1%; Score 28; DB 16; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVEVFP 13
Db 2 KVEVFP 7

RESULT 35
US-09-935-430-333
Sequence 333, Application US/09935430
Publication No. US20030017466A1
GENERAL INFORMATION:
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RAITANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALIVITA-ETD, PIA
APPLICANT: JAKOBOVITZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
FILE REFERENCE: 51158-20050.00
CURRENT APPLICATION NUMBER: US/09/935,430
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,098
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/282,739

PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 333
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-333

Query Match 34.1%; Score 28; DB 10; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPKLX 8
Db 4 PPKLX 9

RESULT 36
US-10-277-292-333
Sequence 333, Application US/10277292
Publication No. US20030199470A1
GENERAL INFORMATION:
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RAITANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALIVITA-ETD, PIA
APPLICANT: JAKOBOVITZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
FILE REFERENCE: 51158-20050.00
CURRENT APPLICATION NUMBER: US/10/277,292
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US/09/935,430
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,098
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/282,739
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 333
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-333

Query Match 34.1%; Score 28; DB 14; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPKLX 8
Db 4 PPKLX 9

RESULT 37
US-10-280-340-333
Sequence 333, Application US/10280340
Publication No. US20030207835A1
GENERAL INFORMATION:
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RAITANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA

```

; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 333
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-333

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```

Query Match          34.1%; Score 28; DB 15; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 3 LKPFKL 8
DB 4 PMPKLK 9

```

```

RESULT 38
US-10-884-862-63
; Sequence 63, Application US/10884862
; Publication No. US20050048071A1
; GENERAL INFORMATION:
; APPLICANT: BAE, JOO-eun
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES
; FILE REFERENCE: 047940-0239
; CURRENT APPLICATION NUMBER: US/10/884,862
; PRIOR FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: US 60/484689
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-862-63

```

```

Query Match          34.1%; Score 28; DB 17; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LKPFKL 7
DB 3 LKPFKL 9

```

```

RESULT 39
US-10-884-862-146
; Sequence 146, Application US/10884862
; Publication No. US20050048071A1
; GENERAL INFORMATION:
; APPLICANT: BAE, JOO-eun
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES
; FILE REFERENCE: 047940-0239
; CURRENT APPLICATION NUMBER: US/10/884,862
; PRIOR FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: US 60/484689

```

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; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-862-146

```

```

Query Match          34.1%; Score 28; DB 17; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LKPFKL 7
DB 2 LKPFKL 8

```

```

RESULT 40
US-09-935-430-269
; Sequence 269, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-269

```

```

Query Match          34.1%; Score 28; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 3 LKPFKL 8
DB 5 PMPKLK 10

```

```

Search completed: June 7, 2005, 23:31:41
Job time : 69.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:56:36 ; Search time 13.9091 Seconds
(without alignments)
103.763 Million cell updates/sec

Title: US-10-691-157-8
Perfect score: 82
Sequence: 1 LKPPFKLKEVFPFP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	40.2	18	2	A60915
2	24	28.3	17	2	S78736
3	23.5	28.7	18	2	S04229
4	23	28.0	9	2	PC7073
5	22	26.8	13	2	CS3275
6	22	26.8	17	2	G85956
7	22	26.8	18	2	A42576
8	22	26.8	18	2	A61220
9	21.5	26.2	16	2	A48301
10	21	25.6	8	2	S66646
11	21	25.6	11	1	XASNBA
12	21	25.6	15	2	PS0452
13	21	25.6	15	2	PA0060
14	21	25.6	16	2	PH0758
15	21	25.6	16	2	H40065
16	20.5	25.0	14	2	H64008
17	20	24.4	6	2	A61049
18	20	24.4	10	2	A60624
19	20	24.4	10	2	A60410
20	20	24.4	10	2	A90917
21	20	24.4	11	2	A90345
22	20	24.4	11	2	PA0028
23	20	24.4	11	2	S07207
24	20	24.4	13	2	S32475
25	20	24.4	14	2	PH1566
26	20	24.4	15	1	LRECF
27	20	24.4	15	2	PA0026
28	20	24.4	15	2	PA0024
29	20	24.4	15	2	PA0088

30	20	24.4	15	2	PD0444	coupling factor 6
31	20	24.4	16	2	A53337	regulatory protein
32	20	24.4	17	2	A37823	diacylglycerol S
33	20	24.4	18	2	S14661	photosystem I prot
34	20	24.4	18	2	S09731	photosystem I prot
35	20	24.4	18	2	A61392	brain-associated s
36	20	24.4	18	2	H75063	hypothetical prote
37	19	23.2	9	2	S66635	alpha-2-macroglobu
38	19	23.2	10	2	S65432	angiotensin I - ho
39	19	23.2	10	2	A61218	angiotensin I - ho
40	19	23.2	10	2	B61218	alpha-gliadin 4Ha
41	19	23.2	12	2	C20907	Ig kappa-1 chain J
42	19	23.2	13	2	S32474	lymadpamide 4 - g
43	19	23.2	14	2	A01250	angiotensin precu
44	19	23.2	15	2	A60834	angiotensin I prec
45	19	23.2	15	2	S29207	angiotensin I prec
46	19	23.2	15	2	C61511	avenin gamma-4 - o
47	19	23.2	16	2	S33590	milk band B protei
48	19	23.2	16	2	A20190	beta-crystallin A3
49	19	23.2	16	2	PN0149	hypodermin B - ear
50	18.5	22.6	17	2	S59481	beta-glialine 13 -
51	18	22.0	8	2	A46306	hydroxyproline-ric
52	18	22.0	9	2	I46023	spasmogenic toxin
53	18	22.0	10	2	S74147	growth hormone rec
54	18	22.0	11	2	S78026	glyceraldehyde-3-p
55	18	22.0	11	2	PC2254	ribosomal protein
56	18	22.0	11	2	S33519	Cyochrome P450 3A
57	18	22.0	12	2	PA0098	probable secreted
58	18	22.0	12	2	PH1567	ribosomal protein
59	18	22.0	13	2	A60458	cerebrin 28 - huma
60	18	22.0	13	2	B44957	protocatechuate 3,
61	18	22.0	13	2	S23640	protein I7 - commo
62	18	22.0	13	2	S21152	Ig kappa chain J s
63	18	22.0	15	2	B31061	tryptophyllin-rela
64	18	22.0	15	2	A28965	hypothetical prote
65	18	22.0	16	2	D45193	ribulose-bisphosph
66	18	22.0	17	2	S29165	zinc finger protei
67	18	22.0	17	2	I55612	quinallidine oxide
68	17.5	21.3	15	2	A41436	thyroid hormone re
69	17	20.7	9	2	S35358	alpha-macroglobuli
70	17	20.7	9	2	A4873	ribosomal protein
71	17	20.7	10	1	XASNPC	caldesmon - rabbit
72	17	20.7	10	2	JC1367	angiotensin-conver
73	17	20.7	10	2	H28027	thyroliiberin poten
74	17	20.7	10	2	A60476	protein p11 - curi
75	17	20.7	10	2	B3143	S-layer protein -
76	17	20.7	10	2	A33143	pneumadin - rat
77	17	20.7	11	2	G42762	proteasome endope
78	17	20.7	11	2	S23306	substance P - Atla
79	17	20.7	11	2	A61033	ranacthykinin A -
80	17	20.7	11	2	D61033	glutathione transf
81	17	20.7	12	2	S17869	histone H2B - huma
82	17	20.7	12	2	S65409	enterotoxin C-1 -
83	17	20.7	12	2	A60757	Ig kappa chain J1
84	17	20.7	12	2	A20907	hypothetical prote
85	17	20.7	13	2	H64124	lymadpamide 2 - g
86	17	20.7	13	2	S32472	Ig kappa chain J s
87	17	20.7	13	2	S23638	22k exoantigen -
88	17	20.7	14	2	C33098	superoxide dismuta
89	17	20.7	16	2	B58503	glutathione kinase
90	17	20.7	16	2	T44936	superoxide dismuta
91	17	20.7	17	2	C37520	modulin kinase
92	17	20.7	17	2	S50901	glutathione transf
93	17	20.7	17	2	S33609	chlorophyll a/b-di
94	17	20.7	17	2	C49255	extensin - maize (
95	17	20.7	17	2	PC2319	T-cell receptor be
96	17	20.7	18	2	B35910	proteasome endope
97	17	20.7	18	2	I78841	neurofibromatosis-
98	17	20.7	18	2	A45138	chromoprotein rec
99	16.5	20.1	18	2	A61620	arsenite oxidase I
100	16.5	20.1	19	2	S10891	loquatmyotropin I
						ubiquitin thioleat

ALIGNMENTS

RESULT 1

A60915 enkephalin-degrading aminopeptidase (EC 3.4.-.-), puromycin-sensitive - rat (fragment)

N:Alternate names: aminoenkephalinase; aminopeptidase MII

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: A60915

R:Dieter, S.H.; Slaughter, C.A.; Orth, K.; Noomaw, C.R.; Hersh, L.B.

J. Neurochem. 54, 547-554, 1990

A:Title: Comparison of the soluble and membrane-bound forms of the puromycin-sensitive

A:Reference number: A60915; PMID:90132681; PMID:2299352

A:Accession: A60915

A:Molecule type: protein

A:Residues: 1-18 <DYE>

A:Cross-references: UNIPROT:Q7M076

A>Note: this sequence represents the N-terminus of both soluble and membrane-associated

C:Superfamily: membrane alanyl aminopeptidase

C:Keywords: hydrolase

Query Match

Best Local Similarity 40.2%; Score 33; DB 2; Length 18;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 KPFPKLKVEVFP 13

Db 4 RPPERLPTVSP 15

RESULT 2

S78756 ribosomal protein MRP-15, mitochondrial - bovine (fragments)

C:Species: Bos primigenius taurus (cattle)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C:Accession: S78756

R:Grack, H.R.

submitted to the Protein Sequence Database, May 1999

A:Reference number: S78756

A:Accession: S78756

A:Molecule type: protein

A:Residues: 1-12/13-17 <GRA>

C:Keywords: mitochondrion

Query Match

Best Local Similarity 29.3%; Score 24; DB 2; Length 17;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PFPKLKVE 10

Db 3 PFEELLEVE 10

RESULT 3

S04229 N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24k chain - rat (fragment)

N:Alternate names: glycosylasparaginase

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993

C:Accession: S04229

R:Tollersrud, O.K.; Aronson Jr., N.N.

Biochem. J. 260, 101-108, 1989

A:Title: Purification and characterization of rat liver glycosylasparaginase.

A:Reference number: S04228; PMID:89374025; PMID:2775174

A:Accession: S04229

A:Molecule type: protein

A:Residues: 1-18 <TOL>

C:Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase

C:Keywords: hydrolase

Query Match

Best Local Similarity 28.7%; Score 23.5; DB 2; Length 18;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 3 PFPKLKVEVFP 14

Db 3 PLP-LVNTWTFP 13

RESULT 4

PC7073 ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C:Accession: PC7073

R:Tangita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kano, M.; Matsui, T.; Watanabe, Y.;

Electrophoresis 21, 1853-1871, 2000

A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t

A:Reference number: PC7072

A:Accession: PC7073

A:Molecule type: protein

A:Residues: 1-9 <TSU>

A:Cross-references: UNIPROT:O9CVK7

C:Keywords: brain; core protein; oxidoreductase

Query Match

Best Local Similarity 28.0%; Score 23; DB 2; Length 9;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKFPKTK 8

Db 2 LKVAPKVK 9

RESULT 5

CS3275 Ig kappa-1 chain J3 segment b95 allotype - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996

C:Accession: CS3275

R:Avadi, H.; Marche, P.N.; Cazenave, P.A.

Immunogenetics 34, 201-207, 1991

A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.

A:Reference number: A53275; PMID:91372868; PMID:1905995

A:Accession: CS3275

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-13 <DNA>

A>Note: sequence extracted from NCBI backbone (NCBI:56069, NCBI:P56164)

C:Comment: This J3 segment may not be functional because of substitutions in the 7 mer a

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 26.8%; Score 22; DB 2; Length 13;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PFKLVEVFP 13

Db 5 PFKLEIKP 13

RESULT 6

G85956 hypothetical protein 24331 [imported] - Escherichia coli (strain O157:H7, substrain EDLs

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: G85956

R:Perina, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaeser, J.D.; Rose, D.J.; Mayhew

Iller, L.; Grobbeck, B.J.; Davis, N.W.; Lim, A.; Diallantha, E.; Potamouidis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; PMID:21074935; PMID:11206551

A:Accession: G85956

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-17 <STO>
A:Cross-references: UNIPROT:O8X4A4; GB:AE005174; NID:G12517539; PIDN:AGS8115.1; GSPDB:C
A:Experimental source: strain O157:H7, substrain EDL933
C:GeneID:8
A:Gene: 24331

Query Match
Best Local Similarity 80.0%; Score 22; DB 2; Length 17;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 VFPP 15
DB 4 VSPFP 8

RESULT 7
A42576
steroid receptor complex Hsp56 60K component - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998
C:Accession: A42576
R:Yem, A.W.; Tomaselli, A.G.; Heinrichson, R.L.; Zurcher-Neely, H.; Ruff, V.A.; Johnson, J. Biol. Chem. 267, 2868-2871, 1992
A:Title: The Hsp56 component of steroid receptor complexes binds to immobilized FK506 an
A:Reference number: A42576; MUID:92147620; PMID:1371107
A:Accession: A42576
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <YEM>
A:Experimental data: thymus
A:Note: sequence extracted from NCBI backbone (NCBIP:80696)
C:Superfamily: human FK506-binding protein FKBP5; BGBP-type peptidylprolyl isomerase hc
C:Keywords: steroid hormone receptor

Query Match
Best Local Similarity 57.1%; Score 22; DB 2; Length 18;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 KVEVPP 14
DB 11 EVELPEP 17

RESULT 8
A61220
epsilon receptor modulating protein (EC 3.4.21.-) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: A61220
R:Matsumita, S.; Katz, D.H. Cell. Immunol. 137, 253-259, 1991
A:Title: The murine epsilon receptor modulating protein: a novel serine protease which m
A:Reference number: A61220; MUID:91356570; PMID:1679381
A:Accession: A61220
A:Molecule type: protein
A:Residues: 1-18 <MAT>
A:Cross-references: UNIPROT:Q7M060
A:Comment: This serine proteinase from a T cell hybridoma does not reduce levels of CD23
C:Keywords: hydrolase; serine proteinase

Query Match
Best Local Similarity 80.0%; Score 22; DB 2; Length 18;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPFPK 6
DB 2 KPAPK 6

RESULT 9
A48301
glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - Synechococcus sp. (PCC 6301) (fr
C:Species: Synechococcus sp.

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C:Accession: A48301
R:Grimm, B.; Bull, A.; Welinder, K.G.; Gough, S.P.; Kannangara, C.G. Carlsberg Res. Commun. 54, 67-79, 1989
A:Title: Purification and partial amino acid sequence of the glutamate 1-semialdehyde am
A:Reference number: A48301; MUID:89374545; PMID:2505791
A:Accession: A48301
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <GRI>
C:Keywords: intramolecular transferase; isomerase

Query Match
Best Local Similarity 38.5%; Score 21.5; DB 2; Length 16;
Matches 5; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 LKPPKLV-EVF 12
DB 3 INPFTIKSDIEP 15

RESULT 10
S66646
cardioacceleratory protein 2b - tobacco hornworm
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66646
R:Huesmann, G.R.; Cheung, C.C.; Lot, P.K.; Lee, T.D.; Swiderrek, K.M.; Tumbilz, N.J. FASEB Lett. 371, 311-314, 1995
A:Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide from the t
A:Reference number: S66646; MUID:96013159; PMID:7556618
A:Accession: S66646
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <HUE>
A:Cross-references: UNIPROT:Q7M3N2

Query Match
Best Local Similarity 50.0%; Score 21; DB 2; Length 8;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 EVVPP 15
DB 1 ELYAPF 6

RESULT 11
XASNBA
bradykinin-potentiating peptide B - marmoset
C:Species: Aotus blommofsi (marmoset)
C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
C:Accession: A01254
R:Kato, H.; Suzuki, T. Proc. Jpn. Acad. 46, 176-181, 1970
A:Reference number: A01254
A:Accession: A01254
A:Molecule type: protein
A:Residues: 1-11 <KAT>
A:Cross-references: UNIPROT:P01021
A:Note: the sequence of the natural peptide was confirmed by the synthesis and analysis
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; veno
P11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match
Best Local Similarity 57.1%; Score 21; DB 1; Length 11;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKPPK 7
DB 3 LPPPK 9

RESULT 12
PS0452
32K protein 3306 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C:Accession: PS0452
R:Tsugita, A.; Miyake, N.
submitted to JIPID, April 1993
A:Reference number: PS0208
A:Accession: PS0452
A:Molecule type: protein
A:Residues: 1-15 <TSU>
A:Experimental source: bran, strain Nihonbare
C:Comment: molecular weight 32K, pI 5.3.

Query Match 25.6%; Score 21; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPKXL 7
|||
Db 6 PPKL 10

RESULT 13
PA0060
protein QP200037 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0060
R:Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A:Reference number: PA0051
A:Accession: PA0060
A:Molecule type: protein
A:Residues: 1-15 <CHO>

Query Match 25.6%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKPPK 6
|||
Db 2 LRPLPE 7

RESULT 14
PH0758
T-cell receptor beta chain (B22) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0758
R:Caenova, J.L.; Romero, P.; Wiemann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0758
A:Molecule type: mRNA
A:Residues: 1-16 <CAS>
A:Cross-references: EMBL:X60853; NID:G50743; PID:CAA43243.1; PID:G50744
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 25.6%; Score 21; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 PPKXLVEVF 12
|||
Db 5 PTKGSNTVEVF 14

RESULT 15
I4065
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C:Species: Buchnera aphidicola
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I4065
R:Roubaksh, D.; Baumann, P.
Gene 155, 107-112, 1995
A:Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (endosymbiont)
A:Reference number: I40651; MUID:95212914; PMID:7535281
A:Accession: I4065
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: UNIPROT:Q44610; EMBL:U10499; NID:G854717; PID:AAA79128.1; PID:G8547
C:Genetics:
A:Gene: aroL
C:Keywords: oxidoreductase

Query Match 25.6%; Score 21; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPKLK 8
|||
Db 9 PPKLR 13

RESULT 16
HE4008
hypothetical protein HI0492 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998
C:Accession: HE4008
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: HE4000; MUID:95350630; PMID:7542800
A:Accession: HE4008
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-14 <TRIG>
A:Cross-references: GB:U2731; GB:L42023; NID:G1573465; PID:G1573478; TIGR:HI0492

Query Match 25.0%; Score 20.5; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 LKP-PPKL 7
|||
Db 1 MKPKTPKM 8

RESULT 17
A61049
halo-toxin - Pseudomonas syringae pv. mori
C:Species: Pseudomonas syringae pv. mori
A:Note: host mulberry tree
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
C:Accession: A61049
R:Kajimoto, T.; Yokomizo, K.; Yabito, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.;
Chem. Lett. 00, 679-680, 1989
A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri
A:Reference number: A61049
A:Accession: A61049
A:Molecule type: protein
A:Residues: 1-6 <KAJ>
A:Note: sequence confirmed by synthesis
C:Comment: This toxin is one of the etiological agents of halo bright disease in mulberry

C:Keywords: toxin

Query Match 24.4%; Score 20; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5
|||
DB 1 PFP 3

RESULT 18

A60624

angiotensin I - Japanese quail

C:Species: Coturnix coturnix japonica (Japanese quail)

C>Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jul-2004

C:Accession: A60624

R:Taket, Y.; Hasegawa, Y.

Gen. Comp. Endocrinol. 79, 12-22, 1990

A:Title: Vasopressor and depressor effects of native angiotensins and inhibition of the

A:Reference number: A60624; MUID:90284684; PMID:2191893

A:Accession: A60624

A:Molecule type: protein

A:Residues: 1-10 <TRK>

A:Cross-references: UNIPROT:P01018

C:Superfamily: Serpin

C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match

Best Local Similarity 24.4%; Score 20; DB 2; Length 10;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 KYVYVPP 14
:|:|:|
DB 2 RYVYVHF 8

RESULT 19

A60410

beta-neoendorphin / dynorphin precursor - guinea pig

N:Alternate names: alpha-neoendorphin; proenkephalin B precursor

C:Species: Cavia porcellus (guinea pig)

C>Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 21-Jan-2000

C:Accession: A60410

R:Murphy, R.; Turner, C.A.

Peptides 11, 65-68, 1990

A:Title: Isolation and microsequence analysis of guinea pig alpha-neo-endorphin.

A:Reference number: A60410; MUID:90259864; PMID:2342931

A:Accession: A60410

A:Molecule type: protein

A:Residues: 1-10 <MUR>

C:Superfamily: proenkephalin

C:Keywords: neuropeptide; opioid peptide

Query Match 24.4%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKPPK 6
||:|:|
DB 5 LRYVPP 10

RESULT 20

A90917

angiotensin precursor - chicken (fragment)

C:Species: Gallus gallus (chicken)

C>Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 09-Jul-2004

C:Accession: A90917; A01250

R:Nakayama, T.; Nakajima, T.; Sokane, H.

Chem. Pharm. Bull. 21, 2085-2087, 1973

A:Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its

A:Reference number: A90917; MUID:74127845; PMID:4361802

A:Accession: A90917

A:Molecule type: protein

A:Residues: 1-10 <NAK>

A:Cross-references: UNIPROT:P01018

C:Keywords: blood pressure control; hormone; vasoconstrictor

F:1-10/Product: angiotensin I #status experimental <AN1>

F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 24.4%; Score 20; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 KYVYVPP 14
:|:|:|
DB 2 RYVYVHF 8

RESULT 21

A90345

angiotensin precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 09-Jul-2004

C:Accession: A90345; A01250

R:Elliot, D.F.; Peart, W.S.

Biochem. J. 65, 246-254, 1957

A:Title: The amino acid sequence in a hypertensin.

A:Reference number: A90345

A:Accession: A90345

A:Molecule type: protein

A:Residues: 1-10 <ELL>

A:Cross-references: UNIPROT:P01017

C:Keywords: blood pressure control; hormone; vasoconstrictor

F:1-10/Product: angiotensin I #status experimental <AN1>

F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 24.4%; Score 20; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 KYVYVPP 14
:|:|:|
DB 2 RYVYVHF 8

RESULT 22

PA0028

protein QA300042 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997

C:Accession: PA0028

R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

Submitted to JPIID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional

A:Reference number: PA0001

A:Accession: PA0028

A:Molecule type: protein

A:Residues: 1-11 <KAM>

A:Experimental source: seed

C:Keywords: seed

Query Match 24.4%; Score 20; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5
|||
DB 6 PFP 8

RESULT 23

S07207

Crinia-angiotensin, skin - frog (Crinia georgiana)

C:Species: Crinia georgiana

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Aug-2004
 C;Accession: S07207
 R;Erpamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.
 R;Experiment 35, 1132-1133, 1979
 A;Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II-1
 A;Reference number: S07207; MUID:80024575; PMID:488254
 A;Accession: S07207
 A;Molecule type: protein
 A;Residues: 1-11 <ERS>
 A;Cross-references: UNIPROT:P09037

Query Match 24.4%; Score 20; DB 2; Length 11;
 Best Local Similarity 40.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 PKLKVEVPF 14
 | : : | | |
 DB 2 PEDRIYVHPF 11

RESULT 24
 S32475
 LymadFamide 5 - great pond snail
 C;Species: Lymnaea stagnalis (great pond snail)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S32475
 R;Johnsen, A.H.; Rehfeld, J.F.
 R;Johnsen, A.H.; Rehfeld, J.F.
 Bur. J. Biochem. 213, 875-879, 1993
 A;Title: LymnadFamide, a new family of neuropeptides from the pond snail, Lymnaea stagnalis
 A;Reference number: S32475; MUID:93238777; PMID:8477756
 A;Accession: S32475
 A;Molecule type: protein
 A;Residues: 1-13 <OH>
 A;Cross-references: UNIPROT:P80182; PIDN:AA626366.1; PID:g299833
 A;Experimental source: ganglia
 C;Keywords: amidated carboxyl end; neuropeptide
 F;13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 24.4%; Score 20; DB 2; Length 13;
 Best Local Similarity 30.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 3 PPKLKVEVPF 12
 | : : |
 DB 1 PPDRISSAPF 10

RESULT 25
 PH1566
 cerebrin 30 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
 C;Accession: PH1566
 R;Deone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.
 J. Neurochem. 61, 533-540, 1993
 A;Title: Micropurification of two human cerebrospinal fluid proteins by high performance
 A;Reference number: PH1566; MUID:93329419; PMID:8336140
 A;Accession: PH1566
 A;Molecule type: protein
 A;Residues: 1-14 <LEO>

Query Match 24.4%; Score 20; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 3.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 PKLKVEVPF 13
 | : : | | |
 DB 2 PEAQVSVQP 10

RESULT 26
 LFECF
 phe operon leader peptide - Escherichia coli (strain K-12)

N;Alternate names: attenuator peptide
 C;Species: Escherichia coli
 C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
 C;Accession: A03593; B36494; A65038
 R;Zurawski, G.; Brown, K.; Kittingly, D.; Yanofsky, C.
 Proc. Natl. Acad. Sci. U.S.A. 75, 4271-4275, 1978
 A;Title: Nucleotide sequence of the leader region of the phenylalanine operon of Escherichia coli
 A;Reference number: A03593; MUID:79033820; PMID:360214
 A;Accession: A03593
 A;Molecule type: DNA
 A;Residues: 1-15 <ZUR>
 A;Cross-references: UNIPROT:P03057; GB:V00314; GB:J01658; NID:g42378; PIDN:CAA23600.1; P
 R;Gavin, N.; Davidson, B.E.
 J. Biol. Chem. 265, 21532-21535, 1990
 A;Title: pheAO mutants of Escherichia coli have a defective pheA attenuator.
 A;Reference number: A36494; MUID:91072346; PMID:2254312
 A;Accession: B36494
 A;Molecule type: DNA
 A;Residues: 1-15 <GAV>
 A;Cross-references: GB:M58024; GB:J05694; NID:g147178; PIDN:AAA62783.1; PID:g147180
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64720; MUID:97426617; PMID:9278503
 A;Accession: A65038
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-15 <BLAT>
 A;Cross-references: GB:A000346; GB:U00096; NID:g2367141; PIDN:AACT5647.1; PID:g1789350;
 A;Experimental source: strain K-12, substrain MG1655
 C;Genetics:
 A;Gene: pheU, pheA
 A;Map position: 56 min
 C;Superfamily: pheA leader peptide

Query Match 24.4%; Score 20; DB 1; Length 15;
 Best Local Similarity 33.3%; Pred. No. 4e+03;
 Matches 5; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 1 LKPPKLKVEVPF 15
 : : | | |
 DB 1 MKHIDFFPAFFPTFP 15

RESULT 27
 PA0026
 protein QA300027 - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C;Accession: PA0026
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Teugita, A.
 submitted to JIPID, July 1994
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensiona
 A;Reference number: PA0001
 A;Accession: PA0026
 A;Molecule type: protein
 A;Residues: 1-15 <KAM>
 A;Experimental source: leaf

Query Match 24.4%; Score 20; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 4e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 LKVEVPF 14
 | | | | |
 DB 2 LKVYGYXP 9

RESULT 28
 PA0024
 protein QA300050 - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)

CjDate: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
CjAccession: PA0024
RjKano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A>Description: Separation and characterization of Arabidopsis proteins by two-dimensions
A.Reference number: PA0001
AjAccession: PA0024
AjMolecule type: protein
AjResidues: 1-15 <KAN>
AjExperimental source: seed

Query Match 24.4%; Score 20; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 6 PPP 8

RESULT 29
PA0088
Protein QP200051 - fungus (Fusarium sporotrichioides) (fragment)
CjSpecies: Fusarium sporotrichioides
CjDate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
CjAccession: PA0088
RjChow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A>Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A.Reference number: PA0051
AjAccession: PA0088
AjMolecule type: protein
AjResidues: 1-15 <CHO>

Query Match 24.4%; Score 20; DB 2; Length 15;
Best Local Similarity 27.3%; Pred. No. 4e+03;
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 PRLKVEVPP 15
|:|:|
Db 3 PDIPXDYPAP 13

RESULT 30
PD0444
coupling factor 6 mitochondrial - mouse (fragment)
CjSpecies: Mus musculus (house mouse)
CjDate: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999
CjAccession: PD0444
RjKawakami, T.; Uchida, T.; Sakai, T.; Kano, M.; Morimasa, T.; Tsugita, A.
submitted to JIPID, August 1998
A>Description: Proteome analysis of mouse brain.
A.Reference number: PD0441
AjContents: Striatum
AjAccession: PD0444
AjMolecule type: protein
AjResidues: 1-15 <KAN>
CjKeywords: mitochondrion

Query Match 24.4%; Score 20; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKPPKLYVE 10
|||
Db 4 LDPVQKLFVD 13

RESULT 31
A53337
regulatory protein tyrR - Escherichia coli (fragment)
CjSpecies: Escherichia coli
CjDate: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 07-May-1999

CjAccession: A53337
RjArguet, V.P.; Wilson, T.J.; Davidson, B.E.
J. Biol. Chem. 269, 5171-5178, 1994
A>Title: Purification of the Escherichia coli regulatory protein TyrR and analysis of its
A.Reference number: A53337; MUID:94148980; PMID:8106498
AjAccession: A53337
AjStatus: preliminary
AjMolecule type: protein
AjResidues: 1-16 <ARG>

Query Match 24.4%; Score 20; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKVEVP 12
::|
Db 1 MRLVEVF 6

RESULT 32
A37823
dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - bovine (fragment)
CjSpecies: Bos primigenius taurus (cattle)
CjDate: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
CjAccession: A37823
RjRahmatullah, M.; Radke, G.A.; Andrews, P.C.; Roche, T.E.
J. Biol. Chem. 265, 14512-14517, 1990
A>Title: Changes in the core of the mammalian-pyruvate dehydrogenase complex upon select
A.Reference number: A37823; MUID:90354445; PMID:2167319
AjAccession: A37823
AjStatus: preliminary
AjMolecule type: protein
AjResidues: 1-17 <RAH>
AjCross-references: UNIPROT:Q7M2M8
CjKeywords: acyltransferase; coenzyme A

Query Match 24.4%; Score 20; DB 2; Length 17;
Best Local Similarity 55.6%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PRLKVEVPP 13
||:|
Db 2 PKGRVFPVSP 10

RESULT 33
S14661
photosystem I protein psal - maize (fragment)
CjSpecies: Zea mays (maize)
CjDate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
CjAccession: S14661
RjKangasjarvi, J.; Gengenbach, B.G.
submitted to the EMBL Data Library, March 1991
A>Description: Nucleotide sequence of maize plastid genome BamHI 14 fragment.
A.Reference number: S14660
AjAccession: S14661
AjStatus: preliminary
AjMolecule type: DNA
AjResidues: 1-18 <KAN>
CjCross-references: EMBL:X58080; NID:g12429; PIDN:CAA41109.1; PID:g12431
CjSuperfamily: photosystem I P700 apoprotein

Query Match 24.4%; Score 20; DB 2; Length 18;
Best Local Similarity 42.9%; Pred. No. 4.9e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 PRLKVEV 11
|:|:|
Db 8 PEVKLAV 14

RESULT 34
S09731

photosystem I protein psal - spinach chloroplast (fragment)
C:Species: chloroplast Spinacia oleracea (spinach)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 19-Jan-1996
C:Accession: S09731
R:Reuch, M.; Hirano, A.; Miyama, T.; Inoue, Y.
FEBS Lett. 263, 274-278, 1990
A>Title: Polypeptide composition of higher plant photosystem I complex. Identification o
A:Reference number: S09730; MUID:90242987; PMID:2185953
A:Accession: S09731
A:Molecule type: protein
A:Residues: 1-18 <IRK>
C:Genetics:
A:Gene: psal
A:Genome: chloroplast
C:Superfamily: photosystem I protein psal
C:Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem I; th
Query Match 24.4%; Score 20; DB 2; Length 18;
Best Local Similarity 42.9%; Pred. No. 4.9e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 4; Gaps 1;
QY 4 FPKLVE---VFP 13
Db 3 FPSIFVPLVGLVFP 16
RESULT 35
A61392
brain-associated small cell lung cancer antigen - human (fragment)
N:Alternate names: BASCA
C:Species: Homo sapiens (man)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Sep-1994
C:Accession: A61392
R:Umezawa, Y.; Kuge, S.; Kikyo, N.; Shirai, T.; Watanabe, J.; Fujiwara, M.; Okabe, T.
Jpn. J. Clin. Oncol. 21, 251-255, 1991
A>Title: Identity of brain-associated small cell lung cancer antigen and the CD56 (NKH-1
A:Reference number: A61392; MUID:92046737; PMID:1719260
A:Accession: A61392
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <DME>
Query Match 24.4%; Score 20; DB 2; Length 18;
Best Local Similarity 42.9%; Pred. No. 4.9e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 7 LKVEVFP 13
Db 1 IQVDIVP 7
RESULT 36
H75063
hypothetical protein PAB7382 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H75063
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: H75063
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <KAW>
A:Cross-references: UNIPROT:Q9UYK7; GB:AJ248287; GB:AL096836; NID:95458657; PIND:CB5040
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB7382
Query Match 24.4%; Score 20; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLVKE 10
Db 2 KLVKE 6
RESULT 37
S66635
alpha-2-macroglobulin isoform 1 - bovine (fragment)
C:Species: Bos primigenius indicus (zebu cattle)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66635
R:Doimer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottru
FEBS Lett. 372, 93-95, 1995
A>Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain o
A:Reference number: S66634; MUID:96032553; PMID:7556651
A:Accession: S66635
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DOL>
A:Cross-references: UNIPROT:Q7M2N8
Query Match 23.2%; Score 19; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 FPF 14
Db 4 FPF 6
RESULT 38
S65432
angiotensin I - horn fly (fragment)
C:Species: Haematobia irritans (horn fly)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65432
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Ridding, G.; Elyin, C.; Kemp, D.; Willadsen, P
Eur. J. Biochem. 237, 414-423, 1996
A>Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran
A:Reference number: S65431; MUID:96215437; PMID:8647080
A:Accession: S65432
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <WID>
A:Note: the source is designated as Haematobia irritans exigua
Query Match 23.2%; Score 19; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 8 KVEVFP 14
Db 2 RYTHPF 8
RESULT 39
A61218
alpha-gliadin 4Ha - grass (Haynaldia villosa) (fragment)
C:Species: Haynaldia villosa, Despyrum villosum
C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C:Accession: A61218
R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.
Biochem. Genet. 29, 207-211, 1991
A>Title: alpha-type prolamin are encoded by genes on chromosomes 4Ha and 6Ha of Haynald
A:Reference number: A61218; MUID:91315394; PMID:1853356
A:Accession: A61218
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SHE>
A:Cross-references: UNIPROT:Q7M1F7
C:Keywords: seed; storage protein

Query Match 23.2%; Score 19; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPPKXK 8
 | | | | |
 Db 5 PVVPOLO 10

RESULT 40

B61218
 alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)
 C:Species: Haynaldia villosa, Dasyphyum villosum
 C:Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #ext_change 09-Jul-2004
 C:Accession: B61218
 R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.
 Biochem. Genet. 29, 207-211, 1991
 A>Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia
 A:Reference number: A61218; WUID:91315394; PMID:1859356
 A:Accession: B61218
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <SHS>
 A:Cross-references: UNIPROT:Q7M1P6
 C:Keywords: seed; storage protein

Query Match 23.2%; Score 19; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPPKXK 8
 | | | | |
 Db 4 PVVPOLO 9

Search completed: June 7, 2005, 23:20:42
 Job time : 13.9091 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 66 Seconds
(without alignments)
116.382 Million cell updates/sec

Title: US-10-691-157-8
Perfect score: 82
Sequence: 1 LKPFKLVKVEVPPFP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	40.2	18	2	07M076
2	30	36.6	14	2	P82435
3	29	35.4	11	2	07RBB2
4	29	35.4	15	2	09S929
5	29	35.4	16	2	09BGG8
6	26	31.7	15	2	06LAI1
7	26	31.7	18	2	09QV11
8	25	30.5	17	2	09JIA7
9	24	29.3	10	2	06QV66
10	24	29.3	15	2	06LC13
11	24	29.3	16	2	06QVE1
12	24	29.3	16	2	09R4J0
13	24	29.3	17	2	09T529
14	23	28.0	8	2	06R4Q8
15	23	28.0	11	1	PVK3_BIACR
16	23	28.0	11	1	PVK3_BIADU
17	23	28.0	11	1	PVK3_GROPO
18	23	28.0	11	1	PVK3_LEUMA
19	23	28.0	11	1	PVK3_NAUCI
20	23	28.0	16	1	FOR2_MVRGU
21	23	28.0	17	2	09TRH5
22	23	28.0	18	2	006711
23	23	28.0	18	2	067216
24	23	28.0	11	2	09QV66
25	22	26.8	16	2	08LVE0
26	22	26.8	16	2	08LVE1
27	22	26.8	16	2	08LVE2
28	22	26.8	16	2	08MC15
29	22	26.8	16	2	08MC17
30	22	26.8	16	2	08MC19
31	22	26.8	16	2	08MC21

32	22	26.8	16	2	08MC23
33	22	26.8	16	2	08MC25
34	22	26.8	16	2	08MC27
35	22	26.8	16	2	08MC29
36	22	26.8	16	2	08MC31
37	22	26.8	16	2	08MC33
38	22	26.8	16	2	08MC35
39	22	26.8	16	2	08MC37
40	22	26.8	16	2	08MC39
41	22	26.8	16	2	08MC41
42	22	26.8	16	2	08MC43
43	22	26.8	16	2	08MC45
44	22	26.8	16	2	08MC47
45	22	26.8	16	2	08MC49
46	22	26.8	16	2	08MC51
47	22	26.8	16	2	08MC53
48	22	26.8	16	2	08MC58
49	22	26.8	16	2	08MC60
50	22	26.8	16	2	08MC62
51	22	26.8	16	2	08MC64
52	22	26.8	16	2	08MC66
53	22	26.8	16	2	08MC68
54	22	26.8	16	2	08MC70
55	22	26.8	16	2	08MC72
56	22	26.8	16	2	08MC74
57	22	26.8	16	2	08MC76
58	22	26.8	16	2	08MC78
59	22	26.8	16	2	08MC80
60	22	26.8	16	2	08MC82
61	22	26.8	16	2	08MC84
62	22	26.8	16	2	08MC86
63	22	26.8	16	2	08MC88
64	22	26.8	16	2	08MC90
65	22	26.8	16	2	08MC92
66	22	26.8	16	2	08MC94
67	22	26.8	16	2	08MC96
68	22	26.8	16	2	08MC98
69	22	26.8	16	2	08MC100
70	22	26.8	16	2	08MC102
71	22	26.8	16	2	08MC104
72	22	26.8	16	2	08MC106
73	22	26.8	16	2	08MC108
74	22	26.8	16	2	08MC110
75	22	26.8	16	2	08MC112
76	22	26.8	16	2	08MC114
77	22	26.8	16	2	08MC116
78	22	26.8	16	2	08MC118
79	22	26.8	16	2	08MC120
80	22	26.8	16	2	08MC122
81	22	26.8	16	2	08MC124
82	22	26.8	16	2	08MC126
83	22	26.8	16	2	08MC128
84	22	26.8	16	2	08MC130
85	22	26.8	16	2	08MC132
86	22	26.8	16	2	08MC134
87	22	26.8	16	2	08MC136
88	22	26.8	16	2	08MC138
89	22	26.8	16	2	08MC140
90	22	26.8	16	2	08MC142
91	22	26.8	16	2	08MC144
92	22	26.8	16	2	08MC146
93	22	26.8	16	2	08MC148
94	22	26.8	16	2	08MC150
95	22	26.8	16	2	08MC152
96	22	26.8	16	2	08MC154
97	22	26.8	16	2	08MC156
98	22	26.8	16	2	08MC158
99	22	26.8	16	2	08MC160
100	22	26.8	16	2	08MC162

ALIGNMENTS

08mc23	sonneratia
08mc25	sonneratia
08mc27	lagerstroem
08mc29	dubanga gr
08mc31	lagerstroem
08mc33	rotala indi
08mc35	heimia myrt
08mc37	lawsonia in
08mc39	amannia ba
08mc41	neasea lued
08mc43	sonneratia
08mc45	decodon ver
08mc47	peplis port
08mc49	peplis acti
08mc51	cuphea lanc
08mc53	woodfordia
08mc58	daphniphyll
08mc60	cericidiphyll
08mc62	saxifraga s
08mc64	triticum ae
08mc66	rhodococcus
08mc68	sinapis alb
08mc70	sinapis alb
08mc72	eschschia
08mc74	eschschia
08mc76	plasmidium
08mc78	plasmidium
08mc80	plasmidium
08mc82	plasmidium
08mc84	plasmidium
08mc86	plasmidium
08mc88	plasmidium
08mc90	plasmidium
08mc92	plasmidium
08mc94	plasmidium
08mc96	plasmidium
08mc98	plasmidium
08mc100	plasmidium
08mc102	plasmidium
08mc104	plasmidium
08mc106	plasmidium
08mc108	plasmidium
08mc110	plasmidium
08mc112	plasmidium
08mc114	plasmidium
08mc116	plasmidium
08mc118	plasmidium
08mc120	plasmidium
08mc122	plasmidium
08mc124	plasmidium
08mc126	plasmidium
08mc128	plasmidium
08mc130	plasmidium
08mc132	plasmidium
08mc134	plasmidium
08mc136	plasmidium
08mc138	plasmidium
08mc140	plasmidium
08mc142	plasmidium
08mc144	plasmidium
08mc146	plasmidium
08mc148	plasmidium
08mc150	plasmidium
08mc152	plasmidium
08mc154	plasmidium
08mc156	plasmidium
08mc158	plasmidium
08mc160	plasmidium
08mc162	plasmidium
08mc164	plasmidium
08mc166	plasmidium
08mc168	plasmidium
08mc170	plasmidium
08mc172	plasmidium
08mc174	plasmidium
08mc176	plasmidium
08mc178	plasmidium
08mc180	plasmidium
08mc182	plasmidium
08mc184	plasmidium
08mc186	plasmidium
08mc188	plasmidium
08mc190	plasmidium
08mc192	plasmidium
08mc194	plasmidium
08mc196	plasmidium
08mc198	plasmidium
08mc200	plasmidium

RESULT 1

Q7RB2
ID Q7RB2 PRELIMINARY; PRT; 18 AA.
AC Q7RB2; 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY06234;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angioli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoabhi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CATION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
DR EMBL, ABL01002084; EAA18412.1; -.
KW Hypothetical protein.
SQ SEQUENCE 11 AA; 1326 MW; 59A5901E69D5B337 CRC64;

Query Match
Best Local Similarity 40.2%; Score 33; DB 2; Length 18;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 KPPKLVFP 13
: ||| |
Db 4 RPPKLVFP 15

RESULT 2
P82435
ID P82435 PRELIMINARY; PRT; 14 AA.
AC P82435;
DT 01-JUN-2000 (TREMBlrel. 14, Created)
DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
DT 29 kDa cell wall protein (Fragment).
DE Nicotiana tabacum (Common tobacco).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; OC Lamiales; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;
RN (1)
RP SEQUENCE.
RC STRAIN=cv.
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Stabas A.R., Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed tobacco culture."
RL Planta 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
DR GO; GO:0005618; Cell wall; IEA.
KW Cell wall.
FT NON TER
SQ SEQUENCE 14 AA; 1645 MW; CA0D490EF7F851B2 CRC64;

Query Match
Best Local Similarity 36.6%; Score 30; DB 2; Length 14;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 PPKLVFP 14
: ||| |
Db 2 YPKLVFP 12

RESULT 3

Q7RB2
ID Q7RB2 PRELIMINARY; PRT; 11 AA.
AC Q7RB2;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY06234;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angioli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoabhi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CATION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
DR EMBL, ABL01002084; EAA18412.1; -.
KW Hypothetical protein.
SQ SEQUENCE 11 AA; 1326 MW; 59A5901E69D5B337 CRC64;

Query Match
Best Local Similarity 35.4%; Score 29; DB 2; Length 11;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKPPK 8
: ||| |
Db 4 LKSPKSK 11

RESULT 4
Q9S929
ID Q9S929 PRELIMINARY; PRT; 15 AA.
AC Q9S929;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Pyruvate-5-carboxylate reductase, PSOR (Fragment).
OS Glycine max (soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; OC Euphorbiales; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
RN (1)
RP SEQUENCE.
RC MEDLINE=91378472; PubMed=1898034;
RA Chilson O.P., Kelly-Chilson A.B., Siegel N.R.;
RT "Pyruvate-5-carboxylate reductase in soybean nodules: isolation/partial primary structure/evidence for isozymes."
RL Arch. Biochem. Biophys. 288:350-357(1991).
FT NON TER
SQ SEQUENCE 15 AA; 1715 MW; D9821F73FD524 CRC64;

Query Match
Best Local Similarity 35.4%; Score 29; DB 2; Length 15;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 VEVFP 15
: ||| |

Db 1 MEIPPIP 7

RESULT 5

Q9BG68 PRELIMINARY; PRT; 16 AA.
AC Q9BG68;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 24, Last annotation update)
DE Thyroid hormone receptor alpha (Fragment).
OS Name=TRKAI;
OS Sorex araneus (Eurasian common shrew) (European shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.
OX NCBI_TaxId=42254;
RN (1)
RP SEQUENCE FROM N.A.
RA Lartin D., Serov O., Zhdanova N.;
RT "Mapping of five genes from human chromosome 17 to chromosome hn of
the common shrew (Sorex araneus).";
RL Acta Theriol. 45:143-146(2000).
DR EMBL; AF314827; AAK13419.1; -
DR GO; GO:0004872; P:receptor activity; IEA.
KW Receptor.
FT NON_TER
SQ SEQUENCE 16 AA; 1951 MW; 7751663BF5F52E2 CRC64;

Query Match 35.4%; Score 29; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 9.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PPKLKEVP 12
Db 3 PPKLKEVP 11

RESULT 6

Q6LAI1 PRELIMINARY; PRT; 15 AA.
AC Q6LAI1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Andropin (Fragment).
OS Name=And;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Montemayor;
RX MEDLINE=98393576; PubMed=9725836;
RA Ramos-Onsins S., Aguade M.;
RT "Molecular Evolution of the Cecropin multigene family in Drosophila:
functional genes vs pseudogenes.";
RT Genetics 150:157-171(1998).
DR EMBL; Y16853; CAA76430.1; -
DR EMBL; Y16854; CAA76436.1; -
DR EMBL; Y16855; CAA76442.1; -
DR EMBL; Y16856; CAA76448.1; -
DR EMBL; Y16857; CAA76454.1; -
DR EMBL; Y16858; CAA76460.1; -
DR EMBL; Y16859; CAA76466.1; -
DR EMBL; Y16861; CAA76476.1; -
DR EMBL; Y16862; CAA76476.1; -
FT NON_TER
SQ SEQUENCE 15 AA; 1659 MW; C86F9313DEE24182 CRC64;

Query Match 31.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.7e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KPPKLT 7
Db 6 KPPKLT 11

RESULT 7

Q9QV11 PRELIMINARY; PRT; 18 AA.
AC Q9QV11;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sucrase-alpha-dextrinase subunit beta, S-D subunit beta
(Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10118;
RN (1)
RP SEQUENCE.
RX MEDLINE=92031479; PubMed=1931964;
RA Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.;
RT "Structural and functional correlates of sucrase-alpha-dextrinase in
intact brush border membranes.";
RL Biochemistry 30:10399-10408(1991).
FT NON_TER
SQ SEQUENCE 18 AA; 2122 MW; 68F1ABA87B24E49 CRC64;

Query Match 31.7%; Score 26; DB 2; Length 18;
Best Local Similarity 55.6%; Pred. No. 3.3e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPKLKEVP 11
Db 7 PPKLKEVP 15

RESULT 8

Q9JIA7 PRELIMINARY; PRT; 17 AA.
AC Q9JIA7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE Fibroblast growth factor homologous factor 3 isoform 1B
(Fragment).
OS Name=FHR-3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20112823; PubMed=10644718; DOI=10.1074/jbc.275.4.2589;
RA Munoz-Saujan I., Smallwood P.M., Nathans J.;
RT "Isoform diversity among fibroblast growth factor homologous factors
is generated by alternative promoter usage and differential
splicing.";
RL J Biol Chem. 275:2589-2597(2000).
DR EMBL; AF199604; AAF31391.1; -
FT NON_TER
SQ SEQUENCE 17 AA; 1870 MW; 9A0E0364E96D949 CRC64;

Query Match 30.5%; Score 25; DB 2; Length 17;
Best Local Similarity 62.5%; Pred. No. 4.5e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKPPKLT 8
Db 3 LKPPKLT 10

RESULT 9

06QV6 PRELIMINARY; PRT; 10 AA.

AC 06QV6; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 RN Ribonuclease H (Fragment).
 GN Name=RNase H;
 OS Phaseolus vulgaris (kidney bean) (French bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
 NCBI_TaxID=3885;

RP SEQUENCE FROM N.A.
 RX PubMed=15060605; DOI=10.1139/g03-102;
 RA Galindo L.M., Galtan E., Baccam P., Tohme J.;
 RT "Isolation and characterization of RNase-LTR sequences of Ty1-copia
 RT retrotransposons in common bean (Phaseolus vulgaris L.).";
 RL Genome 47:84-95(2004).
 DR EMBL; AY524233; AAS18530.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 1113 MW; AE2362376321A726 CRC64;

Query Match 29.3%; Score 24; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 3.9e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPFPK 6
 Db 6 KPFPK 10

RESULT 10

06LC13 PRELIMINARY; PRT; 15 AA.

AC 06LC13; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 RN Na+-phosphate cotransporter type II (Fragment).
 GN Name=NP2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RX MEDLINE=93317607; PubMed=8327470;
 RA Maggnin S., Werner A., Markovich D., Sorribas V., Strange G.,
 RA Biber U., Murer H.;
 RT "Expression cloning of human and rat renal cortex Na/Pi cotransport."
 RT Proc. Natl. Acad. Sci. U.S.A. 90:5979-5983(1993).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=96293539; PubMed=8633007; DOI=10.1073/pnas.93.14.7409;
 RA Hartman C.M., Hewson A.S., Kos C.H., Hilfinger H., Sounounou Y.,
 RA Murer H., Tenenhouse H.S.;
 RT "Structure of murine and human renal type II Na+-phosphate
 RT cotransporter genes (Npt2 and NPT2).";
 RT Proc. Natl. Acad. Sci. U.S.A. 93:7409-7414(1996).
 DR EMBL; U56684; AAD14856.1; -.

FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1770 MW; 23810E2056D88BAB CRC64;

Query Match 29.3%; Score 24; DB 2; Length 15;
 Best Local Similarity 44.4%; Pred. No. 5.8e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 KPFPK 10
 Db 7 KPFPK 15

RESULT 11

06QV61 PRELIMINARY; PRT; 16 AA.

AC 06QV61; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 RN Ribonuclease H (Fragment).
 GN Name=RNase H;
 OS Phaseolus vulgaris (kidney bean) (French bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
 NCBI_TaxID=3885;

RP SEQUENCE FROM N.A.
 RX PubMed=15060605; DOI=10.1139/g03-102;
 RA Galindo L.M., Galtan E., Baccam P., Tohme J.;
 RT "Isolation and characterization of RNase-LTR sequences of Ty1-copia
 RT retrotransposons in common bean (Phaseolus vulgaris L.).";
 RL Genome 47:84-95(2004).
 DR EMBL; AY524258; AAS18555.1; -.

FT NON_TER 1 1
 SQ SEQUENCE 16 AA; 1935 MW; 3E60812E8E2D6A23 CRC64;

Query Match 29.3%; Score 24; DB 2; Length 16;
 Best Local Similarity 80.0%; Pred. No. 6.2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPFPK 6
 Db 6 KPFPK 10

RESULT 12

09R4U0 PRELIMINARY; PRT; 16 AA.

AC 09R4U0; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 RN LIMONATE dehydrogenase (Fragment).

OS Arthrobacter globiformis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococciaceae; Micrococcaceae; Arthrobacter.
 NCBI_TaxID=1665;

RP SEQUENCE.
 RX MEDLINE=96045380; PubMed=7546548; DOI=10.1016/0031-9422(94)00953-Q;
 RA Sunayda C.G., Omura M., Hasegawa S.;
 RT "Limonate dehydrogenase from Arthrobacter globiformis: the native
 RT enzyme and its N-terminal sequence.";
 RL Phytochemistry 40:17-20(1995).
 SQ SEQUENCE 16 AA; 1759 MW; 514B2E906FD5984 CRC64;

Query Match 29.3%; Score 24; DB 2; Length 16;
 Best Local Similarity 55.6%; Pred. No. 6.2e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPFPK 11
 Db 2 KPFPK 10

RESULT 13

09T5Z9 PRELIMINARY; PRT; 17 AA.

AC 09T5Z9;

```

DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATPase8;
OS Pimelodella chagresi.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Pimelodidae; Pimelodella.
OK NCBI_TaxID=71257;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98291472; PubMed=9628002;
RA Berningham E., Martin A.P.;
RT "Comparative mtDNA phylogeography of neotropical freshwater fishes:
RT testing shared history to infer the evolutionary landscape of lower
RT Central America."
RL Mol. Ecol. 7:499-517(1998).
DR EMBL; AF040423; AAC77594.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 17 AA; 2113 MW; 40325B578612222A CRC64;

Query Match 29.3%; Score 24; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 6.6e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 KLVKEVFPFP 15
DB 6 KLVKEVFPFP 15

RESULT 14
O6R408 PRELIMINARY; PRT; 8 AA.
ID O6R408
AC O6R408;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Alpha-S1-casein (Fragment).
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN (1)
RP SEQUENCE FROM N.A.
RA Mishra S.S., Bhattacharya T.K., Sharma A., Dayal S., Vohra V.,
RA Shelkh F.D., Kumar P.;
RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF514427; AAS00439.1; -.
FT NON TER
FT NON TER
SQ SEQUENCE 8 AA; 920 MW; 633879D2CB0769D7 CRC64;

Query Match 28.0%; Score 23; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 3 PPKKLVFP 12
DB 1 PPP---EVF 6

RESULT 15
PVK3 BLACR STANDARD; PRT; 11 AA.
ID PVK3 BLACR
AC P83933; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

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DE Periviscerokinin-3 (Uem-PVK-3).
OS Blaberus craniifer (Beach's head cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberridae; Blaberus.
OX NCBI_TaxID=6982;
RN (1)
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES
FT MOD RES
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKKL 7
DB 7 PPKPV 11

RESULT 16
PVK3 BLADU STANDARD; PRT; 11 AA.
ID PVK3 BLADU
AC P83934; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Periviscerokinin-3 (Uem-PVK-3).
OS Blaptica dubia (Argentinian wood cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Blaptica.
OX NCBI_TaxID=132935;
RN (1)
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES
FT MOD RES
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKKL 7
DB 7 PPKPV 11

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RESULT 17
PVK3 GROPO
ID PVK3 GROPO STANDARD; PRT; 11 AA.
AC P83935; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Periviscerokinin-3 (Lem-PVK-3).
OS Gromphadorina porterosa (Madagascan hissing cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Gromphadorhina.
OX NCBI_TaxID=36953;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 11 Valine amide.
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9F2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKL 7
Db 7 PPRV 11

RESULT 18
PVK3 LEUMA
ID PVK3 LEUMA STANDARD; PRT; 11 AA.
AC P83931; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Periviscerokinin-3 (Lem-PVK-3).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 11 Valine amide.
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9F2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKL 7
Db 7 PPRV 11

RESULT 19
PVK3 NAUCI
ID PVK3 NAUCI STANDARD; PRT; 11 AA.
AC P83932; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Periviscerokinin-3 (Lem-PVK-3).
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Nauphoeta.
OX NCBI_TaxID=6990;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 11 Valine amide.
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9F2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKL 7
Db 7 PPRV 11

RESULT 20
FOR2 MYRGU
ID FOR2 MYRGU STANDARD; PRT; 16 AA.
AC P81437;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Formacin 2.
OS Myrmecia gulosa (Red bulldog ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Formicidae; Myrmecinae; Myrmecini; Myrmecia.
OX NCBI_TaxID=36170;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RC TISSUE=Hemolymph;
RX MEDLINE=98165787; PubMed=9497332; DOI=10.1074/jbc.273.11.6139;
RA Mackintosh J.A., Veal D.A., Beattie A.J., Goolley A.A.;
RT "Isolation from an ant Myrmecia gulosa of two inducible O-glycosylated
RT proline-rich antibacterial peptides."
RL J. Biol. Chem. 273:6139-6143(1998).

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SQ SEQUENCE 11 AA; 1147 MW; 2F4D9F2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKL 7
Db 7 PPRV 11

RESULT 19
PVK3 NAUCI
ID PVK3 NAUCI STANDARD; PRT; 11 AA.
AC P83932; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Periviscerokinin-3 (Lem-PVK-3).
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Nauphoeta.
OX NCBI_TaxID=6990;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 11 Valine amide.
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9F2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKL 7
Db 7 PPRV 11

RESULT 20
FOR2 MYRGU
ID FOR2 MYRGU STANDARD; PRT; 16 AA.
AC P81437;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Formacin 2.
OS Myrmecia gulosa (Red bulldog ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Formicidae; Myrmecinae; Myrmecini; Myrmecia.
OX NCBI_TaxID=36170;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RC TISSUE=Hemolymph;
RX MEDLINE=98165787; PubMed=9497332; DOI=10.1074/jbc.273.11.6139;
RA Mackintosh J.A., Veal D.A., Beattie A.J., Goolley A.A.;
RT "Isolation from an ant Myrmecia gulosa of two inducible O-glycosylated
RT proline-rich antibacterial peptides."
RL J. Biol. Chem. 273:6139-6143(1998).

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CC -1- FUNCTION: Antibacterial peptide. Has activity against E.coli but
 CC none against other Gram-negative bacteria and Gram-positive
 CC bacteria.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- INDUCTION: By bacterial infection.
 CC -1- PTM: O-linked glycan consists of a Gal-GalNAc disaccharide, O-
 CC glycosylation is essential for full biological activity.
 CC Antibiotic: Direct protein sequencing; Glycoprotein; Hemolymph;
 KW Insect immunity.
 FT CARBOHYD 11 11 O-linked (GalNAc...)
 SQ SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BC2E0AE CRC64;

Query Match 28.0%; Score 23; DB 1; Length 16;
 Best Local Similarity 60.0%; Pred. No. 9.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 PEPKLV 7
 DB 12 PYPRL 16

RESULT 21

O9TRH5 PRELIMINARY; PRT; 17 AA.
 AC O9TRH5;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
 DE Alpha-S1-casein homolog (Fragment).
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93231344; PubMed=1299613; DOI=10.1016/0014-5793(92)80664-3;
 RA Neutrocom B., Giuffrida M.G., Conci A.;
 RT "Isolation of a new ligand-carrying casein fragment from bovine
 RT mammary gland microsomes";
 RL FEBS Lett. 305:189-191(1992).
 SQ SEQUENCE 17 AA; 1950 MW; 8890EF0685A0537F CRC64;

Query Match 28.0%; Score 23; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 9.6e+03;
 Matches 6; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

OY 3 PEPKLV 12
 DB 4 PEP---EVF 9

RESULT 22

O06711 PRELIMINARY; PRT; 18 AA.
 AC O06711;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Ubiquitin (Fragment).
 GN Name=UB1;
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YPH1;
 RX MEDLINE=94024010; PubMed=8211183;
 RA Ota I.M., Vazhnevsky A.;
 RT "A yeast protein similar to bacterial two-component regulators";
 RL Science 262:566-569(1993).
 DR EMBL; U01835; AAC48913.1; -.

FT NON TER 1 1
 SQ SEQUENCE 18 AA; 2249 MW; D13K4F7C1DBBFD1 CRC64;

Query Match 28.0%; Score 23; DB 2; Length 18;
 Best Local Similarity 62.5%; Pred. No. 1e+04;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LKPPKLV 8
 DB 11 LRPKGLK 18

RESULT 23

O67216 PRELIMINARY; PRT; 18 AA.
 AC O67216;
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Photosystem I apoprotein A1 (Fragment).
 GN Name=psaA;
 OS Pennisetum americanum (Pearl millet).
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC PACAD clade; Panicoideae; Paniceae; Pennisetum.
 OC NCBI_TaxID=4543;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nallal S.C., Nekkalaipudi S.C., Podile A.R.;
 RT "Pennisetum glaucum clone PGB788 coding for IRP170.";
 RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY694132; ANU2166.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 18 18
 SQ SEQUENCE 18 AA; 2111 MW; 008E617FE6845893 CRC64;

Query Match 28.0%; Score 23; DB 2; Length 18;
 Best Local Similarity 44.4%; Pred. No. 1e+04;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 PEPKLV 11
 DB 6 PEPVKLV 14

RESULT 24

O90YF6 PRELIMINARY; PRT; 11 AA.
 AC O90YF6;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
 DE Pancreas transcription factor1 p48 subunit (Fragment).
 GN Name=PTF1p48;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SV;
 RX MEDLINE=21219338; PubMed=11318877;
 RA Obata J., Yano M., Miyura H., Goto T., Nakayama R., Mibu Y., Oka C.,
 RA Kawauchi M.;
 RT "p48 subunit of mouse PTF1 binds to RBP-Jkappa/CBF-1, the
 RT intracellular mediator of Notch signalling, and is expressed in the
 RT neural tube of early stage embryos";
 RL Genes Cells 6:345-360(2001).
 DR EMBL; AB035674; BAA8247.1; -.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1327 MW; CA4662F8E3372732 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 9.1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKPFK 6
 |||||
 DB 6 LKGFPR 11

RESULT 25

Q8LVE0 PRELIMINARY; PRT; 16 AA.

AC Q8LVE0; 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Psaa (Fragment).
 GN Name=psaa;
 OS Trapa maximowiczii.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Trapa.
 OX NCBI_TaxId=162053;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035729; AAL14139.1; -;
 DR EMBL; AY035730; AAL14141.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;
 Best Local Similarity 44.4%; Pred. No. 1.3e+04;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PPKLKVEV 11
 |||||
 DB 6 PEPEVKILV 14

RESULT 26

Q8LVE1 PRELIMINARY; PRT; 16 AA.

AC Q8LVE1; 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Psaa (Fragment).
 GN Name=psaa;
 OS Punica granatum (Pomegranate).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Punica.
 OX NCBI_TaxId=22663;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035724; AAL14129.1; -;
 DR EMBL; AY035742; AAL14165.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;
 Best Local Similarity 44.4%; Pred. No. 1.3e+04;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PPKLKVEV 11
 |||||
 DB 6 PEPEVKILV 14

RESULT 27

Q8LVE2 PRELIMINARY; PRT; 16 AA.

AC Q8LVE2; 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Psaa (Fragment).
 GN Name=psaa;
 OS Lythrum salicaria (Purple loosestrife).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Lythrum.
 OX NCBI_TaxId=13129;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035727; AAL14135.1; -;
 DR EMBL; AF421495; AAM45853.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;
 Best Local Similarity 44.4%; Pred. No. 1.3e+04;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PPKLKVEV 11
 |||||
 DB 6 PEPEVKILV 14

RESULT 28

Q8MC15 PRELIMINARY; PRT; 16 AA.

AC Q8MC15; 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Psaa (Fragment).
 GN Name=psaa;
 OS Fuchsia hybrid cultivar.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Onagraceae; Fuchsia.
 OX NCBI_TaxId=133545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).

DR EMBL; AY035746; AAL14173.1; -
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER

SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
FT NON TER

Query Match
Best Local Similarity 44.4%; Score 22; DB 2; Length 16;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 PEPKXKVEV 11
| | | | |
| | | | |
DB 6 PEPKXKIV 14

RESULT 29

O8MC17 PRELIMINARY; PRT; 16 AA.

AC O8MC17;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Psaa (Fragment).
GN Name=psaa;
OS Ludwigia hyssopifolia.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Onagraceae; Ludwigia.
OX NCBI_TaxID=155013;
RN [1]
RP SEQUENCE FROM N.A.

RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035745; AAL14171.1; -
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER

SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
FT NON TER

Query Match
Best Local Similarity 44.4%; Score 22; DB 2; Length 16;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 PEPKXKVEV 11
| | | | |
| | | | |
DB 6 PEPKXKIV 14

RESULT 30

O8MC19 PRELIMINARY; PRT; 16 AA.

AC O8MC19;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Psaa (Fragment).
GN Name=psaa;
OS Quisqualis indica (Rangoon creeper).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Combretaceae; Quisqualis.
OX NCBI_TaxID=3956;
RN [1]
RP SEQUENCE FROM N.A.

RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";

RL Int. J. Plant Sci. 163:215-225(2002).

DR EMBL; AY035744; AAL14169.1; -
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER

SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
FT NON TER

Query Match
Best Local Similarity 44.4%; Score 22; DB 2; Length 16;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 PEPKXKVEV 11
| | | | |
| | | | |
DB 6 PEPKXKIV 14

RESULT 31

O8MC21 PRELIMINARY; PRT; 16 AA.

AC O8MC21;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Psaa (Fragment).
GN Name=psaa;
OS Combretum wallichii.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Combretaceae; Combretum.
OX NCBI_TaxID=131243;
RN [1]
RP SEQUENCE FROM N.A.

RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035743; AAL14167.1; -
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER

SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
FT NON TER

Query Match
Best Local Similarity 44.4%; Score 22; DB 2; Length 16;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 PEPKXKVEV 11
| | | | |
| | | | |
DB 6 PEPKXKIV 14

RESULT 32

O8MC23 PRELIMINARY; PRT; 16 AA.

AC O8MC23;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Psaa (Fragment).
GN Name=psaa;
OS Sonneratia alba.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Sonneratia.
OX NCBI_TaxID=122812;
RN [1]
RP SEQUENCE FROM N.A.

RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal

RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035741; AAL14163.1; "-
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 PEPKUKVEV 11
| | | | |
| | | | |
Db 6 PEPEVKILV 14

RESULT 33

Q8MC25 PRELIMINARY; PRT; 16 AA.

ID Q8MC25
AC Q8MC25;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Psaa (Fragment).
DN Name=psaa;
OS Sonneratia apetala.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Sonneratia.
OX NCBI_TaxID=122813;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035740; AAL14161.1; "-
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 PEPKUKVEV 11
| | | | |
| | | | |
Db 6 PEPEVKILV 14

RESULT 34

Q8MC27 PRELIMINARY; PRT; 16 AA.

ID Q8MC27
AC Q8MC27;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Psaa (Fragment).
DN Name=psaa;
OS Lagerstroemia villosa.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Lagerstroemia.
OX NCBI_TaxID=162025;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based

RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035739; AAL14159.1; "-
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 PEPKUKVEV 11
| | | | |
| | | | |
Db 6 PEPEVKILV 14

RESULT 35

Q8MC29 PRELIMINARY; PRT; 16 AA.

ID Q8MC29
AC Q8MC29;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Psaa (Fragment).
DN Name=psaa;
OS Duabanga grandiflora.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Duabanga.
OX NCBI_TaxID=122808;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035738; AAL14157.1; "-
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 PEPKUKVEV 11
| | | | |
| | | | |
Db 6 PEPEVKILV 14

RESULT 36

Q8MC31 PRELIMINARY; PRT; 16 AA.

ID Q8MC31
AC Q8MC31;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Psaa (Fragment).
DN Name=psaa;
OS Lagerstroemia speciosa (Queen crape myrtle).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Lagerstroemia.
OX NCBI_TaxID=122810;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;

RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psal-yct3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences."
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035737; AAL14151.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PEPKAKVEY 11
| | | | |
| | | | |
DB 6 PEPVKILIV 14

RESULT 37

Q8MC33 PRELIMINARY; PRT; 16 AA.
AC Q8MC33;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Psal (Fragment).
GN Name=psal;
GN Rotala indica.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Rotala.
OX NCBI_TaxID=162024;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psal-yct3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences."
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035736; AAL14153.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PEPKAKVEY 11
| | | | |
| | | | |
DB 6 PEPVKILIV 14

RESULT 38

Q8MC35 PRELIMINARY; PRT; 16 AA.
AC Q8MC35;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Psal (Fragment).
GN Name=psal;
GN Heimia myrtifolia.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Heimia.
OX NCBI_TaxID=135798;
RN [1]
RP SEQUENCE FROM N.A.

RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psal-yct3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences."
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035735; AAL14151.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PEPKAKVEY 11
| | | | |
| | | | |
DB 6 PEPVKILIV 14

RESULT 39

Q8MC37 PRELIMINARY; PRT; 16 AA.
AC Q8MC37;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Psal (Fragment).
GN Name=psal;
GN Lawsonia inermis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Lawsonia.
OX NCBI_TaxID=141191;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psal-yct3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences."
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035734; AAL14149.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PEPKAKVEY 11
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| | | | |
DB 6 PEPVKILIV 14

RESULT 40

Q8MC39 PRELIMINARY; PRT; 16 AA.
AC Q8MC39;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Psal (Fragment).
GN Name=psal;
GN Ammannia baccifera.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Ammannia.
OX NCBI_TaxID=162022;
RN [1]
RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
on Chloroplast rbcL Gene, psal-ycf3 Spacer, and Nuclear rDNA Internal
Transcribed Spacer (ITS) Sequences";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035733; AAL14147.1; -.
KW GO; GO:0009507; C:chloroplast; IEA.
FT Chloroplast.
SQ NON TER 16 16
SEQUENCE 16 AA; 1895 MM; 517FE691B89355B9 CRC64;
Query Match 26.8%; Score 22; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 3 PEPKIKVEY 11
DB 6 PEPVKILV 14

Search completed: June 7, 2005, 23:19:04
Job time : 67 secs